

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 November 2003 (27.11.2003)

PCT

(10) International Publication Number
WO 03/097810 A2

(51) International Patent Classification⁷: **C12N**

(21) International Application Number: PCT/US03/15712

(22) International Filing Date: 15 May 2003 (15.05.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
10/146,772 15 May 2002 (15.05.2002) US
10/241,742 9 September 2002 (09.09.2002) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US 10/241,742 (CIP)
Filed on 9 September 2002 (09.09.2002)
US 10/146,772 (CIP)
Filed on 15 May 2002 (15.05.2002)

(71) Applicant (for all designated States except US): **DI-VERSA CORPORATION** [US/US]; 4955 Directors Place, San Diego, CA 92121 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **DESANTIS, Grace** [CA/US]; 3520 Lebon Drive, Apt. 5223, San Diego, CA 92121 (US). **SHORT, Jay, M.** [US/US]; 681 Paseo Delicias, Box 7214, Rancho Santa Fe, CA 92067 (US). **BURK, Mark** [US/US]; 12634 Intermezzo Way, San Diego, CA 92130 (US). **WONG, Kevin** [US/US]; 11304

Trebol Street, San Diego, CA 92126 (US). **FARWELL, Robert** [US/US]; 4415 Terreno Court, San Diego, CA 92124 (US). **CHATMAN, Kelly** [US/US]; P.O. Box 429, Solana Beach, CA 92075 (US).

(74) Agent: **EINHORN, Gregory, P.**; Fish & Richardson P.C., 4350 La Jolla Village Drive, Suite 500, San Diego, CA 92122 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NITRILASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

(57) Abstract: The invention relates to nitrilases and to nucleic acids encoding the nitrilases. In addition methods of designing new nitrilases and method of use thereof are also provided. The nitrilases have increased activity and stability at increased pH and temperature.



WO 03/097810 A2

NITRILASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority to U.S. Patent Application Serial
5 No. (USSN) 10/241,742, filed September 9, 2002, and USSN 10/146,772, filed May 15,
2002, which claims the benefit of priority to USSN 60/351,336, filed January 22, 2002,
USSN 60/309, 006, filed July 30, 2001, and USSN 60/300,189, filed June 21, 2001; and is a
continuation-in-part of USSN 09/751,299, filed December 28, 2000, which claims the benefit
of priority to each of USSN 60/254,414, filed December 7, 2000, and USSN 60/173,609,
10 filed December 29, 1999. These applications are hereby incorporated by reference into the
subject application in their entireties for all purposes.

COPYRIGHT NOTIFICATION

[0002] Pursuant to 37 C.F.R. §1.71(e), a portion of this patent document contains
material which is subject to copyright protection. The copyright owner has no objection to
15 the facsimile reproduction by anyone of the patent document or the patent disclosure, as it
appears in the Patent and Trademark Office patent file or records, but otherwise reserves all
copyright rights whatsoever.

FIELD OF THE INVENTION

[0003] The invention relates generally to the field of molecular biology, biochemistry and
20 chemistry, and particularly to enzymatic proteins having nitrilase activity. The invention also
relates to polynucleotides encoding the enzymes, and to uses of such polynucleotides and
enzymes.

BACKGROUND OF THE INVENTION

[0004] There are naturally occurring enzymes which have great potential for use in
25 industrial chemical processes for the conversion of nitriles to a wide range of useful products
and intermediates. Such enzymes include nitrilases which are capable of converting nitriles
directly to carboxylic acids. Nitrilase enzymes are found in a wide range of mesophilic
micro-organisms, including species of *Bacillus*, *Norcardia*, *Bacteridium*, *Rhodococcus*,

micro-organisms, including species of *Bacillus*, *Nocardia*, *Bacteridium*, *Rhodococcus*, *Micrococcus*, *Brevibacterium*, *Alcaligenes*, *Acinetobacter*, *Corynebacterium*, *Fusarium* and *Klebsiella*. Additionally, there are thermophilic nitrilases which exist in bacteria.

[0005] There are two major routes from a nitrile to an analogous acid: (1) a nitrilase catalyzes the direct hydrolysis of a nitrile to a carboxylic acid with the concomitant release of ammonia; or (2) a nitrile hydratase adds a molecule of water across the carbon-nitrogen bonding system to give the corresponding amide, which can then act as a substrate for an amidase enzyme which hydrolyzes the carbon-nitrogen bond to give the carboxylic acid product with the concomitant release of ammonia. The nitrilase enzyme therefore provides the more direct route to the acid.

[0006] A nitrile group offers many advantages in devising synthetic routes in that it is often easily introduced into a molecular structure and can be carried through many processes as a masked acid or amide group. This is only of use, however, if the nitrile can be unmasked at the relevant step in the synthesis. Cyanide represents a widely applicable C₁-synthon (cyanide is one of the few water-stable carbanions) which can be employed for the synthesis of a carbon framework. However, further transformations of the nitrile thus obtained are impeded due to the harsh reaction conditions required for its hydrolysis using normal chemical synthesis procedures. The use of enzymes to catalyze the reactions of nitriles is attractive because nitrilase enzymes are able to effect reactions with fewer environmentally hazardous reagents and by-products than in many traditional chemical methods. Indeed, the chemoselective biocatalytic hydrolysis of nitriles represents a valuable alternative because it occurs at ambient temperature and near physiological pH.

[0007] The importance of asymmetric organic synthesis in drug design and discovery has fueled the search for new synthetic methods and chiral precursors which can be utilized in developing complex molecules of biological interest. One important class of chiral molecules is the α -substituted carboxylic acids, which include the α -amino acids. These molecules have long been recognized as important chiral precursors to a wide variety of complex biologically active molecules, and a great deal of research effort has been dedicated to the development of methods for the synthesis of enantiomerically pure α -amino acids and chiral medicines.

[0008] Of particular use to synthetic chemists who make chiral medicines would be an enzyme system which is useful under non-sterile conditions, which is useful in non-biological laboratories, which is available in a form convenient for storage and use; which has broad

substrate specificity, which acts on poorly water soluble substrates; which has predictable product structure; which provides a choice of acid or amide product; and which is capable of chiral differentiation. Accordingly, there is a need for efficient, inexpensive, high-yield synthetic methods for producing enantiomerically pure α -substituted carboxylic acids, such as, for example, α -amino acids and α -hydroxy acids.

[0009] In addition, often, the discovery or evolution of an enzyme to perform a particular transformation can be aided by the availability of a convenient high throughput screening or selection process. While a surrogate substrate may be used when an effective ultra high throughput (UHTP) screen is not available, it may be desirable to screen directly for an enzyme that performs specifically the desired transformation. The challenges of designing an UHTP screen is evident when, for example, the discovery or evolution program is aimed at uncovering a stereoselective transformation to generate only one stereoisomer or enantiomer. In this case, there is a paucity of high throughput screening methods available. While, the most straightforward method is to use chiral liquid or gas phase separation to separate the two enantiomers in question, often this approach does not afford the very high throughput capacity that is required. By using mass spectroscopy (MS) techniques, very high throughput screens are possible. However, when applied in a conventional manner, MS does not afford information on chirality or enantioselectivity.

[00010] Another approach is to chemically derivatize the enantiomeric mixture with a single enantiomer compound, thus generating a diasteriomic mixture of compounds that can be characterized by separation on an achiral stationary phase. Again, this is a cumbersome approach and does not lend itself well to high throughput screening.

[00011] Throughout this application, various publications are referenced by author and date. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art as known to those skilled therein as of the date of the invention described and claimed herein.

SUMMARY OF THE INVENTION

[00012] The present invention is directed to an isolated or recombinant nucleic acid comprising nucleotides having a sequence at least about 50% identical to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,

179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, or variants thereof, wherein the nucleic acid encodes a polypeptide having a nitrilase activity. In alternative aspects of the invention, the nucleic acid comprises nucleotides having a sequence at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete identity (100% identical) to the SEQ ID NO: or variants thereof. Exemplary variants may include, for example, the following variations of SEQ ID NO:195, 205, 207, 209, OR 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof. In one aspect of the invention, the variants encode a polypeptide having improved or diminished enantioselectivity, for example, in the conversion of a 3-hydroxyglutarylnitrile (HGN) to (R)-4-Cyano-3-hydroxybutyrate, than the polypeptide encoded by the SEQ ID NO.

[00013] In one aspect of the invention, the nucleic acid comprises nucleotides having a sequence substantially identical to the SEQ ID NO: or variants thereof. In another aspect, the invention provides for an isolated or recombinant nucleic acid comprising consecutive nucleotides having a sequence at least 79 % identical to SEQ ID NO: 33, wherein the nucleic acid encodes a polypeptide having nitrilase activity. The invention provides for a fragment of the nucleic acid, wherein the fragment encodes a polypeptide having nitrilase activity. The invention also provides for an isolated or recombinant nucleic acid complementary to any of the nucleic acids. The invention also provides for an isolated or recombinant nucleic acid

that hybridizes to any one of the nucleic acids under stringent conditions. In one aspect, the stringent conditions comprise at least 50% formamide, and about 37°C to about 42°C.

[00014] The invention provides for a nucleic acid probe comprising from about 15 nucleotides to about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more nucleotides, wherein at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more consecutive nucleotides are at least 50% complementary to a nucleic acid target region within a nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, variants thereof, or their complements. In one aspect, the nucleic acid probe comprises consecutive nucleotides which are at least 55% complementary to the nucleic acid target region. In one aspect, the invention provides for a nucleic acid probe, wherein the consecutive nucleotides are at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% complementary to the nucleic acid target region. In another aspect, the nucleic acid consists essentially of from about 20 to about 50 nucleotides. In other aspects, the nucleic acid can be at least about 20, 25, 30, 35, 40, 45, 50, 75, 100, 150 nucleotides in length.

[00015] The invention provides for a nucleic acid vector capable of replication in a host cell, wherein the vector comprises the nucleic acid of the invention. The invention also provides for a host cell comprising the nucleic acid. The invention also provides for a host organism comprising the host cell. In one aspect, the host organism comprises a gram negative bacterium, a gram positive bacterium or a eukaryotic organism. In another aspect, the gram negative bacterium comprises *Escherichia coli*, or *Pseudomonas fluorescens*. In a

further aspect, the gram positive bacterium comprises *Streptomyces diversa*, *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, or *Bacillus subtilis*. In a further aspect, the eukaryotic organism comprises *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Kluyveromyces lactis*, *Hansenula polymorpha*, or *Aspergillus niger*.

5 [00016] The invention provides for an isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 10 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 15 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, or variants thereof, wherein the polypeptide has nitrilase activity. In one aspect, the polypeptide comprises amino acids having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 20 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% identity to the SEQ ID NO: or variants thereof. Exemplary variants may include, for example, the following variations of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 25 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof.

[00017] The invention also provides for an isolated or recombinant nucleic acid encoding a polypeptide comprising at least 10 consecutive amino acids having a sequence identical to a 10 portion of an amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154,

156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226,
228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262,
264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
5 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334,
336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370,
372, 374, 376, 378, 380, 382, 384, 386, or variants thereof.

[00018] An isolated or recombinant polypeptide comprising amino acids having a
sequence at least about 50% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24,
10 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,
76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116,
118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152,
154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188,
190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224,
15 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260,
262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296,
298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332,
334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
370, 372, 374, 376, 378, 380, 382, 384, 386, or variants thereof, wherein the polypeptide has
20 nitrilase activity. In one aspect of the invention, the polypeptide comprises amino acids
having a sequence at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%,
60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%,
76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%,
92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% identical to the SEQ ID NO:
25 or variants thereof.

[00019] The invention provides an isolated or recombinant nucleic acid comprising
nucleotides having a sequence as set forth in any one of the following SEQ ID NOS:1, 3, 5, 7,
9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,
61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
30 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141,
143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,
179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213,
215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249,

251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof

5 (hereinafter referred to as "Group A nucleic acids"). The invention is also directed to nucleic acids having specified minimum percentages of sequence identity to any of the Group A nucleic acids sequences.

[00020] In another aspect, the invention provides an isolated (purified) or recombinant polypeptide comprising amino acid residues having a sequence as set forth in any one of the
10 following SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200,
15 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380,
20 382, 384, 386, and variants thereof, (hereinafter referred to as "Group B amino acid sequences"). The invention is also directed to purified polypeptides having specified minimum percentages of sequence identity to any of the Group B amino acid sequences.

[00021] The invention provides for a fragment of the polypeptide which is at least 50 amino acids in length, and wherein the fragment has nitrilase activity. Furthermore, the
25 invention provides for a peptidomimetic of the polypeptide or a fragment thereof having nitrilase activity. The invention provides for a codon-optimized polypeptide or a fragment thereof, having nitrilase activity, wherein the codon usage is optimized for a particular organism or cell. Narum et al. *Infect. Immun.* 2001 Dec, 69(12):7250-3 describes codon-optimization in the mouse system. Outchkourov et al. *Protein Expr. Purif.* 2002 Feb;
30 24(1):18-24 describes codon-optimization in the yeast system. Feng et al. *Biochemistry* 2000 Dec 19, 39(50):15399-409 describes codon-optimization in *E. coli*. Humphreys et al. *Protein Expr. Purif.* 2000 Nov, 20(2):252-64 describes how codon usage affects secretion in *E. coli*.

[00022] In one aspect, the organism or cell comprises a gram negative bacterium, a gram positive bacterium or a eukaryotic organism. In another aspect of the invention, the gram negative bacterium comprises *Escherichia coli*, or *Pseudomonas fluorescens*. In another aspect of the invention, the gram positive bacterium comprise *Streptomyces diversa*,

5 *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, or *Bacillus subtilis*. In another aspect of the invention, the eukaryotic organism comprises *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Kluyveromyces lactis*, *Hansenula polymorpha*, or *Aspergillus niger*.

[00023] In another aspect, the invention provides for a purified antibody that specifically
10 binds to the polypeptide of the invention or a fragment thereof, having nitrilase activity. In one aspect, the invention provides for a fragment of the antibody that specifically binds to a polypeptide having nitrilase activity.

[00024] The invention provides for an enzyme preparation which comprises at least one of the polypeptides of the invention, wherein the preparation is liquid or dry. The enzyme
15 preparation includes a buffer, cofactor, or second or additional protein. In one aspect the preparation is affixed to a solid support. In one aspect of the invention, the solid support can be a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof. In another aspect, the preparation can be encapsulated in a gel or a bead.

[00025] The invention further provides for a composition which comprises at least one
20 nucleic acid of the invention which comprises at least one polypeptide of the invention or a fragment thereof, or a peptidomimetic thereof, having nitrilase activity, or any combination thereof.

[00026] The invention provides for a method for hydrolyzing a nitrile to a carboxylic acid comprising contacting the molecule with at least one polypeptide of the invention or a
25 fragment thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity. In one aspect, the conditions comprise aqueous conditions. In another aspect, the conditions comprise a pH of about 8.0 and/or a temperature from about 37° C to about 45° C.

[00027] The invention provides for a method for hydrolyzing a cyanohydrin moiety or an
30 aminonitrile moiety of a molecule, the method comprising contacting the molecule with at least one polypeptide of the invention, or a fragment thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.

[00028] The invention provides for a method for making a chiral α -hydroxy acid molecule, a chiral amino acid molecule, a chiral β -hydroxy acid molecule, or a chiral gamma-hydroxy acid molecule, the method comprising admixing a molecule having a cyanohydrin moiety or an aminonitrile moiety with at least one polypeptide having an amino acid sequence at least 50% identical to any one of the Group B amino acid sequences or a fragment thereof, or a peptidomimetic thereof, having enantio-selective nitrilase activity. In one aspect, the chiral molecule is an (*R*)-enantiomer. In another aspect, the chiral molecule is an (*S*)-enantiomer. In one aspect of the invention, one particular enzyme can have R-specificity for one particular substrate and the same enzyme can have S-specificity for a different particular substrate.

[00029] The invention also provides for a method for making a composition or an intermediate thereof, the method comprising admixing a precursor of the composition or intermediate, wherein the precursor comprises a cyanohydrin moiety or an aminonitrile moiety, with at least one polypeptide of the invention or a fragment or peptidomimetic thereof having nitrilase activity, hydrolyzing the cyanohydrin or the aminonitrile moiety in the precursor thereby making the composition or the intermediate thereof. In one aspect, the composition or intermediate thereof comprises (*S*)-2-amino-4-phenyl butanoic acid. In a further aspect, the composition or intermediate thereof comprises an L-amino acid. In a further aspect, the composition comprises a food additive or a pharmaceutical drug.

[00030] The invention provides for a method for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid. In one aspect, the *ee* is at least 95% or at least 99%. In another aspect, the hydroxyglutaryl nitrile comprises 1,3-dicyano-2-hydroxy-propane or 3-hydroxyglutaronitrile. In a further aspect, the polypeptide has an amino acid sequence of any one of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity.

[00031] The invention also provides a method for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

[00032] The invention provides a method for making an (*R*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of any one of the Group B amino acid sequences or any fragment or peptidomimetic thereof having appropriate nitrilase activity. In one aspect, the (*R*)-mandelic acid comprises (*R*)-2-chloromandelic acid. In another aspect, the (*R*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*R*)-mandelic acid, a pyridyl derivative of (*R*)-mandelic acid or a thienyl derivative of (*R*)-mandelic acid or a combination thereof.

[00033] The invention provides a method for making an (*S*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of Group B sequences or any fragment or peptidomimetic thereof having nitrilase activity. In one aspect, the (*S*)-mandelic acid comprises (*S*)-methyl benzyl cyanide and the mandelonitrile comprises (*S*)-methoxy-benzyl cyanide. In one aspect, the (*S*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*S*)-mandelic acid, a pyridyl derivative of (*S*)-mandelic acid or a thienyl derivative of (*S*)-mandelic acid or a combination thereof.

[00034] The invention also provides a method for making an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyllactic acid derivative, the method comprising admixing a phenyllactonitrile with at least one polypeptide selected from the group of the Group B amino acid sequences or any active fragment or peptidomimetic thereof that selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

[00035] The invention provides for a method for making the polypeptide of the invention or a fragment thereof, the method comprising (a) introducing a nucleic acid encoding the polypeptide into a host cell under conditions that permit production of the polypeptide by the host cell, and (b) recovering the polypeptide so produced.

[00036] The invention provides for a method for generating a nucleic acid variant encoding a polypeptide having nitrilase activity, wherein the variant has an altered biological activity from that which naturally occurs, the method comprising (a) modifying the nucleic acid by (i) substituting one or more nucleotides for a different nucleotide, wherein the nucleotide comprises a natural or non-natural nucleotide; (ii) deleting one or more nucleotides, (iii) adding one or more nucleotides, or (iv) any combination thereof. In one aspect, the non-natural nucleotide comprises inosine. In another aspect, the method further

comprises assaying the polypeptides encoded by the modified nucleic acids for altered nitrilase activity, thereby identifying the modified nucleic acid(s) encoding a polypeptide having altered nitrilase activity. In one aspect, the modifications of step (a) are made by PCR, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis, ligase chain reaction, *in vitro* mutagenesis, ligase chain reaction, oligonucleotide synthesis, any DNA-generating technique and any combination thereof. In another aspect, the method further comprises at least one repetition of the modification step (a).

[00037] The invention further provides a method for making a polynucleotide from two or more nucleic acids, the method comprising: (a) identifying regions of identity and regions of diversity between two or more nucleic acids, wherein at least one of the nucleic acids comprises a nucleic acid of the invention; (b) providing a set of oligonucleotides which correspond in sequence to at least two of the two or more nucleic acids; and, (c) extending the oligonucleotides with a polymerase, thereby making the polynucleotide.

[00038] The invention further provides a screening assay for identifying a nitrilase, the assay comprising: (a) providing a plurality of nucleic acids or polypeptides comprising at least one of the nucleic acids of the invention, or at least one of the polypeptides of the invention; (b) obtaining polypeptide candidates to be tested for nitrilase activity from the plurality; (c) testing the candidates for nitrilase activity; and (d) identifying those polypeptide candidates which are nitrilases. In one aspect, the method further comprises modifying at least one of the nucleic acids or polypeptides prior to testing the candidates for nitrilase activity. In another aspect, the testing of step (c) further comprises testing for improved expression of the polypeptide in a host cell or host organism. In a further aspect, the testing of step (c) further comprises testing for nitrilase activity within a pH range from about pH 3 to about pH 12. In a further aspect, the testing of step (c) further comprises testing for nitrilase activity within a pH range from about pH 5 to about pH 10. In another aspect, the testing of step (c) further comprises testing for nitrilase activity within a temperature range from about 4 °C to about 80 °C. In another aspect, the testing of step (c) further comprises testing for nitrilase activity within a temperature range from about 4 °C to about 55 °C. In another aspect, the testing of step (c) further comprises testing for nitrilase activity which results in an enantioselective

reaction product. In another aspect, the testing of step (c) further testing for nitrilase activity which results in a regio-selective reaction product.

[00039] The invention provides for use of the nucleic acids of the invention, or a fragment or peptidomimetic thereof having nitrilase activity, in a process designed to optimize one
5 aspect of the gene or one aspect of the polypeptide encoded by the gene. In one aspect, the process comprises introducing modifications into the nucleotide sequence of the nucleic acid. In another aspect, the modifications are introduced by PCR, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble
0 mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis, ligase chain reaction, *in vitro* mutagenesis, ligase chain reaction, oligonucleotide synthesis, any other DNA-generating technique or any combination thereof. In a further aspect, the process is repeated.

[00040] The invention provides for use of the polypeptide of the invention, or a fragment
5 or peptidomimetic thereof having nitrilase activity, in an industrial process. In one aspect, the process is for production of a pharmaceutical composition, the process is for production of a chemical, the process is for production of a food additive, the process is catalyzing the breakdown of waste, or the process is production of a drug intermediate. In a further aspect, the process comprises use of the polypeptide to hydrolyze a hydroxyglutaryl nitrile substrate.
0 In a further aspect, the process is for production of LIPITOR™. In another aspect, the polypeptide used comprises a polypeptide having consecutive amino acids of the sequence SEQ ID NO:44, 196, 208, 210, or 238 or a fragment thereof having nitrilase activity. In another aspect, the process is production of a detergent. In another aspect, the process is production of a food product.

5 [00041] The invention provides for use of a nucleic acid of the invention, or a fragment thereof encoding a polypeptide having nitrilase activity, in the preparation of a transgenic organism.

[00042] The invention provides for a kit comprising (a) the nucleic acid of the inventions, or a fragment thereof encoding a polypeptide having nitrilase activity, or (b) the polypeptide
0 of the invention, or a fragment or a peptidomimetic thereof having nitrilase activity, or a combination thereof; and (c) a buffer.

[00043] The invention provides for a method for modifying a molecule comprising: (a) mixing a polypeptide of the invention or a fragment or peptidomimetic thereof having

nitrilase activity, with a starting molecule to produce a reaction mixture; (b) reacting the starting molecule with the polypeptide to produce the modified molecule.

[00044] The invention provides for a method for identifying a modified compound comprising: (a) admixing a polypeptide of the invention, or a fragment or peptidomimetic thereof having nitrilase activity, with a starting compound to produce a reaction mixture and thereafter a library of modified starting compounds; (b) testing the library to determine whether a modified starting compound is present within the library which exhibits a desired activity; (c) identifying the modified compound exhibiting the desired activity.

[00045] The invention provides a screening assay for enantioselective transformation comprising: (a) providing a molecule having two prochiral or enantiotopic moieties; (b) labeling at least one prochiral or enantiotopic moiety of the molecule; (b) modifying at least one of the two moieties by a selective catalyst; and (c) detecting results by mass spectroscopy. The screening assay can be used to determine or monitor the % enantiomeric excess (ee) or determine the % diastomeric excess (de). An exemplary label useful in the assay is a heavier isotope or a lighter isotope. The selective catalyst useful in the assay can be an enzyme. The screening assay may be performed with both moieties labeled. The screening assay may be performed in both directions, *i.e.*, from the reactants to the products as well as from the products to the reactants.

[00046] The invention provides for a computer readable medium having stored thereon a nucleic acid of the invention, e.g., a nucleic acid comprising at least one nucleotide sequence selected from the group consisting of: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70,

72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, and variants thereof.

[00047] The invention provides for a computer system comprising a processor and a data storage device, wherein the data storage device has stored thereon a nucleic acid of the invention, e.g., a nucleic acid comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374,

376, 378, 380, 382, 384, 386, and variants thereof. In one aspect, the computer system further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that identifies polymorphisms.

5 **[00048]** The invention provides for a method for identifying a feature in a sequence which comprises: (a) inputting the sequence into a computer; (b) running a sequence feature identification program on the computer so as to identify a feature within the sequence; and (c) identifying the feature in the sequence, wherein the sequence comprises a nucleic acid of the invention, e.g., a nucleic acid comprising at least one of SEQ ID NOS:1-386, its variants, or
10 any combination thereof.

[00049] The invention provides for an assay for identifying a functional fragment of a polypeptide which comprises: (a) obtaining a fragment of at least one polypeptide of the invention; (b) contacting at least one fragment from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase
15 activity; (c) measuring the amount of reaction product produced by each at least one fragment from step (b); and (d) identifying the at least one fragment which is capable of producing a nitrilase reaction product; thereby identifying a functional fragment of the polypeptide. In one aspect, the fragment of step (a) is obtained by synthesizing the fragment. In another aspect, the fragment of step (a) is obtained by fragmenting the polypeptides.

20 **[00050]** The invention provides for an assay for identifying a functional variant of a polypeptide which comprises: (a) obtaining at least one variant of at least one polypeptide of the invention; (b) contacting at least one variant from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity; (c) measuring the amount of reaction product produced by each at least one variant
25 from step (b); and (d) identifying the at least one variant which is capable of producing a nitrilase reaction product; thereby identifying a functional variant of the polypeptide.

BRIEF DESCRIPTION OF THE DRAWINGS

[00051] Figure 1 shows chemical reaction schemes wherein stereoselective nitrilases hydrolyze a cyanohydrin or an aminonitrile to produce a chiral α -hydroxy acid or α -amino
30 acid.

[00052] Figure 2 illustrates an OPA based cyanide detection assay used for identifying the presence of nitrilase activity.

[00053] Figure 3 is an illustration of a spectroscopic system for the detection and quantification of α -hydroxy acids based on stereoselective lactate dehydrogenases.

[00054] Figure 4 is an illustration of a spectroscopic system for the detection and quantification of α -amino acids based on stereoselective amino acid oxidase.

5 [00055] Figure 5 is a flow diagram illustrating the steps of a nitrilase screening method.

[00056] Figures 6A-6E are chromatograms characteristic of the substrate and product combination for D-phenylglycine showing a blank sample (Fig. 6A), an enzymatic reaction sample (Fig. 6B); a negative control consisting of cell lysate in buffer (Fig. 6C); a chiral analysis of phenylglycine (Fig. 6D); and coelution of the nitrile peak with the D-enantiomer (Fig. 6E).

10 [00057] Figures 7A-7E illustrate chromatograms which are characteristic of substrate and product combinations for (*R*)-2-chloromandelic acid. Fig. 7A shows only 2-chloromandelonitrile in buffer; Fig. 7B shows a chloromandelic acid standard. The chromatogram in Fig. 7C shows the appearance of product and the reduction of substrate peaks.

[00058] Figures 8A-8B illustrate chromatograms characteristic of substrate and product combinations for (*S*)-phenyllactic acid.

[00059] Figures 9A-9B illustrate chromatograms characteristic of substrate and product combinations for L-2-methylphenylglycine.

20 [00060] Figures 10A-10C illustrate chromatograms characteristic of substrate and product combinations for L-*tert*-leucine.

[00061] Figures 11A-11C illustrate chromatograms characteristic of substrate and product combinations for (*S*)-2-amino-6-hydroxy hexanoic acid.

25 [00062] Figures 12A-12D illustrate chromatograms characteristic of substrate and product combinations for 4-methyl-D-leucine and 4-methyl-L-leucine.

[00063] Figures 13A-13B illustrate chromatograms characteristic of substrate and product combinations for (*S*)-cyclohexylmandelic acid.

[00064] Figures 14A-14B illustrate two exemplary standard curves for quantitation in connection with the screening assay of the invention.

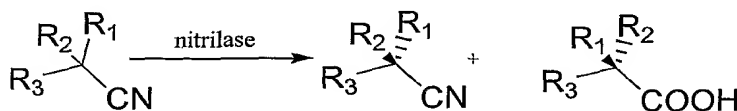
30 [00065] Figure 15 illustrates selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[00066] Figure 16 illustrates selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[00067] Figure 17 illustrates an exemplary nitrilase reaction of the invention.

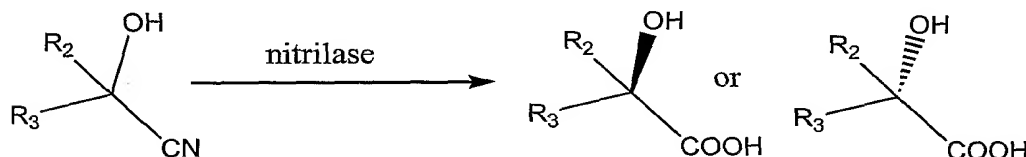
DETAILED DESCRIPTION OF THE INVENTION

[00068] The present invention relates to nitrilases, nucleic acids encoding nitrilases, and uses therefor. As used herein, the term “nitrilase” encompasses any polypeptide having any nitrilase activity, for example, the ability to hydrolyze nitriles into their corresponding carboxylic acids and ammonia. Nitrilases have commercial utility as biocatalysts for use in the synthesis of enantioselective aromatic and aliphatic amino acids or hydroxy acids.

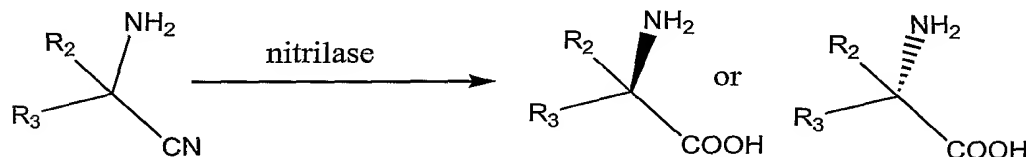


[00069] Nitrilase chemistry is as follows:

[00070] A nitrilase reaction for the preparation of hydroxy acids is as follows:



[00071] A nitrilase reaction for the preparation of amino acids is as follows:



[00072] In addition, in each of the foregoing hydrolysis reactions, two water molecules are consumed and one ammonia molecule is released.

[00073] There are several different types of assays which can be performed to test for the presence of nitrilase activity in a sample or to test whether a particular polypeptide exhibits nitrilase activity. For example, assays can detect the presence or absence of products or by-products from a chemical reaction catalyzed by a nitrilase. For example, the presence of nitrilase activity can be detected by the production of α -hydroxy acids or α -amino acids from, respectively, cyanohydrins or aminonitriles, and the level of nitrilase activity can be

quantified by measuring the relative quantities of the reaction products produced. Figure 1 shows chemical reaction schemes using stereoselective nitrilases to create chiral α -hydroxy acids or α -amino acids in high yield. The starting material is an aldehyde or an imine which is produced from an aldehyde by reaction with ammonia. Reaction of the aldehyde or imine with hydrogen cyanide results in the production of enantiomeric mixtures of the corresponding cyanohydrins and aminonitriles. A stereoselective nitrilase can then be used to stereoselectively convert one enantiomer into the corresponding α -hydroxy acid or α -amino acid. Figure 3 illustrates schematically the stereoselective nitrilase-dependent production and spectrophotometric detection of α -hydroxy acids based on lactate dehydrogenase conversion of the α -hydroxy acids to the corresponding α -keto acids and concomitant oxidation-reduction of a detectable dye. Figure 4 illustrates schematically the stereoselective nitrilase-dependent production and spectrophotometric detection of α -amino acids based on amino acid oxidase conversion of the α -amino acids to the corresponding α -keto acids and concomitant oxidation-reduction of a detectable dye.

[00074] Nitrilases contemplated for use in the practice of the present invention include those which stereoselectively hydrolyze nitriles or cyanohydrins into their corresponding acids and ammonia. In one aspect, nitrilases of the invention can stereoselectively hydrolyze nitriles or cyanohydrins into their corresponding acids and ammonia. Nitrilases include, for example, nitrilases of the invention, e.g., those set forth in the Group B amino acid sequences. Some nitrilases which stereoselectively hydrolyze their substrates are set forth in the Tables hereinbelow.

[00075] The nitrilases of the invention share the following additional characteristics:

- (1) full-length amino acid sequences from about 333 amino acids to about 366 amino acids,
- (2) aggregation and activity as homo-multimers of about 2 subunits to about 16 subunits,
- (3) presence of a catalytic triad of the consecutive amino acids Glu-Lys-Cys, (4) pH optima from about pH 5 to about pH 9, and (5) temperature optima from about 0°C to about 100°C, or from about 40°C to about 50°C.

Consensus Sequences Among New Nitrilases

[00076] The nitrilases disclosed herein were studied using bioinformatics and sequence comparison programs and the following consensus information was collected. Three regions of conserved motifs were identified within the nitrilase polypeptides. These correspond to the catalytic triad (E-K-C) present in nitrilase enzymes. (H. Pace and C. Brenner (Jan. 15,

2001) "The Nitrilase Superfamily: classification, structure and function" *Genome Biology* Vol. 2, No. 1, pp 1-9.)

[00077] The abbreviations used herein are conventional one letter codes for the amino acids: A, alanine; B, asparagine or aspartic acid; C, cysteine; D aspartic acid; E, glutamate, glutamic acid; F, phenylalanine; G, glycine; H histidine; I isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine; Z, glutamine or glutamic acid. See L. Stryer, *Biochemistry*, 1988, W. H. Freeman and Company, New York.

[00078] The computer sequence comparisons made among the nitrilase polypeptide sequences of the invention resulted in the identification of these motifs within each amino acid sequence:

F	P	<u>E</u>	t	<i>f</i>	r	<u>R</u>	<u>K</u>	L	.	P	T	L	.	<u>C</u>	W	<u>E</u>	h	.	.	P
---	---	----------	---	----------	---	----------	----------	---	---	---	---	---	---	----------	---	----------	---	---	---	---

[00079] The following residues (those that are underlined) are completely conserved among all of the identified nitrilases: the third amino acid in the first motif or region (E, glutamate); the second residue in the second motif (R, arginine); the third residue in the second motif (K, lysine); the third residue in the third motif (C, cysteine); and the fifth residue in the third motif (E, glutamate).

[00080] In the boxes, upper case letters indicate 90% or greater consensus among the nitrilases of the invention, while lower case letters indicate 50% or greater consensus. An italicized letter indicates 30% or greater consensus among the nitrilases of the invention. A dot in a box indicates a residue which is not conserved.

[00081] The sequences of nitrilases in the nitrilase branch of the nitrilase superfamily were described as having a catalytic triad in the Pace and Brenner article (*Genome Biology*, 2001, Vol. 2, No. 1, pp. 1-9). However, the catalytic triad regions of the nitrilases of this invention differ from those previously identified in the Pace and Brenner reference in the following ways:

[00082] Differences in the first motif: The F in the first box of the first motif is conserved in 90% of the nitrilases of the invention, rather than in only 50% of those previously identified. The fourth residue of the first motif is a "t", threonine in the nitrilases of this invention, and it is found at 50% or greater consensus. However, that residue was identified by Pace and Brenner as "a" (alanine). The last residue of the first motif was

identified as "f" (phenylalanine) and was indicated to occur at 50% or greater consensus. However, the nitrilases of this invention only show "f" (phenylalanine occurring at 30% consensus.

[00083] Differences in the second motif: There is an "r" (arginine) in the first box of

5 the second motif of the nitrilases of this invention. However, the Pace and Brenner consensus shows an "h" (histidine) in that position. The "R" (arginine) in the second box is completely conserved in the nitrilases of the present invention, however that residue only appears at 90% consensus in the Pace and Brenner reference. The "L" (leucine) in the fourth box of the second motif is conserved in 90% or more of the nitrilases of this invention.

10 However, the Pace and Brenner nitrilases only showed conservation of that residue in 50% of the sequences. Similarly, the "P" (proline) at the sixth box of the second motif is conserved in 90% or more of the nitrilases of this invention. However, the Pace and Brenner nitrilases only showed conservation of that residue in 50% of the sequences.

[00084] Differences in the third motif: The "L in the first box is conserved at 90% or
15 greater in the nitrilases of the invention. However, the Pace and Brenner reference only shows that residue appearing 50% of the time. Finally, the sixth box in the third motif in the nitrilases of the invention show a histidine 50% of the time or more. However, the Pace and Brenner reference indicates that that position shows an asparagine ("n") 50% of the time.

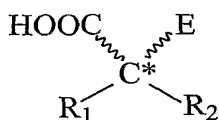
[00085] The invention provides for an isolated polypeptide having nitrilase activity which
20 polypeptide comprises three regions, wherein the first region comprises five amino acids and wherein the first amino acid of the first region is F and the fourth amino acid of the first region is T. The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three regions, wherein the second region comprises seven amino acids and wherein the first amino acid of the second region is R, wherein the second
25 amino acid of the second region is R, and wherein the sixth amino acid of the second region is P. The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three regions, wherein the third region comprises nine amino acids and wherein the first amino acid of the third region is L and the sixth amino acid of the third region is H.

30 **[00086]** The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three consensus subsequences, wherein the first consensus subsequence is FPETF, wherein the second consensus subsequence is RRKLXPT, and wherein the third consensus subsequence is LXCWEHXXP.

[00087] The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three consensus subsequences, wherein the first consensus subsequence is FP₂EXX, wherein the second consensus subsequence is XRKLXPT, and wherein the third consensus subsequence is LXCWEXXXP.

5

[00088] In accordance with the present invention, methods are provided for producing enantiomerically pure α -substituted carboxylic acids. The enantiomerically pure α -substituted carboxylic acids produced by the methods of the present invention have the following structure:



10

wherein:

$\text{R}_1 \neq \text{R}_2$ and R_1 and R_2 are otherwise independently -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, or heterocyclic, wherein said substituents are lower alkyl, hydroxy, alkoxy, amino, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, or halogen or optionally R_1 and R_2 are directly or indirectly covalently joined to form a functional cyclic moiety, and E is $-\text{N}(\text{R}_x)_2$ or $-\text{OH}$, wherein each R_x is independently -H or lower alkyl.

15

[00089] As used herein, the term "alkyl" refers to straight or branched chain or cyclic hydrocarbon groups of from 1 to 24 carbon atoms, including methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, tert-butyl, n-pentyl, n-hexyl, and the like. The term "lower alkyl" refers to monovalent straight or branched chain or cyclic radicals of from one to about six carbon atoms.

20

[00090] As used herein, "alkenyl" refers to straight or branched chain or cyclic hydrocarbon groups having one or more carbon-carbon double bonds, and having in the range of about 2 to about 24 carbon atoms.

25

[00091] As used herein, "alkynyl" refers to straight or branched chain or cyclic hydrocarbon groups having at least one carbon-carbon triple bond, and having in the range of about 2 to about 24 carbon atoms.

[00092] As used herein, "cycloalkyl" refers to cyclic hydrocarbon groups containing in the range of about 3 to about 14 carbon atoms.

30

[00093] As used herein, "heterocyclic" refers to cyclic groups containing one or more heteroatoms (*e.g.*, N, O, S, P, Se, B, etc.) as part of the ring structure, and having in the range of about 3 to about 14 carbon atoms.

[00094] As used herein, "aryl" refers to aromatic groups (*i.e.*, cyclic groups with conjugated double-bond systems) having in the range of about 6 to about 14 carbon atoms.

[00095] As used herein with respect to a chemical group or moiety, the term "substituted" refers to such a group or moiety further bearing one or more non-hydrogen substituents. Examples of such substituents include, without limitation, oxy (*e.g.*, in a ketone, aldehyde, ether, or ester), hydroxy, alkoxy (of a lower alkyl group), amino, thio, mercapto (of a lower alkyl group), cycloalkyl, substituted cycloalkyl, heterocyclic, substituted heterocyclic, aryl, substituted aryl, heteroaryl, substituted heteroaryl, aryloxy, substituted aryloxy, halogen, trifluoromethyl, cyano, nitro, nitrone, amino, amido, -C(O)H, acyl, oxyacyl, carboxyl, carbamate, sulfonyl, sulfonamide, sulfonyl, and the like.

[00096] In preferred aspects, the enantiomerically pure α -substituted carboxylic acid produced by the methods of the present invention is an α -amino acid or α -hydroxy acid. In some aspects, the enantiomerically pure α -amino acid is D-phenylalanine, D-phenylglycine, L-methylphenylglycine, L-*tert*-leucine, D-alanine, or D-hydroxynorleucine ((*S*)-2-amino-6-hydroxy hexanoic acid), R-pantolactone, 2-chloromandelic acid, or (*S*)- or (*R*)-mandelic acid and the enantiomerically pure α -hydroxy acid is (*S*)-cyclohexylmandelic acid. As used herein, a "small molecule" encompasses any molecule having a molecular weight from at least 25 Daltons.

[00097] The term "about" is used herein to mean approximately, roughly, around, or in the region of. When the term "about" is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term "about" is used herein to modify a numerical value above and below the stated value by a variance of 20 percent up or down (higher or lower).

[00098] As used herein, the word "or" means any one member of a particular list and also includes any combination of members of that list.

[00099] The phrase "nucleic acid" as used herein refers to a naturally occurring or synthetic oligonucleotide or polynucleotide, whether DNA or RNA or DNA-RNA hybrid, single-stranded or double-stranded, sense or antisense, which is capable of hybridization to a complementary nucleic acid by Watson-Crick base-pairing. Nucleic acids of the invention can also include nucleotide analogs (*e.g.*, BrdU), and non-phosphodiester internucleoside

linkages (*e.g.*, peptide nucleic acid (PNA) or thiodiester linkages). In particular, nucleic acids can include, without limitation, DNA, RNA, cDNA, gDNA, ssDNA or dsDNA or any combination thereof. In some aspects, a "nucleic acid" of the invention includes, for example, a nucleic acid encoding a polypeptide as set forth in the Group B amino acid sequences, and variants thereof. The phrase "a nucleic acid sequence" as used herein refers to a consecutive list of abbreviations, letters, characters or words, which represent nucleotides. In one aspect, a nucleic acid can be a "probe" which is a relatively short nucleic acid, usually less than 100 nucleotides in length. Often a nucleic acid probe is from about 50 nucleotides in length to about 10 nucleotides in length. A "target region" of a nucleic acid is a portion of a nucleic acid that is identified to be of interest.

[000100] A "coding region" of a nucleic acid is the portion of the nucleic acid which is transcribed and translated in a sequence-specific manner to produce into a particular polypeptide or protein when placed under the control of appropriate regulatory sequences. The coding region is said to encode such a polypeptide or protein.

[000101] The term "gene" refers to a coding region operably joined to appropriate regulatory sequences capable of regulating the expression of the polypeptide in some manner. A gene includes untranslated regulatory regions of DNA (*e.g.*, promoters, enhancers, repressors, etc.) preceding (upstream) and following (downstream) the coding region (open reading frame, ORF) as well as, where applicable, intervening sequences (*i.e.*, introns) between individual coding regions (*i.e.*, exons).

[000102] "Polypeptide" as used herein refers to any peptide, oligopeptide, polypeptide, gene product, expression product, or protein. A polypeptide is comprised of consecutive amino acids. The term "polypeptide" encompasses naturally occurring or synthetic molecules.

[000103] In addition, as used herein, the term "polypeptide" refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *e.g.*, peptide isosteres, and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides can be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification can be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide can have many types of modifications. Modifications include, without

limitation, acetylation, acylation, ADP-ribosylation, amidation, covalent cross-linking or cyclization, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, disulfide bond formation, demethylation, formation of cysteine or pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pergylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See Proteins – Structure and Molecular Properties 2nd Ed., T.E. Creighton, W.H. Freeman and Company, New York (1993); Posttranslational Covalent Modification of Proteins, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)).

[000104] As used herein, the term "amino acid sequence" refers to a list of abbreviations, letters, characters or words representing amino acid residues.

[000105] As used herein, the term "isolated" means that a material has been removed from its original environment. For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides can be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and would be isolated in that such a vector or composition is not part of its original environment.

[000106] As used herein with respect to nucleic acids, the term "recombinant" means that the nucleic acid is covalently joined and adjacent to a nucleic acid to which it is not adjacent in its natural environment. Additionally, as used herein with respect to a particular nucleic acid in a population of nucleic acids, the term "enriched" means that the nucleic acid represents 5% or more of the number of nucleic acids in the population of molecules. Typically, the enriched nucleic acids represent 15% or more of the number of nucleic acids in the population of molecules. More typically, the enriched nucleic acids represent 50%, 90% or more of the number of nucleic acids in the population molecules.

[000107] "Recombinant" polypeptides or proteins refer to polypeptides or proteins produced by recombinant DNA techniques, *i.e.*, produced from cells transformed by an exogenous recombinant DNA construct encoding the desired polypeptide or protein. "Synthetic" polypeptides or proteins are those prepared by chemical synthesis (*e.g.*, solid-phase peptide synthesis). Chemical peptide synthesis is well known in the art (see, *e.g.*,

Merrifield (1963), *Am. Chem. Soc.* **85**:2149-2154; Geysen et al. (1984), *Proc. Natl. Acad. Sci., USA* **81**:3998) and synthesis kits and automated peptide synthesizer are commercially available (e.g., Cambridge Research Biochemicals, Cleveland, United Kingdom; Model 431A synthesizer from Applied Biosystems, Inc., Foster City, CA). Such equipment provides ready
5 access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

[000108] As used herein with respect to pairs of nucleic acid or amino acid sequences, "identity" refers to the extent to which the two sequences are invariant at positions within the sequence which can be aligned. The percent identity between two given sequences can be
10 calculated using an algorithm such as BLAST (Altschul et al. (1990), *J. Mol. Biol.* **215**:403-410). See www.ncbi.nlm.nih.gov/Education/BLASTinfo. When using the BLAST algorithm for sequences no longer than 250 nucleotides or about 80 amino acids ("short queries"), the search parameters can be as follows: the filter is off, the scoring matrix is PAM30, the word size is 3 or 2, the E value is 1000 or more, and the gap costs are 11, 1. For sequences longer
15 than 250 nucleotides or 80 amino acid residues, the default search parameters can be used. The BLAST website provides advice for special circumstances which is to be followed in such circumstances.

[000109] As used herein, "homology" has the same meaning as "identity" in the context of nucleotide sequences. However, with respect to amino acid sequences, "homology" includes
20 the percentage of identical and conservative amino acid substitutions. Percentages of homology can be calculated according to the algorithms of Smith and Waterman (1981), *Adv. Appl. Math.* **2**:482.

[000110] As used herein in the context of two or more nucleic acid sequences, two sequences are "substantially identical" when they have at least 99.5% nucleotide identity,
25 when compared and aligned for maximum correspondence, as measured using the known sequence comparison algorithms described above. In addition, for purposes of determining whether sequences are substantially identical, synonymous codons in a coding region may be treated as identical to account for the degeneracy of the genetic code. Typically, the region for determination of substantial identity must span at least about 20 residues, and most
30 commonly the sequences are substantially identical over at least about 25-200 residues.

[000111] As used herein in the context of two or more amino acid sequences, two sequences are "substantially identical" when they have at least 99.5% identity, when compared and aligned for maximum correspondence, as measured using the known sequence

comparison algorithms described above. In addition, for purposes of determining whether sequences are substantially identical, conservative amino acid substitutions may be treated as identical if the polypeptide substantially retains its biological function.

[000112] "Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through hydrogen bonding at complementary bases. Hybridization assays can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Stringent conditions are defined by concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature, and are well known in the art. Stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In particular, as used herein, "stringent hybridization conditions" include 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 ng/ml sheared and denatured salmon sperm DNA, and equivalents thereof. Variations on the above ranges and conditions are well known in the art.

[000113] The term "variant" refers to polynucleotides or polypeptides of the invention modified at one or more nucleotides or amino acid residues (respectively) and wherein the encoded polypeptide or polypeptide retains nitrilase activity. Variants can be produced by any number of means including, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site-saturated mutagenesis or any combination thereof.

[000114] Methods of making peptidomimetics based upon a known sequence is described, for example, in U.S. Patent Nos. 5,631,280; 5,612,895; and 5,579,250. Use of peptidomimetics can involve the incorporation of a non-amino acid residue with non-amide linkages at a given position. One aspect of the present invention is a peptidomimetic wherein the compound has a bond, a peptide backbone or an amino acid component replaced with a suitable mimic. Examples of unnatural amino acids which may be suitable amino acid mimics include β -alanine, L- α -amino butyric acid, L- γ -amino butyric acid, L- α -amino isobutyric acid, L- ϵ -amino caproic acid, 7-amino heptanoic acid, L-aspartic acid, L-glutamic acid, N- ϵ -Boc-N- α -CBZ-L-lysine, N- ϵ -Boc-N- α -Fmoc-L-lysine, L-methionine sulfone, L-norleucine, L-norvaline, N- α -Boc-N- δ -CBZ-L-ornithine, N- δ -Boc-N- α -CBZ-L-ornithine, Boc-p-nitro-L-phenylalanine, Boc-hydroxyproline, Boc-L-thioprolin.

[000115] As used herein, "small molecule" encompasses a molecule having a molecular weight from about 20 daltons to about 1.5 kilodaltons.

[000116] The molecular biological techniques, such as subcloning, were performed using routine methods which would be well known to one of skill in the art. (Sambrook, J. Fritsch, EF, Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual (2nd ed.), Cold Spring Harbor Laboratory Press, Plainview NY.).

Computer Systems

[000117] In one aspect of the invention, any nucleic acid sequence and/or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15 or 20 nucleic acid sequences as set forth in SEQ ID NOS: 1-386, and sequences substantially identical thereto. In a further aspect, another aspect is the comparison among and between nucleic acid sequences or polypeptide sequences of the invention and the comparison between sequences of the invention and other sequences by a computer. Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

[000118] Aspects of the invention include systems (*e.g.*, internet based systems), particularly computer systems which store and manipulate the sequence information described herein. As used herein, "a computer system" refers to the hardware components, software components, and data storage components used to analyze a sequence (either nucleic acid or polypeptide) as set forth in at least any one of SEQ ID NOS: 1-386 and sequences substantially identical thereto. The computer system typically includes a processor for processing, accessing and manipulating the sequence data. The processor can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

[000119] Typically the computer system is a general purpose system that comprises the processor and one or more internal data storage components for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components.

[000120] In one particular aspect, the computer system includes a processor connected to a bus which is connected to a main memory (preferably implemented as RAM) and one or more internal data storage devices, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the computer system further includes one or more data retrieving device for reading the data stored on the internal data storage devices.

[000121] The data retrieving device may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (*e.g.*, via the internet) etc. In some aspects, the internal data storage device is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

[000122] The computer system includes a display which is used to display output to a computer user. It should also be noted that the computer system can be linked to other computer systems in a network or wide area network to provide centralized access to the computer system. In some aspects, the computer system may further comprise a sequence comparison algorithm. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage means.

Uses of Nitrilases

[000123] Nitrilases have been identified as key enzymes for the production of chiral α -hydroxy acids, which are valuable intermediates in the fine chemicals industry, and as pharmaceutical intermediates. The nitrilase enzymes of the invention are useful to catalyze the stereoselective hydrolysis of cyanohydrins and aminonitriles, producing chiral α -hydroxy- and α -amino acids, respectively.

[000124] Stereoselective enzymes provide a key advantage over chemical resolution methods as they do not require harsh conditions and are more environmentally compatible. The use of nitrilases is of particular interest for the production of chiral amino acids and α -hydroxy acids. Using a stereoselective nitrilase, dynamic resolution conditions can be established, due to the racemisation of the substrate under aqueous conditions. Thus 100% theoretical yields are achievable.

[000125] This invention is directed to the nitrilases which have been discovered and isolated from naturally occurring sources. This invention is also directed to evolving novel genes and gene pathways from diverse and extreme environmental sources. In an effort to develop the most extensive assortment of enzymes available, DNA was extracted directly from samples that have been collected from varying habitats around the globe. From these efforts, the largest collection of environmental genetic libraries in the world was developed. Through extensive high-throughput screening of these libraries, 192 new sequence-unique nitrilase enzymes have been discovered to date. Previous to this invention, fewer than 20 microbial-derived nitrilases had been reported in the literature and public databases.

[000126] Biocatalysts, such as nitrilases, play an important role in catalyzing metabolic reactions in living organisms. In addition, biocatalysts have found applications in the chemical industry, where they can perform many different reactions. Some examples of the advantages of the use of nitrilases is that they provide: high enantio-, chemo- and regio-selectivity; they function under mild reaction conditions; they provide direct access to products – with minimal protection; they have high catalytic efficiencies; they produce reduced waste compared with the chemical alternatives; they are easily immobilized as enzymes or cells; they are recoverable, recyclable and are capable of being manipulated via molecular biological techniques; they can be regenerated in whole cell processes; they are tolerant to organic solvents; and importantly, they can be evolved or optimized. Optimized nitrilases are presented herein as working examples of the invention.

[000127] Nitrilases catalyze the hydrolysis of nitrile moieties generating the corresponding carboxylic acid. Conventional chemical hydrolysis of nitriles requires strong acid or base and high temperature. However, one advantage of the invention is that nitrilases are provided which perform this reaction under mild conditions. Wide ranges of nitrile substrates can be transformed by nitrilases with high enantio-, chemo- and regio- selectivity.

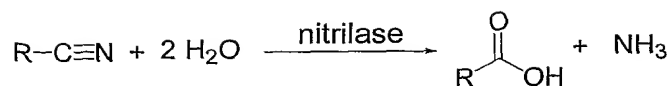


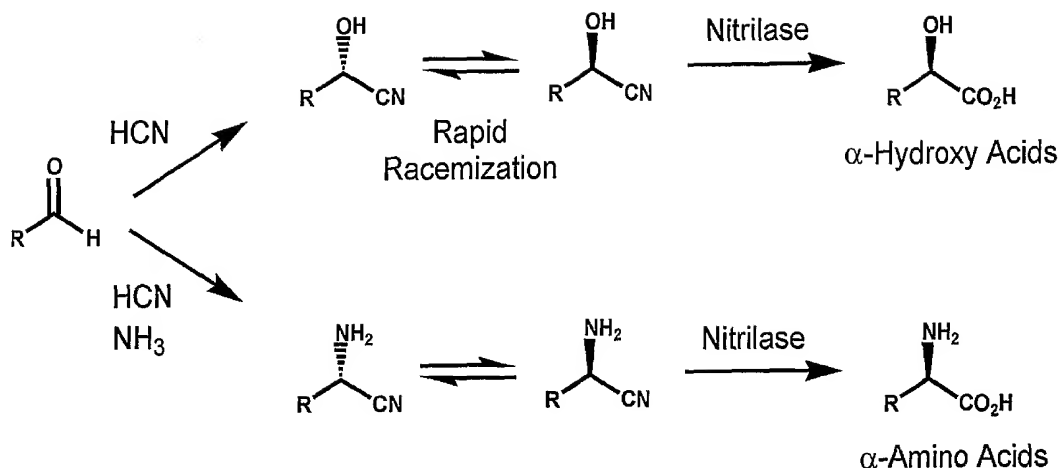
Table 1 - Some characteristics of Nitrilases of the Invention

<u>Previously Discovered Nitrilases</u>		<u>New Nitrilases</u>
Limitations	New Features	Benefits
< 20 reported	>180 newly discovered	Access to a wider substrate range
Homologous	Unique nitrilases, many with little homology to previously known nitrilases	
Narrow substrate Activity spectrum	Broad substrate activity spectrum	
Very few shown to be enantioselective	Enantioselective; both enantiomers accessible	Product with high enantiomeric excess and minimal waste production
Limited stability profile	Stable in a variety of conditions	Potential use in a wide range of process conditions
Inconsistent supply	Consistent supply	Reliable source of product
Not applicable	Amenable to optimization	Good source material leads to better product

5

[000128] Dynamic Kinetic Resolution: The use of the nitrilases allows discrimination between two rapidly equilibrating enantiomers to give a single product in 100% theoretical yield. Nitrilases are utilized for dynamic resolution of key cyanohydrins and aminonitriles to produce enantiomerically pure α -carboxylic and α -amino acids. Newly discovered nitrilases disclosed herein yield products with >95% enantiomeric excess (*ee*) with and >95% yield. The nitrilases perform this transformation efficiently under mild conditions in aqueous solution or in the presence of organic solvent.

10



[000129] These products shown above also include the opposite enantiomers, although they are not shown. In one aspect, the invention provides an isolated nucleic acid having a sequence as set forth in any one of the Group A nucleic acid sequences, having a sequence substantially identical thereto, or having a sequence complementary thereto.

[000130] In another aspect, the invention provides an isolated nucleic acid including at least 20 consecutive nucleotides identical to a portion of a nucleotide sequence as set forth in the Group A nucleic acid sequences, having a sequence substantially identical thereto, or having a sequence complementary thereto.

[000131] In another aspect, the invention provides an isolated nucleic acid encoding a polypeptide having a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000132] In another aspect, the invention provides an isolated nucleic acid encoding a polypeptide having at least 10 consecutive amino acids identical to a portion of a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000133] In yet another aspect, the invention provides a substantially purified polypeptide comprising consecutive amino acid residues having a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000134] In another aspect, the invention provides an isolated antibody that specifically binds to a polypeptide of the invention. The invention also provides for a fragment of the antibody which retains the ability to specifically bind the polypeptide.

[000135] In another aspect, the invention provides a method of producing a polypeptide having a sequence as set forth in the Group B amino acid sequences, and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host cell, wherein the nucleic acid is operably joined to a promoter, and culturing the host cell under conditions that allow expression of the nucleic acid.

[000136] In another aspect, the invention provides a method of producing a polypeptide having at least 10 consecutive amino acids from a sequence as set forth in the Group B amino acid sequences, and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host cell, wherein the nucleic acid is operably joined to a promoter, and culturing the host cell under conditions that allow expression of the nucleic acid, thereby producing the polypeptide.

[000137] In another aspect, the invention provides a method of generating a variant of a nitrilase, including choosing a nucleic acid sequence as set forth in the Group A nucleic acid sequences, and changing one or more nucleotides in the sequence to another nucleotide, deleting one or more nucleotides in the sequence, or adding one or more nucleotides to the sequence.

[000138] In another aspect, the invention provides assays for identifying functional variants of the Group B amino acid sequences that retain the enzymatic function of the polypeptides of the Group B amino acid sequences. The assays include contacting a polypeptide comprising consecutive amino acid residues having a sequence identical to a sequence of the Group B amino acid sequences or a portion thereof, having a sequence substantially identical to a sequence of the Group B amino acid sequences or a portion thereof, or having a sequence which is a variant of a sequence of the Group B amino acid sequences that retains nitrilase activity, with a substrate molecule under conditions which allow the polypeptide to function, and detecting either a decrease in the level of substrate or an increase in the level of a specific reaction product of the reaction between the polypeptide and the substrate, thereby identifying a functional variant of such sequences.

Modification of Polypeptides of the Invention

[000139] Enzymes are highly selective catalysts. Their hallmark is the ability to catalyze reactions with exquisite stereo-selectivity, regio-selectivity, and chemo-selectivity that is unparalleled in conventional synthetic chemistry. Moreover, enzymes are remarkably versatile. They can be tailored to function in organic solvents, operate at extreme pHs (for example, acidic or basic conditions) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity), and catalyze reactions with compounds that can be structurally unrelated to their natural, physiological substrates except for the enzymatic active site.

[000140] The invention provides methods for modifying polypeptides having nitrilase activity or polynucleotides encoding such polypeptides in order to obtain new polypeptides which retain nitrilase activity but which are improved with respect to some desired characteristic. Such improvements can include the ability to function (*i.e.*, exhibit nitrilase activity) in organic solvents, operate at extreme or uncharacteristic pHs, operate at extreme or uncharacteristic temperatures, operate at extreme or uncharacteristic salinity levels, catalyze reactions with different substrates, etc.

[000141] The present invention directed to methods of using nitrilases so as to exploit the unique catalytic properties of these enzymes. Whereas the use of biocatalysts (*i.e.*, purified or crude enzymes) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds. Each biocatalyst is specific for one functional group, or several related functional groups, and can react with many starting compounds containing this functional group.

[000142] Enzymes react at specific sites within a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of specificity provides the means to identify a single active compound within a library of compounds. The library is characterized by the series of biocatalytic reactions used to produce it, a so-called "biosynthetic history." Screening the library for biological activities and tracing the biosynthetic history identifies the specific

reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies, and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library. (For further teachings on modification of molecules, including small molecules, see PCT Application No. PCT/US94/09174, herein incorporated by reference in its entirety).

[000143] In one exemplification, the invention provides for the chimerization of a family of related nitrilase genes and their encoded family of related products. Thus according to this aspect of the invention, the sequences of a plurality of nitrilase nucleic acids (*e.g.*, the Group A nucleic acids) serve as nitrilase "templates" which are aligned using a sequence comparison algorithm such as those described above. One or more demarcation points are then identified in the aligned template sequences, which are located at one or more areas of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks, which are used to generate chimeric nitrilases. Thus, the demarcation points identified and selected in the nitrilase template molecules serve as potential chimerization points in the assembly of the chimeric nitrilase molecules.

[000144] Typically, a useful demarcation point is an area of local identity between at least two progenitor templates, but preferably the demarcation point is an area of identity that is shared by at least half of the templates, at least two thirds of the templates, at least three fourths of the templates, or at nearly all of the templates.

[000145] The building blocks, which are defined by the demarcation points, can then be mixed (either literally, in solution, or theoretically, on paper or in a computer) and reassembled to form chimeric nitrilase genes. In one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library of all possible combinations. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, however, the order of assembly of each building block in the 5' to 3' direction in each combination is designed to reflect the order in the templates, and to reduce the production of unwanted, inoperative products.

[000146] In some aspects, the gene reassembly process is performed systematically, in order to generate a compartmentalized library with compartments that can be screened systematically, *e.g.*, one by one. In other words, the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of chimeric products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of chimeric molecules to be examined systematically in smaller groups.

[000147] In some aspects, the synthetic nature of the step in which the building blocks are generated or reassembled allows the design and introduction of sequences of nucleotides (*e.g.*, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). The introduction of these nucleotides may be desirable for many reasons, including the potential benefit of creating a useful demarcation point.

[000148] The synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which has two ligatable ends. Some examples of the two ligatable ends on each nucleic acid building block includes, but are not limited to, two blunt ends, or one blunt end and one overhang, or two overhangs. In a further, non-limiting example, the overhang can include one base pair, 2 base pairs, 3 base pairs, 4 base pairs or more.

[000149] A double-stranded nucleic acid building block can be of variable size. Preferred sizes for building blocks range from about 1 base pair (bp) (not including any overhangs) to about 100,000 base pairs (not including any overhangs). Other preferred size ranges are also provided, which have lower limits of from about 1 bp to about 10,000 bp (including every integer value in between), and upper limits of from about 2 bp to about 100,000 bp (including every integer value in between).

[000150] According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that

form an overhang; thus containing no mismatches, apart from any overhang(s).

Alternatively, the two strands of a double-stranded nucleic acid building block can be complementary at fewer than every nucleotide, apart from any overhang(s). In particular, mismatches between the strands can be used to introduce codon degeneracy using methods such as the site-saturation mutagenesis described herein.

[000151] *In vivo* shuffling of molecules is also useful in providing variants and can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves (1) the recognition of homologies; (2) strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally (3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

[000152] Thus, the invention includes a method for producing a chimeric or recombinant polynucleotide from at least a first polynucleotide and a second polynucleotide *in vivo*. The invention can be used to produce a recombinant polynucleotide by introducing at least a first polynucleotide and a second polynucleotide which share at least one region of partial sequence homology (*e.g.*, the Group A nucleic acid sequences, and combinations thereof) into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a recombinant polynucleotide. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

[000153] The invention provides a means for generating recombinant polynucleotides which encode biologically active variant polypeptides (*e.g.*, a nitrilase variant). For example, a polynucleotide may encode a particular enzyme from one microorganism. An enzyme encoded by a first polynucleotide from one organism can, for example, function effectively under a particular environmental condition, *e.g.*, high salinity. An enzyme encoded by a second polynucleotide from a different organism can function effectively under a different environmental condition, such as extremely high temperature. A recombined polynucleotide containing sequences from the first and second original polynucleotides encodes a variant

enzyme which exhibits characteristics of both enzymes encoded by the original polynucleotides. Thus, the enzyme encoded by the recombined polynucleotide can function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

- 5 [000154] A variant polypeptide can exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding nitrilase activity, the resulting variant polypeptide encoded by a recombined polynucleotide can be screened for specialized nitrilase activity obtained from each of the original enzymes, *i.e.*, the temperature or pH at which the nitrilase functions.
- 10 Sources of the original polynucleotides may be isolated from individual organisms (“isolates”), collections of organisms that have been grown in defined media (“enrichment cultures”), or, uncultivated organisms (“environmental samples”). The use of a culture-independent approach to derive polynucleotides encoding novel bioactivities from environmental samples is most preferable since it allows one to access untapped resources of
- 15 biodiversity. The microorganisms from which the polynucleotide may be prepared include prokaryotic microorganisms, such as *Xanthobacter*, *Eubacteria* and *Archaeobacteria*, and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be isolated from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one
- 20 aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms are particularly preferred. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep sea thermal vents, at temperatures below 0°C in arctic waters, in the saturated salt
- 25 environment of the Dead Sea, at pH values around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge.

- [000155] Examples of mammalian expression systems that can be employed to express recombinant proteins include the COS-7, C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors comprise an origin of replication, a suitable promoter and
- 30 enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and polyadenylation sites may be

used to provide the required nontranscribed genetic elements. U.S. Patent No. 6,054,267 is hereby incorporated by reference in its entirety.

[000156] Host cells containing the polynucleotides of interest can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. Clones, which are identified as having a desired enzyme activity or other property may then be sequenced to identify the recombinant polynucleotide sequence encoding the enzyme having the desired activity or property.

[000157] In one aspect, the invention provides for the isolated nitrilases as either an isolated nucleic acid or an isolated polypeptide wherein the nucleic acid or the polypeptide was prepared by recovering DNA from a DNA population derived from at least one uncultivated microorganism, and transforming a host with recovered DNA to produce a library of clones which is screened for the specified protein, *e.g.* nitrilase activity. U.S. Patent No. 6,280,926, Short, provides descriptions of such methods and is hereby incorporated by reference in its entirety for all purposes.

[000158] Therefore, in a one aspect, the invention relates to a method for producing a biologically active recombinant nitrilase polypeptide and screening such a polypeptide for desired activity or property by:

- 1) introducing at least a first nitrilase polynucleotide and a second nitrilase polynucleotide, said at least first nitrilase polynucleotide and second nitrilase polynucleotide sharing at least one region of sequence homology, into a suitable host cell;
- 2) growing the host cell under conditions which promote sequence reorganization resulting in a recombinant nitrilase polynucleotide;
- 3) expressing a recombinant nitrilase polypeptide encoded by the recombinant nitrilase polynucleotide;
- 4) screening the recombinant nitrilase polypeptide for the desired activity or property; and
- 5) isolating the recombinant nitrilase polynucleotide encoding the recombinant nitrilase polypeptide.

[000159] Examples of vectors which may be used include viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, fowlpox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for the hosts of interest (e.g., *Bacillus*, *Aspergillus* and yeast). Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Examples of bacterial vectors include pQE vectors (Qiagen, Valencia, CA); pBluescript plasmids, pNH vectors, and lambda-ZAP vectors (Stratagene, La Jolla, CA); and pTRC99a, pKK223-3, pDR540, and pRIT2T vectors (Pharmacia, Peapack, NJ). Examples of eukaryotic vectors include pXT1 and pSG5 vectors (Stratagene, La Jolla, CA); and pSVK3, pBPV, pMSG, and pSVLSV40 vectors (Pharmacia, Peapack, NJ). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host.

[000160] A preferred type of vector for use in the present invention contains an f-factor (or fertility factor) origin of replication. The f-factor in *E. coli* is a plasmid which effects high frequency transfer of itself during conjugation and less frequent transfer of the bacterial chromosome itself. A particularly preferred aspect is to use cloning vectors referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA.

[000161] The DNA sequence in the expression vector is operably joined to appropriate expression control sequences, including a promoter, to direct RNA synthesis. Useful bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, P_L and trp. Useful eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers.

[000162] In addition, the expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells. Useful selectable markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*.

[000163] The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation

5 [000164] Reductive Reassortment - In another aspect, variant nitrilase polynucleotides can be generated by the process of reductive reassortment. Whereas recombination is an “inter-molecular” process which, in bacteria, is generally viewed as a “recA-dependent” phenomenon, the process of “reductive reassortment” occurs by an “intra-molecular”, recA-independent process. In this aspect, the invention can rely on the ability of cells to mediate
10 reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. The method involves the generation of constructs containing consecutive repeated or quasi-repeated sequences (original encoding sequences), the insertion of these sequences into an appropriate vector, and the subsequent introduction of the vector into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial
15 processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences, and results in the production of novel molecular species. Various treatments may be applied to enhance the rate of reassortment, such as ultra-violet light or DNA damaging chemicals. In addition, host cell
20 lines displaying enhanced levels of “genetic instability” can be used.

[000165] Repeated Sequences - Repeated or “quasi-repeated” sequences play a role in genetic instability. In the present invention, “quasi-repeats” are repeats that are not identical in structure but, rather, represent an array of consecutive sequences which have a high degree of similarity or identity sequences. The reductive reassortment or deletion process in the cell
25 reduces the complexity of the resulting construct by deleting sequences between positions within quasi-repeated sequences. Because the deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units, these sequences provide a large repertoire of potential variants.

[000166] When the quasi-repeated sequences are all ligated in the same orientation, for instance head-to-tail or vice versa, the endpoints of a deletion are, for the most part, equally
30 likely to occur anywhere within the quasi-repeated sequences. In contrast, when the units are presented head-to-head or tail-to-tail, the inverted quasi-repeated sequences can form a

duplex which delineates the endpoints of the adjacent units and thereby favors deletion of discrete units. Therefore, it is preferable in the present invention that the quasi-repeated sequences are joined in the same orientation because random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. Nonetheless, although having fewer of the contiguous sequences in the same orientation decreases the efficiency or reductive reassortment, it may still provide sufficient variation for the effective recovery of novel molecules.

[000167] Sequences can be assembled in a head-to-tail orientation using any of a variety of methods, including the following:

a) Primers can be utilized that include a poly-A head and poly-T tail which, when made single-stranded, would provide orientation. This is accomplished by having the first few bases of the primers made from RNA and hence easily removed by RNase H. b)

Primers can be utilized that include unique restriction cleavage sites. Multiple sites, a battery of unique sequences, and repeated synthesis and ligation steps would be required.

c) The inner few bases of the primer can be thiolated and an exonuclease used to produce properly tailed molecules.

[000168] The recovery of the reassorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The reassorted coding sequences can then be recovered by amplification. The products are recloned and expressed. The recovery of cloning vectors with reduced RI can be effected by:

1) The use of vectors only stably maintained when the construct is reduced in complexity.

2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and then size-fractionated using standard procedures (*e.g.*, agarose gel or column with a low molecular weight cut off).

3) The recovery of vectors containing interrupted genes can be selected when insert size decreases.

4) The use of direct selection techniques wherein an expression vector is used and the appropriate selection is carried out.

[000169] Coding sequences from related organisms may demonstrate a high degree of homology but nonetheless encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of coding sequences with a high degree of identity (quasi-repeats), this process is not limited to nearly identical repeats.

[000170] The following example demonstrates a method of the invention. Quasi-repetitive coding sequences derived from three different species are obtained. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by one or more base pairs at unique positions in the sequences which are designated "A", "B" and "C". The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules. The number of quasi-repeat units can be controlled by the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

[000171] Once formed, the constructs can be size-fractionated on an agarose gel according to published protocols, inserted into a cloning vector, and transfected into an appropriate host cell. The cells can then be propagated to allow reductive reassortment to occur. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an "intra-molecular" mechanism, or mediated by recombination-like events through "inter-molecular" mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

[000172] In another aspect, prior to or during recombination or reassortment, polynucleotides of the invention or polynucleotides generated by the methods described herein can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-adenine) (Sun et al. (1992), *Biochemistry* 31(10):2822-9); an N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (see, for example, van de Poll et al. (1992), *Carcinogenesis* 13(5):751-8); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting

DNA synthesis (see also, Van de Poll et al. (1992), *supra*); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon ("PAH") DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[a]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-BP"), 1,2-dibromo-3-chloropropane ("DBCP"), 2-bromoacrolein (2BA), benzo[a]pyrene-7,8-dihydrodiol-9-10-epoxide ("BPDE"), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-f]-quinoline ("N-hydroxy-IQ"), and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-f]-pyridine ("N-hydroxy-PhIP"). Especially preferred means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

[000173] GSSM™ - The invention also provides for the use of codon primers containing a degenerate N,N,G/T sequence to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, a method referred to as gene site-saturated mutagenesis (GSSM™). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,G/T sequence, and possibly a second homologous sequence. The progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids.

[000174] In one aspect, one such degenerate oligo (comprising one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,G/T cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,G/T sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequences. In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

[000175] In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,G/T triplets, *i.e.*, a degenerate (N,N,G/T)_n sequence.

[000176] In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,G/T sequence. For example, it may be desirable in some instances to use a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use a degenerate N,N,N triplet sequence, or an N,N, G/C triplet sequence.

[000177] It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of the 20 possible amino acids into each and every amino acid position in a polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for the 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

[000178] This invention also provides for the use of nondegenerate oligonucleotides, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

[000179] Thus, in one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

[000180] It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

[000181] In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

[000182] Thus, in a non-limiting exemplification, polynucleotides and polypeptides of the invention can be derived by saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

[000183] In addition to performing mutagenesis along the entire sequence of a gene, mutagenesis can be used to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized can be each integer from about 15 to about 100,000. Thus, instead of mutagenizing every position along a molecule, one can
5 subject every or a discrete number of bases (*e.g.*, a subset totaling from about 15 to about 100,000) to mutagenesis. In one aspect, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized can be a codon. In one aspect, the mutations are introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. For
10 example, cassettes can have from about 1 to about 500 bases. Each nucleotide position in such heterologous cassettes can be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T.

[000184] In a general sense, saturation mutagenesis comprises mutagenizing a complete set of mutagenic cassettes (for example, each cassette is about 1-500 bases in length) in a defined
15 polynucleotide sequence to be mutagenized (for example, the sequence to be mutagenized is from about 15 to about 100,000 bases in length). Thus, a group of mutations (ranging from about 1 to about 100 mutations) is introduced into each cassette to be mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application
20 of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons, and groupings of particular nucleotide cassettes.

[000185] Defined sequences to be mutagenized include a whole gene, pathway, cDNA, entire open reading frame (ORF), promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a “defined
25 sequence” for this purpose may be any polynucleotide that a 15 base-polynucleotide sequence, and polynucleotide sequences of lengths between about 15 bases and about 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

[000186] In a particularly preferred exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,

14, 15, 16, 17, 18, 19, and 20 amino acids at each position, and a library of polypeptides encoded thereby.

[000187] One aspect of the invention is an isolated nucleic acid comprising one of the sequences of the Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the Group A nucleic acid sequences. The isolated nucleic acids may comprise DNA, including cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated nucleic acids may comprise RNA.

[000188] As discussed in more detail below, the isolated nucleic acid sequences of the invention may be used to prepare one of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto.

[000189] Alternatively, the nucleic acid sequences of the invention may be mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of the Group A nucleic acid sequences, and sequences substantially identical thereto. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

[000190] The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of the invention (*e.g.*, the Group B amino acid sequences). Such nucleotide changes may be introduced using techniques such as site-directed mutagenesis, random chemical mutagenesis, exonuclease III deletion, and other recombinant DNA techniques.

Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acid sequences which specifically hybridize to probes

comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the Group A nucleic acid sequences, and sequences substantially identical thereto (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

5 Immobilized Enzyme Solid Supports

[000191] The enzymes, fragments thereof and nucleic acids which encode the enzymes and fragments can be affixed to a solid support. This is often economical and efficient in the use of the enzymes in industrial processes. For example, a consortium or cocktail of enzymes (or active fragments thereof), which are used in a specific chemical reaction, can be attached to a solid support and dunked into a process vat. The enzymatic reaction can occur. Then, the solid support can be taken out of the vat, along with the enzymes affixed thereto, for repeated use. In one aspect of the invention, the isolated nucleic acid is affixed to a solid support. In another aspect of the invention, the solid support is selected from the group of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.

15 [000192] For example, solid supports useful in this invention include gels. Some examples of gels include sepharose, gelatin, glutaraldehyde, chitosan-treated glutaraldehyde, albumin-glutaraldehyde, chitosan-Xanthan, toyopearl gel (polymer gel), alginate, alginate-polylysine, carrageenan, agarose, glyoxyl agarose, magnetic agarose, dextran-agarose, poly(Carbamoyl Sulfonate) hydrogel, BSA-PEG hydrogel, phosphorylated polyvinyl alcohol (PVA),
20 monoaminoethyl-N-aminoethyl (MANA), amino, or any combination thereof.

[000193] Another solid support useful in the present invention are resins or polymers. Some examples of resins or polymers include cellulose, acrylamide, nylon, rayon, polyester, anion-exchange resin, AMBERLITE™ XAD-7, AMBERLITE™ XAD-8, AMBERLITE™ IRA-94, AMBERLITE™ IRC-50, polyvinyl, polyacrylic, polymethacrylate, or any
25 combination thereof. Another type of solid support useful in the present invention is ceramic. Some examples include non-porous ceramic, porous ceramic, SiO₂, Al₂O₃. Another type of solid support useful in the present invention is glass. Some examples include non-porous glass, porous glass, aminopropyl glass or any combination thereof. Another type of solid support which can be used is a microelectrode. An example is a polyethyleneimine-coated
30 magnetite. Graphitic particles can be used as a solid support. Another example of a solid support is a cell, such as a red blood cell.

Methods of immobilization

[000194] There are many methods which would be known to one of skill in the art for immobilizing enzymes or fragments thereof, or nucleic acids, onto a solid support. Some examples of such methods include electrostatic droplet generation, electrochemical means, via adsorption, via covalent binding, via cross-linking, via a chemical reaction or process, via encapsulation, via entrapment, via calcium alginate, or via poly (2-hydroxyethyl methacrylate). Like methods are described in *Methods in Enzymology, Immobilized Enzymes and Cells*, Part C. 1987. Academic Press. Edited by S. P. Colowick and N. O. Kaplan. Volume 136; and *Immobilization of Enzymes and Cells*. 1997. Humana Press. Edited by G. F. Bickerstaff. Series: Methods in Biotechnology, Edited by J. M. Walker.

[000195] Probes - The isolated nucleic acids of the Group A nucleic acid sequences, sequences substantially identical thereto, complementary sequences, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the foregoing sequences may also be used as probes to determine whether a biological sample, such as a soil sample, contains an organism having a nucleic acid sequence of the invention or an organism from which the nucleic acid was obtained. In such procedures, a biological sample potentially harboring the organism from which the nucleic acid was isolated is obtained and nucleic acids are obtained from the sample. The nucleic acids are contacted with the probe under conditions which permit the probe to specifically hybridize to any complementary sequences which are present therein.

[000196] Where necessary, conditions which permit the probe to specifically hybridize to complementary sequences may be determined by placing the probe in contact with complementary sequences from samples known to contain the complementary sequence as well as control sequences which do not contain the complementary sequence. Hybridization conditions, such as the salt concentration of the hybridization buffer, the formamide concentration of the hybridization buffer, or the hybridization temperature, can be varied to identify conditions which allow the probe to hybridize specifically to complementary nucleic acids. Stringent hybridization conditions are recited herein.

[000197] Hybridization may be detected by labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye or an enzyme capable of catalyzing the formation of a detectable product. Many methods for using the labeled probes to detect the presence of complementary nucleic acids in a sample are familiar to those skilled in the art. These include Southern Blots, Northern Blots, colony hybridization procedures, and dot blots.

Protocols for each of these procedures are provided in Ausubel et al. (1997), *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc., and Sambrook et al. (1989), *Molecular Cloning: A Laboratory Manual 2d Ed.*, Cold Spring Harbor Laboratory Press, the entire disclosures of which are incorporated herein by reference.

- 5 **[000198]** In one example, a probe DNA is “labeled” with one partner of a specific binding pair (*i.e.*, a ligand) and the other partner of the pair is bound to a solid matrix to provide ease of separation of target from its source. For example, the ligand and specific binding partner can be selected from, in either orientation, the following: (1) an antigen or hapten and an antibody or specific binding fragment thereof; (2) biotin or iminobiotin and avidin or streptavidin; (3) a sugar and a lectin specific therefor; (4) an enzyme and an inhibitor therefor; (5) an apoenzyme and cofactor; (6) complementary homopolymeric oligonucleotides; and (7) a hormone and a receptor therefor. In one example, the solid phase is selected from: (1) a glass or polymeric surface; (2) a packed column of polymeric beads; and (3) magnetic or paramagnetic particles.
- 10 **[000199]** Alternatively, more than one probe (at least one of which is capable of specifically hybridizing to any complementary sequences which are present in the nucleic acid sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (*e.g.*, an organism from which the nucleic acid was isolated). Typically, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. PCR protocols are described in Ausubel et al. (1997), *supra*, and Sambrook et al. (1989), *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany (1991), *PCR Methods and Applications* 1:5-16; Fahy et al. (1991), *PCR Methods and Applications* 1:25-33; and Walker et al. (1992), *Nucleic Acid Research* **20**:1691-1696, the disclosures of which are incorporated herein by reference in their entireties).
- 20 **[000200]** Probes derived from sequences near the ends of a sequence as set forth in the Group A nucleic acid sequences, and sequences substantially identical thereto, may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the nucleic acid sequences as set forth above. Such methods allow the isolation of genes which encode additional proteins from the host organism.
- 30 **[000201]** An isolated nucleic acid sequence as set forth in the Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or

500 consecutive bases of one of the foregoing sequences may be used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

[000202] In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized.

For example, the length of the nucleic acids, the amount of complementarity between the nucleic acids, the nucleotide sequence composition (*e.g.*, G-C rich v. A-T rich content), and the nucleic acid type (*e.g.*, RNA v. DNA) can be considered in selecting hybridization conditions. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m , is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

[000203] For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

[000204] If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

[000205] Expression Libraries - Expression libraries can be created using the polynucleotides of the invention in combination with expression vectors and appropriate host cells. The library allows for the *in vivo* expression of the polypeptides which are encoded by the polynucleotides of the invention. After such expression libraries have been generated one can include the additional step of "biopanning" such libraries prior to screening by cell sorting. The "biopanning" procedure refers to a process for identifying clones having a specified biological activity by screening for sequence identity in a library of clones prepared by (i) selectively isolating target DNA derived from at least one microorganism by use of at least one probe DNA comprising at least a portion of a DNA sequence encoding a

polypeptide having a specified biological activity (*e.g.*, nitrilase activity); and (ii) optionally transforming a host with the isolated target DNA to produce a library of clones which are screened for the specified biological activity.

[000206] The probe DNA used for selectively isolating the target DNA of interest from the DNA derived from at least one microorganism can be a full-length coding region sequence or a partial coding region sequence of DNA for an enzyme of known activity. The original DNA library can be probed using mixtures of probes comprising at least a portion of DNA sequences encoding enzymes having the specified enzyme activity. These probes or probe libraries are single-stranded and the microbial DNA which is probed has been converted into single-stranded form. The probes that are particularly suitable are those derived from DNA encoding enzymes having an activity similar or identical to the specified enzyme activity that is to be screened.

[000207] Having prepared a multiplicity of clones from DNA selectively isolated from an organism, such clones are screened for a specific enzyme activity and to identify the clones having the specified enzyme characteristics.

[000208] The screening for enzyme activity may be affected on individual expression clones or may be initially affected on a mixture of expression clones to ascertain whether or not the mixture has one or more specified enzyme activities. If the mixture has a specified enzyme activity, then the individual clones may be rescreened for such enzyme activity or for a more specific activity. Thus, for example, if a clone mixture has nitrilase activity, then the individual clones may be recovered and screened to determine which of such clones has nitrilase activity.

[000209] As described with respect to one of the above aspects, the invention provides a process for enzyme activity screening of clones containing selected DNA derived from a microorganism which process includes: screening a library for specified enzyme activity, said library including a plurality of clones, said clones having been prepared by recovering from genomic DNA of a microorganism selected DNA, which DNA is selected by hybridization to at least one DNA sequence which is all or a portion of a DNA sequence encoding an enzyme having the specified activity; and transforming a host with the selected DNA to produce clones which are screened for the specified enzyme activity.

[000210] In one aspect, a DNA library derived from a microorganism is subjected to a selection procedure to select therefrom DNA which hybridizes to one or more probe DNA

sequences which is all or a portion of a DNA sequence encoding an enzyme having the specified enzyme activity by:

(a) contacting the single-stranded DNA population from the DNA library with the DNA probe bound to a ligand under stringent hybridization conditions so as to produce a duplex between the probe and a member of the DNA library;

(b) contacting the duplex with a solid phase specific binding partner for the ligand so as to produce a solid phase complex;

(c) separating the solid phase complex from the non-duplexed members of the DNA library;

(d) denaturing the duplex to release the member of the DNA library;

(e) creating a complementary DNA strand of the member from step (d) so as to make the member a double-stranded DNA;

(f) introducing the double-stranded DNA into a suitable host so as to express a polypeptide which is encoded by the member DNA; and

(g) determining whether the polypeptide expressed exhibits the specified enzymatic activity.

[000211] In another aspect, the process includes a preselection to recover DNA including signal or secretion sequences. In this manner it is possible to select from the genomic DNA population by hybridization as hereinabove described only DNA which includes a signal or secretion sequence. The following paragraphs describe the protocol for this aspect of the invention, the nature and function of secretion signal sequences in general and a specific exemplary application of such sequences to an assay or selection process.

[000212] A particularly aspect of this aspect further comprises, after (a) but before (b) above, the steps of:

(i) contacting the single-stranded DNA population of (a) with a ligand-bound oligonucleotide probe that is complementary to a secretion signal sequence unique to a given class of proteins under hybridization conditions to form a double-stranded DNA duplex;

(ii) contacting the duplex of (i) with a solid phase specific binding partner for said ligand so as to produce a solid phase complex;

(iii) separating the solid phase complex from the single-stranded DNA population of (a);

(iv) denaturing the duplex so as to release single-stranded DNA members of the genomic population; and

(v) separating the single-stranded DNA members from the solid phase bound probe.

[000213] The DNA which has been selected and isolated to include a signal sequence is then subjected to the selection procedure hereinabove described to select and isolate therefrom DNA which binds to one or more probe DNA sequences derived from DNA

5 encoding an enzyme(s) having the specified enzyme activity. This procedure is described and exemplified in U.S. Pat. No. 6,054,267, incorporated herein by reference in its entirety.

[000214] *In vivo* biopanning may be performed utilizing a (fluorescence activated cell sorter) FACS-based machine. Complex gene libraries are constructed with vectors which contain elements which stabilize transcribed RNA. For example, the inclusion of sequences

10 which result in secondary structures such as hairpins which are designed to flank the transcribed regions of the RNA would serve to enhance their stability, thus increasing their half life within the cell. The probe molecules used in the biopanning process consist of

oligonucleotides labeled with reporter molecules that only fluoresce upon binding of the probe to a target molecule. These probes are introduced into the recombinant cells from the

15 library using one of several transformation methods. The probe molecules bind to the transcribed target mRNA resulting in DNA/RNA heteroduplex molecules. Binding of the probe to a target will yield a fluorescent signal that is detected and sorted by the FACS machine during the screening process.

[000215] In some aspects, the nucleic acid encoding one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Optionally, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of the Group B amino acid sequences,

25 sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

[000216] The host cell may be any of the host cells familiar to those skilled in the art,

30 including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, fungal cells, such as yeast,

insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, animal cells such as CHO, COS or Bowes melanoma, and adenoviruses. The selection of an appropriate host is within the abilities of those skilled in the art.

[000217] Where appropriate, the engineered host cells can be cultured in conventional

5 nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (*e.g.*, temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or

10 fragment thereof.

[000218] Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells

employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such

15 methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including

ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction

chromatography, affinity chromatography, hydroxylapatite chromatography and lectin

20 chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography

(HPLC) can be employed for final purification steps.

[000219] Various mammalian cell culture systems can also be employed to express

recombinant protein. Examples of mammalian expression systems include the COS-7 lines

25 of monkey kidney fibroblasts (described by Gluzman (1981), *Cell* **23**:175.), and other cell

lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

[000220] The invention also relates to variants of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least 5,

30 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. In particular, the variants may differ in amino acid sequence from the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination.

[000221] The variants may be naturally occurring or created *in vitro*. In particular, such variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures.

[000222] Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect to the sequence obtained from the natural isolate are generated and characterized. Typically, these nucleotide differences result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

Error Prone PCR

[000223] For example, variants may be created using error prone PCR. In error prone PCR, PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described in Leung et al. (1989), *Technique* 1:11-15 and Caldwell et al. (1992), *PCR Methods Applic.* 2:28-33, the disclosures of which are incorporated herein by reference in their entirety. Briefly, in such procedures, nucleic acids to be mutagenized are mixed with PCR primers and reagents (e.g., reaction buffer, MgCl₂, MnCl₂, Taq polymerase and an appropriate concentration of dNTPs) for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmoles of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl₂, 0.5mM MnCl₂, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

[000224] Variants also may be created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis

is described in Reidhaar-Olson et al. (1988), *Science*, 241:53-57, the disclosure of which is incorporated herein by reference in its entirety. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the cloned DNA to be mutagenized. Clones
5 containing the mutagenized DNA are recovered and the activities of the polypeptides they encode are assessed.

Assembly PCR

[000225] Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large
10 number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in U.S. Pat. No. 5,965,408, the disclosure of which is incorporated herein by reference in its entirety.

Sexual PCR mutagenesis

[000226] Still another method of generating variants is sexual PCR mutagenesis. In sexual
15 PCR mutagenesis, forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described in Stemmer (1994), *Proc. Natl. Acad. Sci. USA* 91:10747-10751, the disclosure of which is incorporated herein by
20 reference in its entirety. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of about 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the
25 purified fragments at a concentration of 10-30 ng/μl in a solution of 0.2mM of each dNTP, 2.2mM MgCl₂, 50mM KCl, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100μl of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that
30 these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent

set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

In vivo Mutagenesis

[000227] Variants may also be created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an *E. coli* strain, which carries mutations in one or more of the DNA repair pathways. Such “mutator” strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427 the disclosure of which is incorporated herein by reference in its entirety.

Cassette Mutagenesis

[000228] Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide “cassette” that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

Recursive Ensemble Mutagenesis

[000229] Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described in Arkin et al. (1992), *Proc. Natl. Acad. Sci. USA*, **89**:7811-7815, the disclosure of which is incorporated herein by reference in its entirety.

Exponential Ensemble Mutagenesis

[000230] In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described in Delegrave et al. (1993), *Biotechnology Research* **11**:1548-1552, the disclosure of which incorporated herein by reference in its entirety.

Random and site-directed mutagenesis

[000231] Random and site-directed mutagenesis is described in Arnold (1993), *Current Opinions in Biotechnology* 4:450-455, the disclosure of which is incorporated herein by reference in its entirety.

5 Shuffling Procedures

[000232] In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as described in U.S. Patent. Nos. 5,965,408 and 5,939,250, each of which is hereby incorporated by reference
10 in their entirety.

[000233] The variants of the polypeptides of the Group B amino acid sequences may be variants in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences are substituted with a conserved or non-conserved amino acid residue (*e.g.*, a conserved amino acid residue) and such substituted amino acid residue may or may
15 not be one encoded by the genetic code.

[000234] Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the following replacements: replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a
20 Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic
25 residue.

[000235] Other variants are those in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences includes a substituent group.

[000236] Still other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example,
30 polyethylene glycol).

[000237] Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence which facilitates purification, enrichment, or stabilization of the polypeptide.

[000238] In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto. In other aspects, the fragment, derivative, or analog includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

[000239] Another aspect of the invention is polypeptides or fragments thereof which have at least about 85%, at least about 90%, at least about 95%, or more than about 95% homology to one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Percent identity may be determined using any of the programs described above which aligns the polypeptides or fragments being compared and determines the extent of amino acid homology or similarity between them. It will be appreciated that amino acid "homology" includes conservative amino acid substitutions such as those described above. In one aspect of the invention, the fragments can be used to generate antibodies. These antibodies can be used to immobilize nitrilases can be used in industrial processes. Polynucleotides encoding the nitrilases of the present invention can be used in a similar way.

[000240] Alternatively, the homologous polypeptides or fragments may be obtained through biochemical enrichment or purification procedures. The sequence of potentially homologous polypeptides or fragments may be determined by proteolytic digestion, gel electrophoresis and/or microsequencing. The sequence of the prospective homologous polypeptide or fragment can be compared to one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or a fragment comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof using any of the programs described herein.

[000241] Another aspect of the invention is an assay for identifying fragments or variants of the Group B amino acid sequences, or sequences substantially identical thereto, which retain the enzymatic function of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto. For example, the fragments or variants of the polypeptides, may be used to catalyze biochemical reactions, which indicate that said fragment or variant retains the enzymatic activity of the polypeptides in Group B amino acid sequences.

[000242] The assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto includes the steps of: contacting the polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function, and
5 detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

[000243] The polypeptides of the Group B amino acid sequences, sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in a variety of applications. For example,
10 the polypeptides or fragments thereof may be used to catalyze biochemical reactions. In accordance with one aspect of the invention, there is provided a process for utilizing a polypeptide of the Group B amino acid sequences, and sequences substantially identical thereto or polynucleotides encoding such polypeptides for hydrolyzing aminonitriles. In such procedures, a substance containing a haloalkane compound is contacted with one of the
15 polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto under conditions which facilitate the hydrolysis of the compound.

[000244] Antibodies - The polypeptides of Group B amino acid sequences, sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies
20 which bind specifically to the enzyme polypeptides or fragments. The resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of the Group B
25 amino acid sequences, sequences substantially identical thereto, or fragments of the foregoing sequences.

[000245] In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or column matrix. The protein preparation is placed in contact with the antibody under conditions under which the antibody specifically binds to one of the polypeptides of the
30 Group B amino acid sequences, sequences substantially identical thereto, or fragments thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

[000246] The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays, and Western Blots.

[000247] The antibodies of the invention can be attached to solid supports and used to immobilize nitrilases of the present invention. Such immobilized nitrilases can be used, as described above, in industrial chemical processes for the conversion of nitriles to a wide range of useful products and intermediates.

[000248] Polyclonal antibodies generated against the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal. The antibody so obtained will then bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

[000249] For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein (1975), *Nature*, **256**:495-497, the disclosure of which is incorporated herein by reference), the trioma technique, the human B-cell hybridoma technique (Kozbor et al. (1983), *Immunology Today* **4**:72, the disclosure of which is incorporated herein by reference), and the EBV-hybridoma technique (Cole et al. (1985), in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, the disclosure of which is incorporated herein by reference in its entirety).

[000250] Techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778, the disclosure of which is incorporated herein by reference in its entirety) can be adapted to produce single chain antibodies to the polypeptides of, for example, the Group B amino acid sequences, or fragments thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments.

[000251] Antibodies generated against a polypeptide of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind to the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, **160**:87-116, which is hereby incorporated by reference in its entirety.

Use of Whole Cells Comprising A Nucleic Acid

[000252] The invention provides for the use of whole cells which have been transformed with nucleic acid (or an active fragment thereof) encoding one or more of the nitrilases of the invention. The invention also provides for the use of such a whole cell in performing a nitrilase reaction on a substrate. Therefore, this invention provides for methods of hydrolyzing a cyanohydrin or aminonitrile linkage using a whole cell comprising at least one nucleic acid or polypeptide disclosed herein (SEQ ID NOS:1-386). For example, a whole cell which is stably transfected (the invention also encompasses transiently transfected or transformed whole cells) with a nucleic acid encoding a nitrilase is one aspect of the invention. Such a cell is useful as a reagent in a reaction mixture to act on a substrate and exhibit nitrilase activity.

Sequence Analysis Software

[000253] Percent identity or homology between two or more sequences is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, Madison, WI). Such software matches similar sequences by assigning a percent identity or homology to various deletions, substitutions and other modifications. The term "percent identity," in the context of two or more nucleic acids or polypeptide sequences, refers to the percentage of nucleotides or amino acid residues that are the same when compared after being aligned for maximum correspondence over a designated region or comparison "window." Under some algorithms, a conservative amino acid substitution can be considered "identical" and a change at a wobble site of a codon can be considered "identical."

[000254] "Alignment" refers to the process of lining up two or more sequences to achieve maximal correspondence for the purpose of assessing the degree of identity or homology, as defined within the context of the relevant alignment algorithm.

[000255] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated for a particular algorithm. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent identity or homology for the test sequences relative to the reference sequence, based on the program parameters.

[000256] A "comparison window", as used herein, is a segment of the contiguous positions in a nucleic acid or an amino acid sequence consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 nucleotides or residues, which may be compared to a reference sequence of the same or different number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith and Waterman (1981), *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970), *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988), *Proc. Natl. Acad. Sci. USA* 85:2444-2448, by computerized implementations of these algorithms, or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, the BLAST program (Basic Local Alignment Search Tool, National Center for Biological Information), BESTFIT, FASTA, and TFASTA (Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Alignment of Multiple Protein Sequence), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLOCKS IMPROVED Searcher), Intervals and Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence

Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction and Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome
5 databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, http://weber.u.Washington.edu/~roach/human_genome_progress2.html) (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M.*
10 *genitalium* (Fraser et al., 1995), *M. jannaschii* (Bult et al., 1996), *H. influenzae* (Fleischmann et al., 1995), *E. coli* (Blattner et al., 1997), and yeast (*S. cerevisiae*) (Mewes et al., 1997), and *D. melanogaster* (Adams et al., 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans*, and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional
15 information are maintained by different organizations, and are accessible via the internet, for example, <http://www.tigr.org/tdb>; <http://www.genetics.wisc.edu>; <http://genome-www.stanford.edu/~ball>; <http://hiv-web.lanl.gov>; <http://www.ncbi.nlm.nih.gov>; <http://www.ebi.ac.uk>; <http://Pasteur.fr/other/biology>; and <http://www.genome.wi.mit.edu>.
[000257] Examples of useful algorithms are the BLAST and the BLAST 2.0 algorithms,
20 which are described in Altschul et al. (1977), *Nuc. Acids Res.* **25**:3389-3402, and Altschul et al. (1990), *J. Mol. Biol.* **215**:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which
25 either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased.
30 Cumulative scores are calculated using the parameter M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the

cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. For nucleotide sequences, the BLASTN program uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989), *Proc. Natl. Acad. Sci. USA* 89:10915).

[000258] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993), *Proc. Natl. Acad. Sci. USA* 90:5873). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, less than about 0.01, or less than about 0.001.

[000259] In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST"). In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

[000260] The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which may be obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are identified (*i.e.*, aligned) by

means of a scoring matrix, many of which are known in the art. In one example, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al. (1992), *Science* **256**:1443-1445; Henikoff and Henikoff (1993), *Proteins* **17**:49-61). In another example, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds. (1978), *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine, *e.g.*, at www.ncbi.nlm.nih.gov.

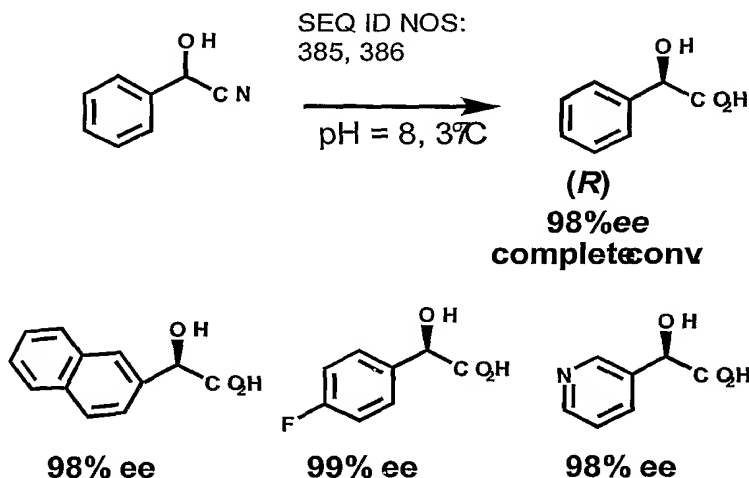
[000261] The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

[000262] In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library, and then testing the small molecules produced in the portion of the library for the presence or absence of the modified small molecule with the desired activity. The specific biocatalytic reactions, which produce the modified small molecule of, desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

[000263] Some aspects of the use of the nitrilases are:

α -hydroxy acid - Nitrilases produce α -hydroxy acids through hydrolysis of cyanohydrins. Production of mandelic acid and derivatives thereof is an example of this. A significant application of this type involves commercial production of (*R*)-mandelic acid in both high yield and high enantioselectivity from mandelonitrile. Mandelic acid and derivatives have found broad application as intermediates and resolving agents for the production of many chiral pharmaceutical and agricultural products. Previous attempts to

employ the few known nitrilases in processes using analogous substrates have been plagued by significantly lower activity, productivity, and selectivity.

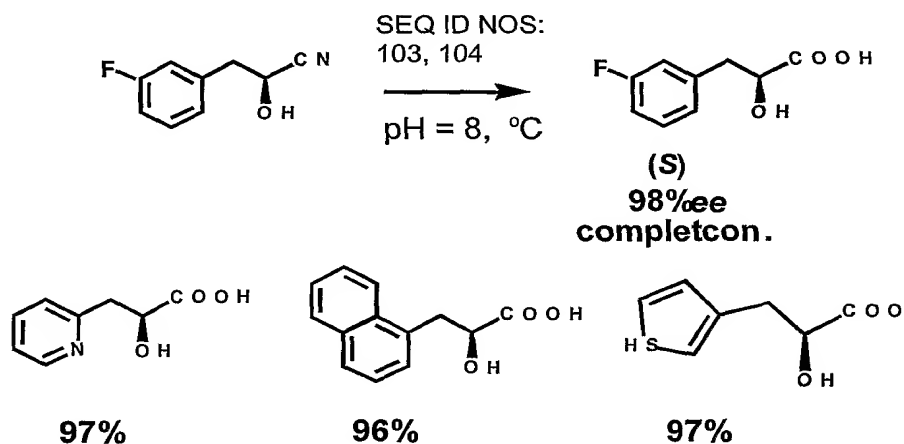


5

Phenylactic acid derivatives

[000264] An additional application is in the production of (*S*)-phenyl lactic acid derivatives in both high yield and high enantioselectivity. Phenyl lactic acid derivatives have found broad application in the production of many chiral pharmaceutical and agricultural products.

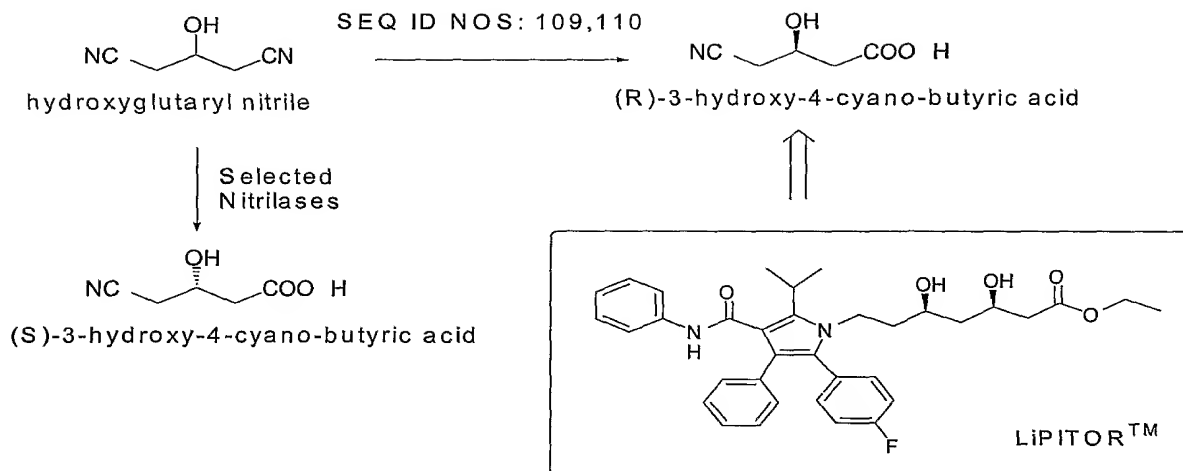
10



β-hydroxy acid

[000265] With important commercial considerations, nitrilases are provided produce either enantiomer of 4-cyano-3-hydroxybutyric acid, the (*R*)-enantiomer of which is a key intermediate in the synthesis of the drug LIPITOR™.

15



[000266] The following nitrilases are more examples of nitrilases useful in converting hydroxyglutaryl nitrile to (R)-3-hydroxy-4-cyano-butyric acid: SEQ ID NOS:205, 206, SEQ ID NOS:207, 208, SEQ ID NOS:195, 196, SEQ ID NOS:43, 44, SEQ ID NOS:321, 322, and SEQ ID NOS:237, 238. The above schematic indicates that "selected nitrilases" can be used to convert hydroxyglutaryl nitrile to (S)-3-hydroxy-4-cyano-butyric acid: SEQ ID NOS:107, 108, SEQ ID NOS:109, 110, SEQ ID NOS:111, 112, SEQ ID NOS:127, 128, SEQ ID NOS:129, 130, SEQ ID NOS:133, 134, SEQ ID NOS:113, 114, SEQ ID NOS:145, 146, SEQ ID NOS:101, 102, SEQ ID NOS:179, 180, SEQ ID NOS:201, 202, SEQ ID NOS:159, 160, SEQ ID NOS:177, 178, SEQ ID NOS:181, 182, SEQ ID NOS:183, 184, SEQ ID NOS:185, 186, SEQ ID NOS:57, 58, SEQ ID NOS:197, 198, SEQ ID NOS:59, 60, SEQ ID NOS:67, 68, and SEQ ID NOS:359, 360.

[000267] The invention will be further described with reference to the following examples; however, it is to be understood that the invention is not limited to such examples. Rather, in view of the present disclosure which describes the current best mode for practicing the invention, many modifications and variations would present themselves to those of skill in the art without departing from the scope and spirit of this invention. All changes, modifications, and variations coming within the meaning and range of equivalency of the claims are to be considered within their scope.

EXAMPLES

Example 1: Phagemid infections

[000268] For each library to be screened for nitrilases, an infection was set up as follows: 5ml of an $OD_{600nm}=1$ resuspension of SEL700 cells and 1ml of the phagemid library to be screened were combined. The combination was incubated in a 37°C waterbath for 45 min.

- 5 [000269] Using the infection, serial dilutions were made in 10mM $MgSO_4$, using 10 μ l aliquots of the infection.

	<u>titer of library</u>	<u>dilutions to make</u>
	$\sim 10^5$ cfu/ml	10^{-1} dilution
	$\sim 10^6$ cfu/ml	10^{-1} , 10^{-2} dilution
10	$\sim 10^7$ cfu/ml	10^{-1} , 10^{-2} , 10^{-3} dilution

[000270] 60 μ l of each of the following dilutions were deposited onto a small LB-kan⁵⁰ plate:

	<u>titer of library</u>	<u>dilutions to make</u>
	$\sim 10^5$ cfu/ml	undiluted infection, 10^{-1} dilution
	$\sim 10^6$ cfu/ml	10^{-1} , 10^{-2} dilutions
15	$\sim 10^7$ cfu/ml	10^{-2} , 10^{-3} dilutions

- [000271] The cells in the infection were centrifuged in a tabletop centrifuge at 4°C, 4.6k rpm, 10 min to form pellets. The supernatant was decanted from the resulting pellets. The cells were resuspended in residual liquid. All of the resuspended cells were deposited onto a single large LB-kan⁵⁰ plate. All plates were incubated at 30°C overnight.
- 20

Example 2: Selection Screenings

- [000272] The cells of each infection plate were resuspended with ~4mls 10mM $MgSO_4$. The resuspensions were placed in a tube. The remaining cells on each plate were resuspended with ~3mls 10mM $MgSO_4$ and combined with the first resuspension from the same plate. The volume of each tube was brought to 12ml with 10mM $MgSO_4$. The tubes were vortexed vigorously. The tubes were centrifuged in a tabletop centrifuge at 4°C and 4.6k for 10min to form pellets. The supernatant was decanted from each resuspension. The washed cells in each tube were resuspended with 10ml 10mM $MgSO_4$. The resuspensions from each library were stored at 4°C until the selection cultures were ready to be set up.
- 25
- 30

[000273] For each resuspension, selection cultures were set up using the following process:

- 1) The nitrilase selection medium was prepared, using: 1XM9 medium with 0.2% glucose, no nitrogen and 50 μ g/ml kanamycin (for pBK phagemid libraries only; use ampicillin for pBS libraries).
- 2) 5ml of the medium was aliquoted into a 50ml screw top conical tube.
- 3) 25 μ l of the stored resuspension was added to the tube.
- 4) 5 μ l of adiponitrile was added to the tube, to bring the final concentration to 8.8mM. Additional nitrile substrates may be used, in place of adiponitrile.
- 5) The resulting combination was cultured at 30°C.

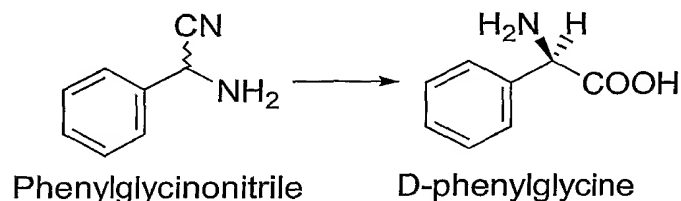
Steps 1-5 were repeated for each nitrile substrate.

Example 3: Isolation of a positive nitrilase clone from selection cultures

[000274] Ten (10) μ l of selection culture with growth was streaked out onto a small LB-kan⁵⁰ plate and allowed to grow for 2 nights at 30°C. Five isolated cfu were picked and each was grown in 2ml nitrilase selection medium at 30°C. Each culture was monitored (where growth indicates positive cfu was picked), and was removed when monitoring indicated that it was in a stationary phase of growth. One (1) ml of culture was used to do a plasmid preparation and was eluted with 40 μ l elution buffer. Five to eight (5-8) μ l DNA was cut with Pst I/Xho I or Sac I/Kpn I restriction enzymes to remove insert from vector. A restriction fragment length polymorphism (RFLP) determination was carried out to identify the size of the insert. The insert was sequenced.

Example 4: Screening and Characterization of Nitrilases

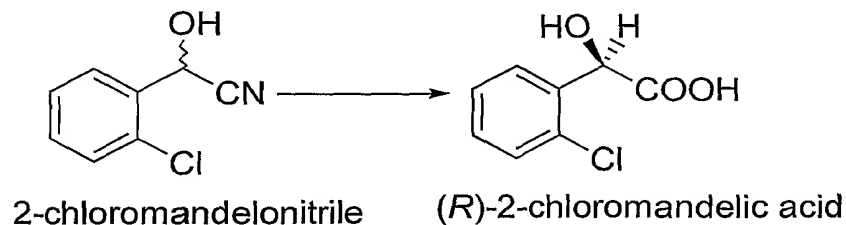
[000275] Nitrilases of the invention were screened against target substrates. Of those showing hydrolytic activity in a primary screen, enzymes with enantioselectivities above 20% enantiomeric excess (*ee*) were selected for further characterization. Those enzymes were selected based on: 1) having activity against one of the substrates of interest and 2) exhibition of greater than 35% *ee* (enantiomeric excess). The results of this screening process are set forth in Table 1 above. The products used for screening were: D-Phenylglycine, L-Phenyllactic acid, (*R*) 2-chloromandelic acid, (*S*)- Cyclohexylmandelic acid, L-2-methylphenylglycine, (*S*)-2-amino-6-hydroxy hexanoic acid, and 4-methyl-L-leucine.

Screening of nitrilases against target substrate D-Phenylglycine

[000276] The hydrolysis of phenylglycinonitrile was performed. Some of these enzymes showed an *ee* higher than 20% and those were selected for preliminary characterization.

[000277] Based on the preliminary characterization experiments, a number of putative hits were identified on phenylglycinonitrile and a large amount of data was accumulated on these enzymes. The data revealed many common properties: the majority of the enzymes had pH optima for activity at pH 7 and, in general, the enantioselectivity was enhanced at the lower pH values. The enzymes were found to be more active at higher temperature, particularly 38°C, although this temperature often resulted in lower enantioselectivities. The use of water-miscible co-solvents in the reaction was shown to be a practical option. The inclusion of 10-25% methanol (v/v) in the enzyme reactions did not substantially affect enzyme activity and in many cases, led to an increase in enantioselectivity. The use of biphasic systems has also shown some promise, with the enzymes maintaining their level of activity with the addition of up to 70% (v/v) of hexane and, in some cases, toluene. The use of ethyl acetate in the biphasic systems, however, led to lower activity.

[000278] Of the enzymes identified active on phenylglycinonitrile, the enantioselectivity of several enzymes was shown to remain above the success criterion of 35% *ee*. The preliminary characterization data indicated that some of the enzymes exhibited high enantioselectivities for D-phenylglycine, with corresponding conversion to product of 40-60%. Further investigation suggested that the rate of activity of some of these enzymes was faster than the rate of racemization of the substrate. Reducing the concentration of enzyme led to improved enantioselectivity; therefore, it appears that some benefit could be gained by control of the relative rates of the chemical racemization and the enzyme activity.

Screening of nitrilases against target substrate (*R*)-2-chloromandelic acid

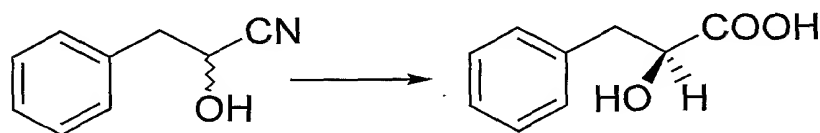
[000279] Enzymes were identified which showed activity on 2-chloromandelonitrile. A high degree of overlap existed between the enzymes which were active on 2-chloromandelonitrile and phenylglycinonitrile. Many of these enzymes also formed a distinct sequence family.

[000280] Higher temperatures and neutral pH appeared to lead to the highest activity for the active enzymes. For the majority of the nitrilases, the enantioselectivity also increased at higher temperatures, particularly 38°C. The enzymes retained their activity in the presence of up to 25% methanol or 10% isopropanol; in many of these cases, the enantioselectivity was also enhanced. Activity in biphasic systems was largely comparable to aqueous conditions, particularly with hexane as the non-aqueous phase; varying tolerances to toluene were observed between the different nitrilases.

Table 2. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-chloromandelonitrile.

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
385, 386	7	38	25% MeOH
169, 170	5	38	25% MeOH, 10% IPA
185, 186	7	38	25% MeOH, 10% IPA
47, 48	7	38	10% MeOH
197, 198	6	55	25% MeOH, 10% IPA
187, 188	7	38	10% MeOH; 40% IPA
217, 218	7	38	25% MeOH, 10% IPA, 70% hexane, 40% toluene
55, 56	7	38	10% MeOH, IPA, 70% hexane
167, 168	9	38	10% MeOH, IPA, 70% hexane
15, 16	7	38	25% MeOH, 10% IPA, 70% hexane, 40% toluene

Screening of nitrilases against target substrate (*S*)-phenyllactic acid:



Phenylacetaldehyde
cyanohydrin

(*S*)-Phenyllactic acid

5

[000281] Many of the nitrilases tested were active on phenylacetaldehyde cyanohydrin. Many of these enzymes were part of two related sequence families and were distinct from those enzymes that were active on phenylglycinonitrile and chloromandelonitrile.

[000282] The pH optima of the enzymes was generally above pH 7 (*i.e.* pH 8 or 9), with higher enantioselectivities being exhibited at these levels. Most of the enzymes showed superior activity at higher temperature, particularly 38°C. The effect of temperature on the enantioselectivities of the enzymes varied; in most cases, this property was slightly lower at

10

higher temperatures. While the enzymes were tolerant towards the addition of co-solvents, particularly 10% (v/v) methanol, no advantage in activity or enantioselectivity was gained by such additions. The use of a biphasic system was again shown to be feasible.

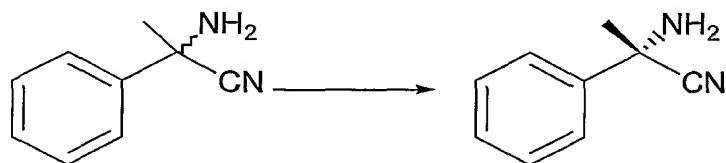
[000283] Table 3. Summary of optimal conditions determined from characterization

5 experiments for enantioselective hydrolysis of phenylacetaldehyde cyanohydrin

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
103, 104	7	55	10% MeOH, IPA
99, 100	8	38	10% MeOH, 70% hexane, toluene
183, 184	9	38	10% MeOH, IPA, 70% toluene, hexane
173, 174	5	38-55	25% MeOH, IPA, 70% hexane, toluene
213, 214	7	38	10% MeOH, 25% IPA, 70% hexane, toluene
61, 62	7	38	10% MeOH, 70% hexane, toluene
205, 206	8	38-55	10% MeOH, IPA, 40% hexane, toluene
207, 208	8	38	10% MeOH, 70% hexane
309, 210	8	38	10% MeOH, 40% hexane, toluene
195, 196	8	38	10% MeOH, 40% hexane, toluene
43, 44	9	38	10% MeOH, 40% hexane
161, 162	9	38	25% MeOH, IPA, 10% hexane, toluene
175, 176	6	38-55	10% MeOH, IPA, 40% hexane

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
293, 294	6	38	10% MeOH, IPA, 40% hexane

Screening of nitrilases against target substrate L-2-methylphenylglycine

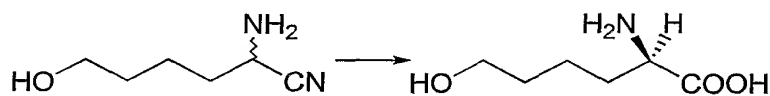


2-methylphenylglycinonitrile

L-2-methylphenylglycine

[000284] Nitrilases have shown activity on this substrate and preferentially yielded the D-2-methylphenylglycine, rather than the required L-2-methylphenylglycine.

Screening of nitrilases against target substrate L-hydroxynorleucine ((S)-2-amino-6-hydroxy hexanoic acid)

5-hydroxypentanal
aminonitrile

L-hydroxynorleucine

[000285] A number of nitrilases, which showed activity on 2-amino-6-hydroxy hexanenitrile, were isolated. All of these enzymes showed enantioselectivity towards the L-isomer of the product.

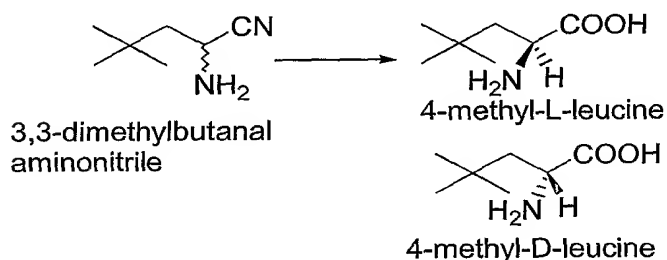
[000286] The enzymes all showed higher enantioselectivities at higher pH and appeared to more susceptible to the addition of solvents than the other nitrilases tested. Although activity was detected in the presence of organic solvents, it was generally lower than that of the aqueous control. Once again, the activity of the enzymes was negatively affected by the acid product and aldehyde starting material.

Table 4. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-amino-6-hydroxy hexanenitrile.

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent
217, 218	9	38	10% MeOH
55, 56	9	38	None
187, 188	9	38	10% MeOH
167, 168	9	38	None
221, 222	9	38	

[000287] A range of hydrolytic activities was observed among the confirmed hit enzymes for 2-amino-6-hydroxy hexanenitrile.

5 Screening of nitrilases against target substrate 4-methyl-D-leucine and 4-methyl-L-leucine

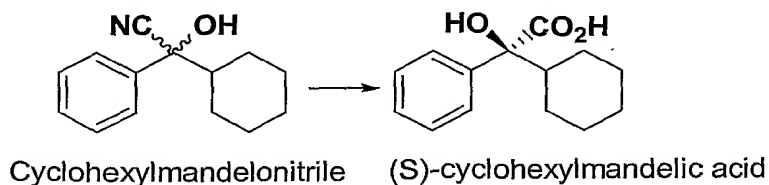


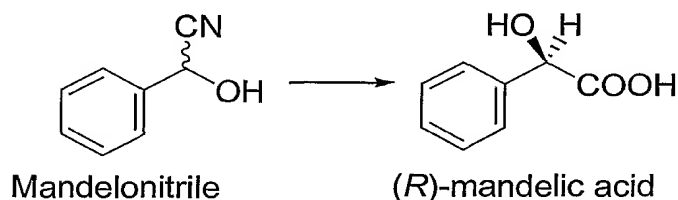
[000288] Hydrolysis of 2-amino-4,4-dimethyl pentanenitrile was performed by several of the nitrilases. Of these, some were shown to hydrolyse the nitrile to the L-isomer of the corresponding acid and were selected for further characterization.

10 Table 5. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-amino-4,4-dimethyl pentanenitrile

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
103, 104	7	23	25% MeOH, 10% IPA
59, 60	8	23	25% MeOH
221, 222	6	38	25% MeOH, 10% IPA

Screening of nitrilases against target substrate (S)-cyclohexylmandelic acid



Screening of nitrilases against target substrate Mandelonitrile

- 5 [000289] The nitrilase collection was also screened on mandelonitrile. The nitrilases actively hydrolyzed both phenylglycinonitrile and chloromandelonitrile.

Enzymatic assay for determination of enantioselectivity

- [000290] In the design of a spectroscopic system for determination of the chiral α -hydroxy acids and α -amino acids, an enzyme based assay which permits the detection of product
10 formation and enantioselectivity was developed and used.

- [000291] Spectroscopic systems for the detection of α -hydroxy- and for α -amino- acids based on lactate dehydrogenase (L-LDH & D-LDH) and on amino acid oxidase (L-AA Oxid & D-AA Oxid) are described in Figures 6 and 7. These enzymes were chosen because they are reported to have reasonably broad substrate ranges while still retaining near absolute
15 enantiospecificity.

- [000292] The overall feasibility of this system has been established (Table 12). Neither the parent hydroxynitrile nor the aminonitrile is metabolized by the secondary or detection enzyme and thus starting material does not interfere. Cell lysate which is not heat treated results in background activity for the LDH system; however, heat inactivation eliminates the
20 background activity. Cell lysate does not appear to interfere in the AA Oxidase assay. One concern is the inactivation of the AA Oxidase, which utilizes a FMN co-factor, by residual cyanide. However, the control studies indicated that at 2 mM PGN (which could release up to 2 mM HCN) inactivation is not a problem. This assay is suitable for automation of 384 well (or possibly greater density) microtiter plates.

- 25 Table 6: Summary of Identification of Secondary Enzyme to Chiral Detection of Acid Product.

SUBSTRATE	ENZYME WITH SUITABLE ACTIVITY FOUND FROM COMMERCIAL SOURCE
Hydroxy Acid Products:	
L-lactic acid	YES
D-lactic acid	YES
L-phenyl lactic acid	YES
D-phenyl lactic acid	YES
S-cyclohexylmandelic acid ¹	<i>Not applicable</i>
R-cyclohexylmandelic acid ¹	<i>Not applicable</i>
Amino Acid Products:	
4-methyl-L-leucine	YES
4-methyl-L/D-leucine	YES (D-unknown)
D-phenylalanine	YES
R-phenylglycine	YES
L-homophenyllactic acid	YES
D-homophenyllactic acid	YES
L-homophenylalanine	YES
D-homophenylalanine	YES
(S)-2-amino-6-hydroxy hexanoic acid	YES
(R/S)-2-amino-6-hydroxy hexanoic acid	YES (D-unknown)
L-methylphenylglycine ¹	1. <i>Not Applicable</i>
D-methylphenylglycine ¹	<i>Not Applicable</i>

¹: The assay will not be applicable to cyclohexylmandelic acid and 2-methylphenylglycine, as tertiary alcohols are not amenable to this particular oxidation

5 Example 5: Standard assay conditions

[000293] The following solutions were prepared:

- Substrate stock solution: 50 mM of the aminonitrile substrate in 0.1 M phosphate buffer (pH 7) or 50 mM of the cyanohydrin substrate in 0.1 M Na Acetate buffer (pH 5)
- Enzyme stock solution: 3.33 ml of 0.1 M phosphate buffer (pH 7) to each vial of 20 mg of lyophilized cell lysate (final concentration 6 mg protein/ml)

[000294] Procedure:

- Add 100 µl of the 50 mM substrate solution to the appropriate number of wells of a 96-well plate
- Add 80 µl of buffer to each well
- Add 20 µl of enzyme solution to each well
- Blank controls were set up by substitution of 20 µl of buffer for the enzyme solution

• Negative controls consisting of 20 µl of enzyme solution in 180 µl of buffer were also included in many of the experiments. Once it had been established that the cell lysate did not interfere with the detection of the products, these controls were not included.

[000295] Sampling of reactions:

5 • The reactions were sampled by removing an aliquot from each well (15-50 µl) and diluting the samples as follows:

• Samples for non-chiral HPLC analysis:

10 • Phenylglycine, 2-chloromandelic acid and phenyllactic acid: initially, the samples were diluted 2-fold with water and a further 2-fold with methanol or acetonitrile (final dilution: 4-fold). It was found that an 8-fold dilution of these samples led to improved chromatographic separation

15 • (S)-2-amino-6-hydroxy hexanoic acid, 4-methylleucine, *t*-leucine, 2-methylphenylglycine and cyclohexylmandelic acid: samples were diluted 1:1 with methanol or acetonitrile. The choice of solvent was based on the solvent used in the HPLC analysis method.

[000296] • Samples for chiral HPLC analysis:

20 • Phenylglycine, 2-chloromandelic acid and phenyllactic acid: as described above for the non-chiral analyses, the samples for chiral analyses were initially diluted 2-fold and in the later stages of the project, at 4-fold.

• (S)-2-amino-6-hydroxy hexanoic acid, 4-methylleucine, *t*-leucine, 2-methylphenylglycine: samples were diluted 1:1 with methanol or acetonitrile.

[000297] • For each experiment, a standard curve of the product was included in the HPLC run. The curve was plotted on an X-Y axis and the concentration of product in the samples calculated from the slope of these curves.

25 [000298] • For the preliminary characterization experiments, samples were taken such that the activity of the enzymes was in the linear phase; this was performed so that differences in the effects of the parameters on the rate of reaction, rather than the complete conversion, could be determined. The sampling times are denoted in the tables included in the text.

[000299] • The samples were analyzed by HPLC, using the methods outlined in Table 20 and 21.

Example 6: Determination of the Effect of pH on enzyme activity and enantioselectivity

[000300] The effect of pH on the enzyme activity and enantioselectivity was studied by performance of the standard assay in a range of different buffers:

0.1 M Citrate Phosphate pH 5

5 0.1 M Citrate Phosphate pH 6

0.1 M Sodium Phosphate pH 7

0.1 M Tris-HCl pH 8

M Tris-HCl pH 9

10 [000301] The samples were analyzed by non-chiral and chiral HPLC methods and examples of the results are presented in Tables 5, 8 and 11 herein.

Example 7: Determination of the effect of temperature on enzyme activity and enantioselectivity

15 [000302] The effect of temperature on the activity and enantioselectivity was investigated by performing the standard assay at room temperature, 38°C and 55°C. The samples were analyzed by non-chiral and chiral HPLC methods and examples of the results are given in Tables 5, 8 and 11 herein.

Example 8: Determination of the Effect of solvents on enzyme activity and enantioselectivity

20 [000303] The enzyme reactions were performed in the presence of cosolvents and as biphasic systems, in order to investigate the effect of water-miscible and water-immiscible solvents on the enzymes. In the presence of cosolvents, the reactions were run under standard conditions, with substitution of the buffer with methanol or isopropanol. The final concentrations of solvent in the reactions was 0, 10, 25 and 40% (v/v).

25 [000304] The biphasic reactions were also carried out under standard conditions, with a layer of water-immiscible organic solvent forming the nonaqueous phase. The solvent was added at the following levels: 0%, 10%, 40% and 70% (v/v) of the aqueous phase. The samples from these reactions were evaporated by centrifugation under vacuum and redissolved in a 50:50 mixture of methanol or acetonitrile and water. The samples were
30 analyzed by non-chiral and chiral HPLC methods.

Example 9: Determination of the Effect of process components on enzyme activity and enantioselectivity

Activity

[000305] The effect of the process components on the activity of the enzymes was established by addition of the individual components to the enzymatic reaction. These components included the starting materials for the nitrile synthesis, aldehyde, cyanide and ammonium, as well as triethylamine, which is added in catalytic amounts to the nitrile synthesis reaction. The concentrations of the reactants were selected with possible process conditions in mind and were adapted to the levels of reactants used in the enzyme assays. In some cases, the solubility of the aldehydes and products was relatively low; in these cases, the highest level of solubility was added to the reactions as the highest level and 10% of this level as the lower value.

[000306] The enzymatic reactions were carried out under standard conditions, with addition of one or more of the following components: benzaldehyde, phenylglycine, phenylacetaldehyde, phenyllactic acid, 2-chlorobenzaldehyde, 2-chloromandelic acid, 5-hydroxypentanal, (S)-2-amino-6-hydroxy hexanoic acid, 4-methylleucine, KCN, Triethylamine, NH₄Cl. Control reactions were performed under standard conditions, with no additive. The samples were analyzed by non-chiral HPLC.

Stability

[000307] The stability of the enzymes to process conditions was monitored by incubation of the enzymes in the presence of the individual reaction components for predetermined time periods, prior to assay of the enzyme activity under standard conditions. In these experiments, the enzymes were incubated at a concentration of 1.2 mg protein/ml in the presence of each of the following reaction components: methanol, benzaldehyde, phenylglycine, phenylacetaldehyde, phenyllactic acid, 2-chlorobenzaldehyde, 2-chloromandelic acid, 5-hydroxypentanal, (S)-2-amino-6-hydroxy hexanoic acid, KCN, NH₄Cl.

Assay conditions:

[000308] At 0, 2, 6 and 24 hours of incubation in the particular additive, 50 µl of the enzyme solution was removed, 50 µl of a 50 mM substrate stock solution added and the enzyme activity assayed under standard conditions. After substrate addition, the reactions were sampled at the following times: Phenylglycinonitrile: 10 mins; Phenylacetaldehyde cyanohydrin: 1 hour; 2-chloromandelonitrile: 2 hours. Control reactions were performed by

incubation of the enzyme in buffer only. The samples were analyzed using non-chiral HPLC methods.

Example 10: Confirmation of putative hit enzymes

[000309] Following the preliminary characterization experiments, the enzymes which were identified as putative hits were assayed under the optimal conditions determined, in order to evaluate their performance, especially in terms of enantioselectivity, when higher conversions were attained. The enzymes were assayed with 25 mM substrate, under the conditions of pH and temperature noted in the tables included in the text. A standard concentration of 0.6 mg/ml protein was used for each of the enzymes, unless otherwise stated.

Example 11: Selected examples of chromatograms from enzyme reactions

[000310] In this section, representative examples of chromatograms for each substrate and product combination will be shown, together with a discussion of some of the challenges encountered with the methods and how they were addressed.

D-Phenylglycine

[000311] Non-chiral analysis showing the substrate peak eluting at 2.6 min and 3.2 min. See Figures 8A-8E. The two peaks were present in all samples containing higher concentrations of the nitrile; the second peak is thought to be a product associated with the nitrile; it decreased with time and was no longer present once complete conversion to the product had taken place. The chromatogram shown in Figure 8A is a blank control, containing only nitrile and buffer; the samples were all diluted with water and solvent as explained in section 1 above. This was repeated for all samples discussed below. An enzymatic reaction sample is shown in the chromatogram in Figure 8B, with the product eluting at 0.4 min.

[000312] Of note in these chromatograms is the small solvent front peak eluting at 0.3 min. Further representation of this peak is given in the chromatogram shown in Figure 8C, in which a negative control consisting of cell lysate in buffer, was run. A very small peak coeluted with the product at 0.4 min. In the initial phase of the project, this peak was regarded as problematic, although the appropriate controls were run with each experiment in order to maintain accuracy. In these experiments, the peak area resulting from the cell lysate, although it was relatively small, was subtracted from the peak areas of the product in the enzymatic reactions. Improvement of this analysis was obtained by further dilution of the samples and the use of lower injection volumes on the HPLC. Following the implementation

of these improvements, interference by this peak was shown to be minimal, as shown in the chromatogram illustrated in Fig. 6C.

[000313] The chiral analysis of phenylglycine is shown in chromatogram in Fig. 6D with the L-enantiomer eluting at 6 min and the D-enantiomer at 11 min. Good resolution between the two isomers was obtained. However, the column used was very sensitive and the characteristics of the column appeared to change over time, resulting in changes in the elution times of the acids. While this was easily detected by the use of the proper controls and standards, a greater problem existed in the coelution of the nitrile peak with the D-enantiomer (chromatogram shown in Fig. 6E). The cause of this coelution was unclear; however, it was easily detected by the use of appropriate standards; in addition, the UV spectrum of the acid was very distinctive, making the use of this tool effective in detecting the coelution. The problem was also easily resolved by adjusting the methanol content in the mobile phase.

(R)-2-chloromandelic acid

[000314] The HPLC analysis of chloromandelic acid and chloromandelonitrile offered many of the challenges associated with the analysis of the phenylglycine samples. From the chromatogram shown in Fig. 7A, which contains only chloromandelonitrile in buffer, it is evident that a peak eluted at the same time as the product in the chromatogram shown in Fig. 7B, which represents a chloromandelic acid standard. The contribution of the cell lysate to this peak was found to be small; it would appear that the greatest contribution to this peak was from the chloromandelonitrile, either from a breakdown product or a contaminant in the nitrile preparation. The peak area remained constant throughout each experiment and, using the appropriate controls, it was found that subtraction of the peak area from that of the product yielded sufficient accuracy. Many attempts were made to change the HPLC conditions so that the product peak eluted at a later time; however, these attempts were not successful. Chromatogram shown in Fig. 7C illustrates the appearance of product and the reduction of the substrate peaks.

[000315] The chiral analysis of chloromandelic acid was almost problem-free. The elution of a small peak at the same time as the (S)-enantiomer presented some concern (the peak at 2.4 min in chromatogram shown in Fig. 7D). However, once it was established that this peak was present in all the samples at the same level, including the blank control, and that it had a different UV spectrum to that of the chloromandelic acid peak, it was not regarded as a problem. Consequently, it was subtracted from the peak eluting at 2.4 min in each sample. The (R)-enantiomer eluted at 3 minutes.

(S)-phenyllactic acid

[000316] The analysis of phenyllactic acid was initially plagued with the same problems discussed for phenylglycine and 2-chloromandelic acid. However, in this case, adjustment of the solvent concentration in the nonchiral HPLC method led to a shift in the retention time of the acid, so that it no longer coeluted with the cell lysate peak. Following this, no problems were encountered with either the nonchiral or chiral methods. Representative nonchiral chromatograms of the product (1.9 min) and cyanohydrin substrate (3.7 min) are shown in Fig. 8A, while the chiral analysis of the acid is shown in Fig. 8B, with the L-enantiomer eluting at 2 min and the opposite enantiomer at 6 min.

L-2-methylphenylglycine

[000317] The analysis of methylphenylglycine was unproblematic, although the nonchiral method did not provide baseline separation between a cell lysate peak and the product peak, as shown in the chromatogram illustrated in Fig. 9A. The amino acid standard for this method was provided in the final stages of the project, thus minimizing the time for method development. In the chromatogram shown in Fig. 9A the amino acid elutes at 0.7 min and the aminonitrile at 5.0 min. Sufficient separation between the two initial peaks was obtained to allow the calculation of approximate conversion to product.

[000318] The chiral analysis of this compound provided good separation between the two enantiomers, as shown in the chromatogram illustrated in Fig. 9B. The L-enantiomer elutes at 5 min and the D-enantiomer at 8 min.

L-tert-leucine

[000319] For the nonchiral analysis of *t*-leucine, the cell lysate presented the most serious problem amongst the group of products for this project. This was compounded by the low spectroscopic properties of the amino acid, leading to difficulty in differentiating the product peak from the cell lysate. Good separation of the individual product enantiomers was obtained by chiral analysis as shown in Fig. 10A. During the primary screen, a small peak eluted at the same time as the L-amino acid standard in certain samples (see Fig. 10B) and was thought to be the amino acid. However, further development of the method and the use of the appropriate controls established that this peak was actually a cell lysate peak.

[000320] The aminonitrile eluted between the two *t*-leucine peaks, as shown in Fig. 10C; this chromatogram also shows the cell lysate peak at 4.8 min. The UV spectrum of the nitrile was distinct from that of the amino acid, making it easier to differentiate from the acid peaks.

L-hydroxynorleucine ((S)-2-amino-6-hydroxy hexanoic acid)

[000321] The chiral analysis of (S)-2-amino-6-hydroxy hexanoic acid was consistent and reliable. By contrast, the nonchiral method presented many problems, primarily as a result of non-separation between the nitrile and the acid peaks. Towards the latter half of the project, a method was developed and used successfully for the confirmation of activities. Prior to this, most of the analysis was performed using the chiral method; standard curves of the products were run in order to quantify the reactions. A representative chromatogram of (S)-2-amino-6-hydroxy hexanoic acid is shown in Figure 11A, with (S)-2-amino-6-hydroxy hexanoic acid eluting at 6 min. The aminonitrile was not detected by this method.

[000322] Separation of the individual 2-amino-6-hydroxy hexanoic acid enantiomers is shown in Fig. 11B. The L-enantiomer elutes first, at 2 min, followed by the D-enantiomer at 3 min. In Fig. 11C, an enzymatic sample is represented; the only area of slight concern is the negative peak preceding the elution of the L-enantiomer. However, it did not appear to interfere significantly with the elution of this enantiomer; method development did not eliminate the negative peak.

4-methyl-D-leucine and 4-methyl-L-leucine

[000323] For the detection of 4-methylleucine, the chiral HPLC method again proved more reliable. The combination of low activities, together with the low sensitivity of the method to the compound led to difficulties in detection using nonchiral HPLC. A 2.5 mM standard of the amino acid is shown in Fig. 12A, with a peak height of approximately 40 mAU; this was substantially lower than those detected for the aromatic compounds. Chromatogram in Fig. 12B shows an enzymatic sample, in which conversion was detected using the chiral HPLC method; while it is not clear, it would appear that the 4-methylleucine peak elutes at 2.7 min and is extremely low in both peak height and area. This peak did not appear in samples which were negative by chiral HPLC analysis.

[000324] The chiral analysis of 4-methyl-L-leucine and 4-methyl-D-leucine did not present any problems. The L-enantiomer eluted at 5 min and the D-enantiomer at 7 min, although some peak shift did occur, as a result of the sensitivity to the column, described in section (i) for phenylglycine. In chromatograms shown in Figs. 14C-14D, the separation of these amino acids is shown; the first sample represents an enzyme which produced both enantiomers and in the second sample, the enzyme preferentially hydrolyzed the L-enantiomer, with a small amount D-amino acid forming.

(S)-cyclohexylmandelic acid

[000325] Chromatograms of the standards for cyclohexylmandelic acid (Fig. 13A) and the corresponding nitrile (Fig. 13B) are shown. The acid eluted at 1.3 min, while the cyanohydrin was observed at 2.5 min. The peak eluting at 2.1 min is thought to be the cyclohexylphenylketone, as shown by the elution of a ketone standard at this point.

Example 12: An Enzyme Library Approach to Biocatalysis: Development of a Nitrilase Platform for Enantioselective Production of Carboxylic Acid Derivatives

[000326] Biocatalytic processes can offer unique advantages in transformations that are challenging to accomplish through conventional chemical methods (Wong, C.-H.;

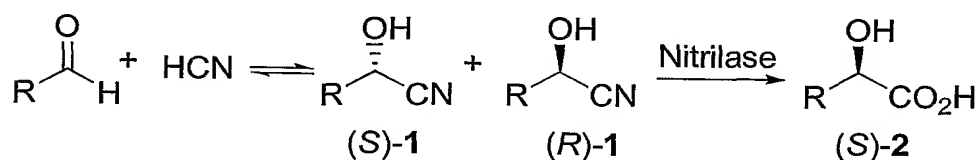
Whitesides, G.M. *Enzymes in Synthetic Organic Chemistry*; Pergamon, New York, 1994; Drauz, K.; Waldmann, H., Roberts, S.M. Eds. *Enzyme Catalysis in Organic Synthesis*; VCH: Weinheim, Germany, 2nd ed., 2002). Nitrilases (EC 3.5.5.1) promote the mild hydrolytic conversion of organonitriles directly to the corresponding carboxylic acids (Kobayashi, M.; Shimizu, S. *FEMS Microbiol. Lett.* **1994**, 120, 217; Bunch, A.W. In *Biotechnology*; Rehm, H.-J.; Reed, G.; Puhler, A.; Stadler, P., Eds.; Wiley-VCH: Weinheim, Germany, Vol. 8a, Chapter 6, pp 277-324; Wieser, M.; Nagasawa, T. In *Stereoselective Biocatalysis*; Patel, R.N., Ed.; Marcel Dekker: New York, 2000, Chapter 17, pp 461-486.) Fewer than fifteen microbially-derived nitrilases have been characterized and reported to date. (Harper, D.B. *Int. J. Biochem.* **1985**, 17, 677; Levy-Schil, S.; Soubrier, F.; Crutz-Le Coq, A.M.; Faucher, D.; Crouzet, J.; Petre, D. *Gene* **1995**, 161, 15; Yu, F. 1999, US Patent 5872000; Ress-Loschke, M.; Friedrich, T.; Hauer, B.; Mattes, R.; Engels, D. PCT Appl. WO 00/23577, April 2000.). Several nitrilases previously have been explored for the preparation of single-enantiomer carboxylic acids, although little progress has been made in the development of nitrilases as viable synthetic tools. This application describes the discovery of a large and diverse set of nitrilases and herein demonstrate the utility of this nitrilase library for identifying enzymes that catalyze efficient enantioselective production of valuable hydroxy carboxylic acid derivatives.

[000327] In an effort to access the most diversified range of enzymes that can be found in Nature, we create large genomic libraries by extracting DNA directly from environmental samples that have been collected from varying global habitats. (For a description of these methods, see: Short, J.M. *Nature Biotech.* **1997**, 15, 1322; Handelsman, J.; Rondon, M.J.; Brady, S.F.; Clardy, J.; Goodman, R.M. *Chem. Biol.* **1998**, 5, R245; Henne, A.; Daniel, R.; Schmitz, R.A.; Gottschalk, G. *Appl. Environ. Microbiol.* **1999**, 65, 3901.). We have

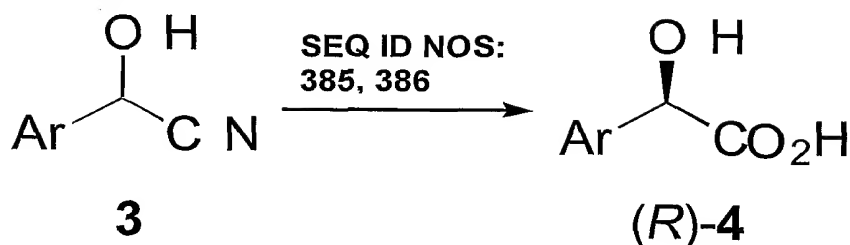
established a variety of methods for identifying novel activities through screening mixed populations of uncultured DNA. (Robertson, D.E.; Mathur, E.J.; Swanson, R.V.; Marrs, B.L.; Short, J.M. *SIM News* **1996**, 46, 3; Short, J.M. US Patent 5,958,672, **1999**; Short J.M. US Patent 6,030,779, **2000**.) Through this approach, nearly 200 new nitrilases have been discovered and characterized. (For a concise description of the studies, see Materials and Methods section below.) All nitrilases were defined as unique at the sequence level and were shown to possess the conserved catalytic triad Glu-Lys-Cys which is characteristic for this enzyme class. (Pace, H.; Brenner, C. *Genome Biology* **2001**, 2, 0001.1-0001.9.) Each nitrilase in our library was overexpressed and stored as a lyophilized cell lysate in order to facilitate rapid evaluation of the library for particular biocatalytic functions.

[000328] The initial investigations focused upon the efficacy of nitrilases for production of α -hydroxy acids **2** formed through hydrolysis of cyanohydrins **1**. Cyanohydrins are well-documented to racemize readily under basic conditions through reversible loss of HCN. (Inagaki, M.; Hiratake, J.; Nishioka, T.; Oda, J.; *J. Org. Chem* **1992**, 57, 5643. (b) van Eikeren, P. US Patent 5,241,087, 1993.) Thus, a dynamic kinetic resolution process is possible whereby an enzyme selectively hydrolyzes only one enantiomer of **1**, affording **2** in 100% theoretical yield and with high levels of enantiomeric purity.

[000329] One important application of this type involves commercial production of (*R*)-mandelic acid from mandelonitrile. (Ress-Loschke, M.; Friedrich, T.; Hauer, B.; Mattes, R.; Engels, D. PCT Appl. WO 00/23577, April 2000; Yamamoto, K.; Oishi, K.; Fujimatsu, I.; Komatsu, K. *Appl. Environ. Microbiol.* **1991**, 57, 3028; Endo, T.; Tamura, K. US Patent 5,296,373, March 1994.) Mandelic acid and derivatives find broad use as intermediates and resolving agents for production of many pharmaceutical and agricultural products. (Coppola, G.M.; Schuster, H.F. *Chiral α -Hydroxy Acids in Enantioselective Synthesis*; Wiley-VCH: Weinheim, Germany: 1997.) However, the few known nitrilases derived from cultured organisms have not been found useful for efficient and selective hydrolysis of analogous substrates.



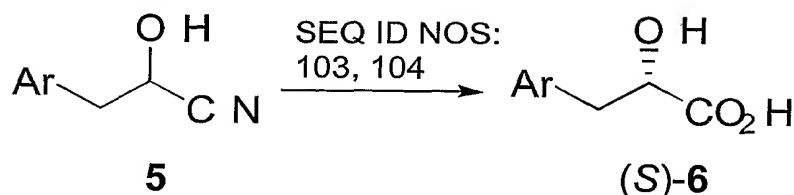
[000330] The nitrilase library was screened for activity and enantioselectivity in the hydrolysis of mandelonitrile (**3a**, Ar = phenyl) to mandelic acid. Preliminary results revealed



that 27 enzymes afforded mandelic acid in >90% ee. One enzyme, SEQ ID NOS:385, 386, was studied in greater detail and was found to be very active for hydrolysis of mandelonitrile. Under standard conditions using 25 mM 3a and 0.12 mg/mL enzyme in 10% MeOH (v/v) 0.1 M phosphate buffer at 37°C and pH 8, (R)-mandelic acid was formed quantitatively within 10 min and with 98% ee. To confirm synthetic utility, the reaction was performed using 1.0 g 3a (50 mM) and 9 mg nitrilase (0.06 mg/mL nitrilase I); after 3 h (R)-mandelic acid was isolated in high yield (0.93 g, 86%) and again with 98% ee.

(a) Reactions were conducted under standard conditions (see text). Reaction time for complete conversion to 4 was 1-3 h. Entries 8-9 were conducted at pH 9 and 5 mM substrate concentration. (b) Specific activities were measured at 5 min transformation timepoints and are expressed as $\mu\text{mol mg}^{-1} \text{ min}^{-1}$. (c) TOF = turnover frequency, mol product/mol catalyst/sec. (d) Enantioselectivities were determined by chiral HPLC analysis. Hydroxy acids were isolated and absolute configurations were determined to be (R) in all cases.

[000331] The substrate scope of SEQ ID NOS:385, 386 was next explored. As shown in Table 13, a broad range of mandelic acid derivatives as well as aromatic and heteroaromatic analogues (4) may be prepared through this method. SEQ ID NOS:385, 386 tolerates aromatic ring substituents in the *ortho*-, *meta*-, and *para*-positions of mandelonitrile derivatives and products of type 4 were produced with high enantioselectivities. Other larger aromatic groups such as 1-naphthyl and 2-naphthyl also are accommodated within the active site, again affording the acids 4 with high selectivity (Table 13, entries 8-9). Finally, 3-pyridyl and 3-thienyl analogues of mandelic acid were prepared readily using this process (Table 13, entries 10-11). This is the first reported demonstration of a nitrilase that affords a range of mandelic acid derivatives and heteroaromatic analogues of type 4. High activity on the more sterically encumbered *ortho*-substituted and 1-naphthyl derivatives is particularly noteworthy.



[000332] We next examined the preparation of aryllactic acid derivatives **6** through hydrolysis of the corresponding cyanohydrins **5**. Phenyllactic acid and derivatives serve as versatile building blocks for the preparation of numerous biologically active compounds.

(Coppola, G.M.; Schuster, H.F. *Chiral α -Hydroxy Acids in Enantioselective Synthesis*;

- 5 Wiley-VCH: Weinheim, Germany: **1997**.) Upon screening our nitrilase library against the parent cyanohydrin **5a** (Ar = phenyl), we found several enzymes that provided **6a** with high enantiomeric excess. One enzyme, SEQ ID NOS: 103, 104, was further characterized. After optimization, SEQ ID NOS:103, 104, was shown to provide (*S*)-phenyllactic acid (**6a**) with complete conversion (50 mM) and very high enantioselectivity (98% ee) over 6 h. The
- 10 highest enantioselectivity previously reported for biocatalytic conversion of **5** to **6** was 75% ee achieved through a whole cell transformation using a *Pseudomonas* strain. (Hashimoto, Y.; Kobayashi, E.; Endo, T.; Nishiyama, M.; Horinouchi, S. *Biosci. Biotech. Biochem.* **1996**, 60, 1279.)

Table 7. Nitrilase II-catalyzed production of aryllactic acid derivatives and analogues **6**^a

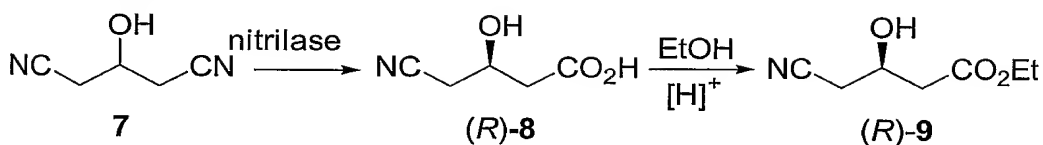
Entry	Ar in 6	Spec. Act. ^b	TOF ^c	% ee ^d
1	C ₆ H ₅	25	16	99
2	2-Me-C ₆ H ₅	160	100	95
3	2-Br-C ₆ H ₅	121	76	95
4	2-F-C ₆ H ₅	155	97	91
5	3-Me-C ₆ H ₅	21	13	95
6	3-F-C ₆ H ₅	22	14	99

7	1-naphthyl	64	40	96
8	2-pyridyl	10.5	6.6	99
9	3-pyridyl	11.6	7.2	97
10	2-thienyl	3.4	2.1	96
11	3-thienyl	2.3	1.4	97

(a) Reaction conditions as in Table 13, except 0.016 mg/mL nitrilase was used. Full conversion to **6** was observed within 6 h. (b)-(d) See Table 13. The absolute configuration was determined to be (*S*) for phenyllactic acid and entries 2-11 were assigned (*S*) based upon identical chiral HPLC peak elution order.

5 [000333] *Ortho* and *meta* substituents appear to be tolerated well by nitrilase II, with *ortho* substituted derivatives surprisingly being converted with higher rates relative to the parent substrate **5a**. Novel heteroaromatic derivatives, such as 2-pyridyl-, 3-pyridyl, 2-thienyl- and 3-thienyllactic acids, were prepared with high conversions and enantioselectivities (entries 8-11). Unexpectedly, *para* substituents greatly lowered the rates
10 of these reactions, with full conversion taking over two weeks under these conditions.

[000334] The final transformation that we examined was desymmetrization of the readily available prochiral substrate 3-hydroxyglutarylnitrile (**7**) (Johnson, F.; Panella, J.P.; Carlson, A.A. *J. Org. Chem.* **1962**, 27, 2241) to afford hydroxy acid (*R*)-**8** which, once esterified to (*R*)-**9**, is an intermediate used in the manufacture of the cholesterol-lowering
15 drug LIPITORTM. Previously reported attempts to use enzymes for this process were unsuccessful and **8** was produced with low selectivity (highest: 22% ee) and the undesired (*S*)-configuration. (Crosby, J.A.; Parratt, J.S.; Turner, N.J. *Tetrahedron: Asymmetry* **1992**, 3, 1547; Beard, T.; Cohen, M.A.; Parratt, J.S.; Turner, N.J. *Tetrahedron: Asymmetry* **1993**, 4, 1085; Kakeya, H.; Sakai, N.; Sano, A.; Yokoyama, M.; Sugai, T.; Ohta, H. *Chem. Lett.* **1991**,
20 1823.)



[000335] The nitrilase library was screened and unique enzymes were discovered and isolated that provided the required product (R)-8 with high conversion (>95%) and >90% *ee*. Using one of the (R)-specific nitrilases, this process was operated on a 1.0 g scale (240 mM 7, 30 mg enzyme, 22°C, pH 7) and after 22 h, (R)-8 was isolated in 98% yield and 95% *ee*. Interestingly, the same screening program also identified nitrilases that afford the opposite enantiomer (S)-8 with 90-98% *ee*. Thus, the extensive screen of biodiversity has uncovered enzymes that provide ready access to either enantiomer of the intermediate 8 with high enantioselectivities. Our discovery of the first enzymes that furnish (R)-8 underscores the advantage of having access to a large and diverse library of nitrilases.

[000336] By plumbing our environmental genomic libraries created from uncultured DNA, we have discovered a large array of novel nitrilases. This study has revealed specific nitrilases that furnish mandelic and aryl lactic acid derivatives, as well as either enantiomer of 4-cyano-3-hydroxybutyric acid in high yield and enantiomeric excess.

Procedures and Analytical Data:

[000337] Hydroxyglutaryl nitrile was purchased from TCI America and used as received. Amino acids used for the preparation of aryl lactic acid standards were purchased from PepTech (Cambridge, MA). (R)-3-hydroxy-4-cyanobutyric acid was obtained from Gateway Chemical Technology (St. Louis, MO). Both (R)- and (S)- mandelic acid and (R)- and (S)- phenyl lactic acid standards were purchased from Sigma Aldrich. All other reagents were purchased from Sigma Aldrich and utilized without further purification. Silica Gel, 70-230 mesh, 60 Å, purchased from Aldrich, was used for chromatographic purifications. All ¹H NMRs and ¹³C NMRs were run on Bruker model AM-500 machines, set at room temperature, 500 MHz and 125MHz respectively for ¹H and ¹³C. Mass analyses and unit mass resolution was achieved by flow injection analysis (FIA) using a Perkin-Elmer Sciex API-4000 TURBOION™ Spray LC/MS/MS system. The LC flow was provided by Shimadzu LC-10Advp pumps, with 0.05% acetic acid and MeOH. Injections were accomplished via a Valco injector valve. The HPLC analysis was done on an Agilent 1100 HPLC with Astec's Chirobiotic R column (100 x 4.6 mm, cat no. 13022 or 150 x 4.6 mm, cat no. 13023) or Daicel's Chiralcel OD column (50 x 4.6 mm, cat no. 14022) and the DAD detector set at 210,

220, 230, and 250 nm. For specific rotations, a Perkin Elmer Model 341 Polarimeter was used, set at 589 nm, Na lamp, at room temperature, with a 100 mm path length cell.

Concentrations for specific rotation are reported in grams per 100 mL of solvent.

Microbiology techniques were executed in accordance to published protocols. (Sambrook, J.

- 5 Fritsch, EF, Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed.), Cold Spring Harbor Laboratory Press, Plainview NY.) Glycolic acid products were isolated and absolute configurations were determined to be (*R*) in all cases by comparison with literature optical rotation data on configurationally defined compounds except for (-)-3-pyridylglycolic acid, which to our knowledge is not known as a single enantiomer. (For mandelic, 2-
10 chloromandelic, 2-methyl mandelic, 3-chloromandelic, 3-bromomandelic and 4-fluoromandelic acid see Hoover, J.R. E.; Dunn, G. L.; Jakas, D.R.; Lam, L.L.; Taggart, J. J.; Guarini, J.R.; Phillips, L. *J. Med. Chem.* **1974**, 17(1), 34-41; For 2-bromo mandelic acid see Collet, A.; Jacques, J.; *Bull. Soc. Chem. Fr.* **1973**, 12, 3330-3331; For 1- and 2-naphthylglycolic acid see Takahashi, I; Y. Aoyagi, I. Nakamura, Kitagawa, A., Matsumoto,
15 K., Kitajima, H. Isa, K. Odashima, K. Koga, K. *Heterocycles* **1999**, 51(6), 1371-88; For 3-thienylglycolic acid Gronowitz, S. *Ark. Kemi*, **1957**, 11, 519-525.)

- [000338] For the aryl lactic acid products, absolute configuration was established to be (*S*) for phenyl lactic acid by comparison with literature optical rotation and for all other phenyl lactic acid products, absolute configurations were predicted based upon elution order
20 using chiral HPLC. Absolute configuration for 3-hydroxy-4-cyano-butanoic acid was established by derivatization to (*R*)-(-)-Methyl (3-O-[benzoyl]-4-cyano)-butanoate and comparison to literature optical rotation data on configurationally defined compound. (3. Beard, T. Cohen, M. A. Parratt, J.S. Turner, N. J. *Tetrahedron:Asymm.* 4(6), **1993**, 1085-1104.)

25 Nitrilase Discovery and Characterization Methods:

1. Nitrilase Selection.

- [000339] An *Escherichia coli* screening host strain, SEL700, was optimized for nitrilase selections on a nitrile substrate. An $Abs_{600nm} = 1$, resuspension of SEL700 screening host in 10 mM $MgSO_4$ was infected with kanamycin-resistant environmental DNA library for 45
30 minutes at 37°C, such that complete screening coverage of the library was achieved. Infected cells, now denoted by kanamycin resistance, were plated on kanamycin LB plates and allowed to grow overnight at 30°C. Titer plates were also made to determine infection

efficiency. Cells were pooled, washed, and resuspended the next morning with 10 mM MgSO₄. Transformed clones were inoculated into M9 media (without nitrogen) with 10 mM of nitrile substrate. M9 media consisted of 1X M9 salts (NH₄Cl omitted), 0.1mM CaCl₂, 1 mM MgSO₄, 0.2 % glucose, and approximately 10 mM of a nitrile selection substrate. The selection cultures were then incubated at 30°C, shaking at 200 rpm, for up to five weeks. Positive nitrilase cultures were identified by growth, due to positive clone's ability to hydrolyze nitrile substrate. Positive clones were isolated by streaking out a selection culture with growth and subsequent secondary culturing of isolated colonies in the same defined media. The DNA from any positive secondary cultures exhibiting re-growth was then isolated and sequenced to confirm discovery of a nitrilase gene and to establish the unique nature of that gene.

2. Nitrilase Biopanning.

[000340] Traditional filter lift hybridization screening protocols are limited to libraries with approximately 10⁶ to 10⁷ members. Attempting to screen one library would require approximately 5,000 filter lifts. Therefore, solution phase and other biopanning formats have been developed for ultra high throughput sequence based screening permitting rapid screening of up to 10⁸ member environmental libraries. In the solution format, the DNA from a large number of library clones is mixed with tagged molecules of interest under conditions which promote hybridization. The tagged clones and hybridized DNA are then removed from solution and washed at some level of stringency to remove clones which do not have sequence identity with the probe. The hybridized DNA is then eluted and recovered. Clones of interest are sequenced and cloned to provide enzyme activities of interest. This method has been demonstrated to achieve up to 1,000-fold enrichment per round for sequences of interest.

3. High Throughput Nitrilase Activity Assay.

[000341] Activity assays were conducted using 25 mM (~3 mg/mL) substrate, 0.1 mg/mL nitrilase in 0.25 mL of assay solution. Assay solutions consisted of 0-10% (v/v) MeOH in 0.1 M sodium phosphate buffer solution at pH 7 to 9 and temperatures 37°C or 22°C. Specific activities were measured at 5 min transformation time point, unless otherwise noted, and are expressed in units $\mu\text{mol mg}^{-1} \text{ min}^{-1}$. Enantiomeric excess and conversion rates were determined by high throughput HPLC analysis comparing enzyme product concentration to standard curves of racemic acid products. Analytical conditions for the products are tabulated below.

Analytical Methods:

	Acid Product	Column	Liquid Chromatography Method	Retention Times of enantiomers (min)
1.1	mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.4 (S); 2.9 (R)
1.2	2-Cl-mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.3 (S); 2.9 (R)
1.3	2-Br-mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 4.0
1.4	2-CH ₃ -mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.1; 3.8
1.5	3-Cl-mandelic	Chirabiotic R 100 x 4.6 mm	10%[0.5% AcOH], 90% CH ₃ CN 1 ml/min	3.1; 3.8
1.6	3-Br-mandelic	Chirabiotic R 100 x 4.6 mm	10%[0.5% AcOH], 90% CH ₃ CN 1 ml/min	3.3; 3.9
1.7	4-F-mandelic	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.7; 4.8
1.8	1-naphthylglycolic acid	Chirabiotic R 100 x 4.6 mm	4%[0.5% AcOH], 96% CH ₃ CN 1 ml/min	3.1; 3.7
1.9	2-naphthylglycolic acid	Chirabiotic R 100 x 4.6 mm	4%[0.5% AcOH], 96% CH ₃ CN 1 ml/min	3.7; 4.7
1.10	3-pyridylglycolic acid	Chirabiotic R 100 x 4.6 mm	5% [0.5% AcOH], 65% H ₂ O, 30% CH ₃ CN, 2 ml/min	4.4; 5.5
1.11	3-thienylglycolic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 2 ml/min	1.4; 2.5
2.1	phenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8 (S); 4.0 (R)
2.2	2-methylphenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.5; 2.8
2.3	2-bromophenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 3.2
2.4	2-fluorophenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.6; 2.9
2.5	3-methylphenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.4; 3.2
2.6	3-fluorophenyl lactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 3.6
2.7	1-naphthyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.7; 3.1
2.8	2-pyridyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.5; 2.9
2.9	3-pyridyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.9; 3.6
2.10	2-thienyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.6; 4.6
2.11	3-thienyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.5; 4.6
	Methyl(3-O [benzoyl]-4-cyano)-butanoate	Daicel OD 50 x 4.6 mm	5% isopropanol, 95% hexane 1 ml/min	4.5 (R); 5.4(S)

Cyanohydrin (Substrate) Synthesis:

- 5 **[000342]** Mandelonitrile Synthesis Method A: Acetone cyanohydrin (685 μ L, 7.5 mmol), aldehyde (5 mmol), and catalytic DIEA (13 μ L, 0.075 mmol) were mixed at 0 °C. The

reactions were stirred on ice for 45 minutes. To drive the equilibrium toward the product, acetone was removed *in vacuo*. Subsequently, crude reactions were acidified with H₂SO₄ (3 μ L) and stored at -20°C. TLC was used to monitor reaction progress (3:1 hexane/ethylacetate (EtOAc)).

- 5 [000343] Mandelonitrile Synthesis Method B: To a solution of KCN (358 mg, 5.5 mmol) in MeOH (1 mL) at 0°C was added aldehyde (5 mmol) and acetic acid (315 μ L, 5.5 mmol). After stirring for one hour on ice, MeOH was removed *in vacuo*, and the crude mixture was partitioned using EtOAc and H₂O. The organic fraction was retained and concentrated *in vacuo*. TLC analysis was used to monitor reaction progress (3:1 Hexanes/EtOAc).
- 10 [000344] Aryl Acetaldehyde Cyanohydrin: Arylacetic acid (50 mmol) was dissolved in 50 ml anhydrous tetrahydrofuran (THF) in a two-neck 500 ml round-bottom flask under N₂(g) atmosphere. To this solution cooled to 0 °C, under vigorous mixing, was added slowly 105 mmol of hexylchloroborane-dimethyl sulfide (2.55 M in methylene chloride). The reaction was allowed to proceed overnight. Excess acetic acid (10 ml) was added to quench and
- 15 acidify the reaction followed by the addition 10 ml water. After stirring at room temperature for 1 hour, solvent was removed *in vacuo* and the residue was dissolved in 100 ml water and extracted with 200 ml EtOAc. The EtOAc layer was dried over sodium sulfate, filtered and then concentrated *in vacuo*. Subsequently, 60 mmol of KCN, followed by 100 ml methanol was added to the residue. The solution was then cooled to 0 °C and acetic acid (60 mmol)
- 20 added. The reaction was stirred for 1-2 hours after all KCN dissolved. Solvents were removed *in vacuo* and residue was dissolved in 100 ml water and 200 ml EtOAc. The aqueous layer was extracted with EtOAc one more time. Combined EtOAc extracts were washed with saturated brine and dried over sodium sulfate, filtered and then concentrated *in vacuo* to obtain crude cyanohydrin product. The cyanohydrin was purified by silica-gel column
- 25 (hexane/EtOAc), as necessary.

[000345] 2-chloro mandelonitrile: ¹H NMR (CDCl₃, 500 MHz) δ 7.69 (m, 1H), 7.41 (m, 1H), 7.36 (m, 2H), 5.84 (s, 1H), 3.07 (br, 1H). ¹³C NMR (CDCl₃, 125 MHz) δ 132.89, 132.73, 131.22, 130.19, 128.48, 127.84, 118.24, 60.87. MS calc'd for [C₈H₆ClNO] 167.01 found 167.9 (LC-MS +).

- 30 [000346] 2-bromomandelonitrile: ¹H NMR (CDCl₃, 500 MHz) δ 7.72 (d, 1H, *J*= 6.58), 7.62 (d, 1H, *J*= 8.35), 7.43 (t, 1H, *J*= 8.42), 7.30 (t, 1H, *J*= 7.00), 5.85 (s, 1H). ¹³C NMR (CDCl₃, 125 MHz) δ 134.550, 133.584, 131.564, 128.819, 128.535, 122.565, 118.153, 63.379.

- [000347] 2-methylmandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ : 7.60 (d, 1H, $J = 7.4$), 7.23-7.35 (m, 3H), 5.66 (s, 1H), 2.44 (s, 3H). ^{13}C NMR (CDCl_3 , 298 K, 125 MHz) δ : 136.425, 133.415, 131.450, 130.147, 127.204, 126.894, 118.952, 18.916. MS calc'd for $[\text{C}_9\text{H}_9\text{NO}]$ 147.07, found 147.2 (ESI +).
- 5 [000348] 3-chloromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.55 (s, 1H), 7.43-7.37 (m, 3H), 5.54 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.183, 135.480, 130.718, 130.303, 127.047, 124.891, 118.395, 63.156. MS calc'd for $[\text{C}_8\text{H}_6\text{ClNO}]$ 167.01 found 167.9 (LC-MS +).
- [000349] 3-bromomandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.69 (s, 1H), 7.56 (d, $J = 6.2$ Hz, 1H), 7.45 (d, $J = 5.5$ Hz, 1H), 7.32 (t, $J = 6.4$ Hz, 1H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.376, 133.201, 130.934, 129.208, 125.359, 123.380, 118.458, 63.006. MS calc'd for $[\text{C}_8\text{H}_6\text{BrNO}]$ 212.0 found 211.9 (LC-MS +).
- 10 [000350] 4-fluoromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 5.54 (s, 1H), 7.13 (m, 2H), 7.51-7.53 (m, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 63.02, 116.44, 118.97, 128.90, 131.54, 132.51, 162.575.
- 15 [000351] 4-chloromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.47 (d, $J = 7.0$ Hz, 2H), 7.42 (d, $J = 7.0$ Hz, 2H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 136.209, 133.845, 129.647, 128.232, 118.630, 63.154. MS calc'd for $[\text{C}_8\text{H}_6\text{ClNO}]$ 167.01 found 167.9 (LC-MS +).
- 20 [000352] 1-naphthyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.14 (d, 1H, $J = 8.5$), 7.92 (t, 2H, $J = 6.1$), 7.82 (d, 1H, $J = 5.7$), 7.62 (t, 1H, $J = 6.1$), 7.56 (t, 1H, $J = 6.1$), 7.50 (t, 1H, $J = 6.1$), 6.18 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.0, 135.7, 134.2, 131.1, 129.2, 127.5, 126.7, 125.8, 125.3, 123.1, 119.0, 62.4; MS calc'd for $[\text{C}_{12}\text{H}_9\text{O}]$ 183.21, found 183.2 (ESI +).
- 25 [000353] 2-naphthyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.03 (s, 1H), 7.92 (d, 1H, $J = 8.6$), 7.87-7.91 (m, 2H), 7.61 (dd, 1H, $J = 6.7, 1.2$), 7.55-7.60 (m, 2H), 5.72 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 134.9, 133.9, 132.7, 129.6, 128.6, 128.0, 127.4, 127.2, 126.4, 123.9, 118.9, 64.1; MS calc'd for $[\text{C}_{12}\text{H}_9\text{O}]$ 183.21, found 183.2 (ESI +).
- [000354] 3-pyridyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ : 8.62 (d, 1H, $J = 1.8$), 8.57 (d, 1H, $J = 5.1$), 7.94 (d, 1H, $J = 8.1$), 7.41 (dd, 1H, $J = 8.1, 5.1$), 5.64 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 149.921, 147.355, 135.412, 133.044, 124.443, 118.980, 61.085. MS calc'd for $[\text{C}_7\text{H}_6\text{N}_2\text{O}]$ 134.05, found 135.2 (ESI +).
- 30

- [000355] 3-thienyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.45 (d, $J = 2.2$ Hz, 1H), 7.56 (dd, $J = 6.2$ Hz, 1H), 7.45 (d, $J = 5.5$ Hz, 1H), 7.32 (t, $J = 6.4$ Hz, 1H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.376, 133.201, 130.934, 129.208, 125.359, 123.380, 118.458, 63.006. MS calc'd for $[\text{C}_6\text{H}_5\text{NOS}]$ 139.01 found 139.9 (LC-MS +).
- 5 [000356] phenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.34 (m, 5H), 4.64 (t, $J = 6.75$ Hz, 1H), 3.11 (d, $J = 6.75$ Hz, 2H), 2.75 (br, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 133.96, 129.91, 129.16, 128.08, 119.47, 62.33, 41.55.
- [000357] 2-methylphenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.11 (m, 4H), 4.61 (t, $J = 6.62$ Hz, 1H), 3.12 (d, $J = 6.62$ Hz, 2H), 2.14 (s, 3H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 136.94, 136.47, 132.57, 130.48, 127.61, 125.75, 120.11, 62.95, 44.73 MS calc'd for $[\text{C}_{10}\text{H}_{11}\text{NO}]$: 161.08, found 162.2 (M+Na, ESI +)
- 10 [000358] 2-bromophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.20 (m, 4H), 4.78 (t, $J = 6.5$ Hz, 1H), 3.26 (d, $J = 6.5$ Hz, 2H). ^{13}C NMR (CDCl_3 , 100 MHz) δ 133.93, 132.82, 131.72, 129.21, 128.12, 124.86, 119.41, 63.02, 44.89.
- 15 [000359] 2-fluorophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.2 (m, 2H), 7.02 (m, 2H), 4.50 (dd, $J = 4.62$ Hz, $J = 7.88$ Hz, 1H), 3.23 (dd, $J = 4.62$ Hz, $J = 14.12$ Hz, 1H), 2.97 (dd, 7.88 Hz, 14.12 Hz, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 132.18, 131.52, 129.66, 129.03, 128.07, 124.05, 115.8, 63.02, 44.79 MS calc'd for $[\text{C}_9\text{H}_8\text{FNO}]$ 165.06, found 164.2 (ESI +).
- 20 [000360] 3-methylphenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.18 (m, 1H), 7.02 (m, 3H), 4.54 (dd, $J = 4.62$ Hz, $J = 8$ Hz, 1H), 3.06 (dd, $J = 4.62$ Hz, $J = 14.38$ Hz, 1H), 2.83 (dd, $J = 8$ Hz, $J = 14.38$ Hz, 1H), 2.36 (s, 3H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 176.25, 138.18, 136.0, 130.97, 128.93, 127.68, 126.58, 76.42, 34.29, 37.69 MS calc'd for $[\text{C}_{10}\text{H}_{12}\text{O}_3]$ 180.08, found 180.0 (ESI +).
- 25 [000361] 3-fluorophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.18 (m, 2H), 6.95 (m, 2H), 4.44 (dd, 1H), 3.11 (dd, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 130.40, 125.53, 124.85, 116.92, 114.87, 114.50, 119.77, 61.97, 41.27.
- [000362] 1-naphthyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.07 (m, 1H), 7.86 (m, 1H), 7.74 (m, 1H), 7.41 (m, 4H), 4.20 (t, $J = 7$ Hz, 1H), 3.33 (d, $J = 6.8$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 177.7, 140.31, 129.74, 129.24, 128.92, 128.26, 127.84, 125.63, 124.53, 124.05, 123.42, 70.58, 38.0 MS calc'd for $[\text{C}_{13}\text{H}_{11}\text{NO}]$ 197.08, found 197.1 (ESI +).
- 30

[000363] 2-pyridyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.50 (m, 1H), 7.85 (m, 1H), 7.48 (m, 1H), 7.34 (m, 1H), 4.42 (m, 1H), 3.19 (dd, $J = 3.5$ Hz, $J = 13.7$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 157.44, 145.69, 140.24, 126.96, 126.16, 122.99, 60.30, 42.60 MS calc'd for $[\text{C}_8\text{H}_8\text{N}_2\text{O}]$ 148.06, found 149.1 (ESI +).

5 [000364] 3-pyridyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.62 (d, 1H, $J = 1.8$), 8.57 (d, 1H, $J = 5.1$), 7.94 (d, 1H, $J = 8.1$), 7.41 (dd, 1H, $J = 8.1$, 5.1), 5.64 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ : 149.921, 147.355, 135.412, 133.044, 124.443, 118.980, 61.085. Exact Mass calculated for $[\text{C}_7\text{H}_6\text{N}_2\text{O}]$: 134.05, found: 135.2 (ESI +).

10 [000365] 2-thienyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.1 (m, 1H), 6.9 (m, 1H), 6.8 (m, 1H), 4.11 (t, $J = 7.0$ Hz, 1H), 2.86 (d, $J = 7.0$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 127.68, 127.41, 125.58, 124.60, 118.70, 63.25, 44.84.

[000366] 3-thienyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.09 (m, 3H), 4.60 (t, $J = 6.25$ Hz, 1H), 3.12 (d, $J = 6.25$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 129.05, 127.16, 125.27, 122.65, 119.87, 61.58, 44.90.

15 [000367] Preparation of racemic mandelic acids standards from corresponding cyanohydrins: (Stoughton, R.W. J. Am. Chem. Soc. 1941, 63, 2376) 2-bromomandelonitrile (230 mg, 1.08 mmol) was dissolved in conc. HCl (1 mL) and stirred at room temperature for 18 h and then at 70 °C for 24 h. After cooling, the reaction mixture was extracted with diethyl ether (4 x 2 mL). Organic extracts were, combined, dried over MgSO_4 , filtered and
20 concentrated *in vacuo*. 2-bromomandelic acid was isolated as a colorless powder (180 mg, 0.78 mmol, 70 % yield).

[000368] Preparation of racemic aryllactic acids standards from corresponding amino acids: Phenylalanine (10 mmol, 1.65g) was dissolved in 30 ml 2N H_2SO_4 at room temperature under N_2 (g) atmosphere. Sodium nitrite (1.4 g in 3 ml aqueous solution, 2 eq) solution was added
25 slowly to the reaction mixture over a period of 3-4 hours with vigorous stirring at room temperature under N_2 (g) atmosphere. The reaction mixture was stirred overnight and the phenyllactic acid product was then extracted into diethylether (3 x 30 ml). Combined ether extracts were dried over MgSO_4 and then filtered and concentrated *in vacuo*. (Kenji, I.; Susumu, A.; Masaru, M.; Yasuyoshi, U.; Koki, Y.; Koichi, K. Patent Number, WO0155074,
30 Publication date: 2001-08-02.)

General Method for Enzymatic Preparation of α -hydroxy acids:

[000369] (*R*)-(-)-Mandelic Acid To a solution of mandelonitrile (1.005 g, 7.56 mmol) in 150 mL of sodium phosphate (100 mM) buffer at pH 8 with 10% v/v methanol, that had been

N₂ (g) sparged, at 37 °C, was added 9 mg of nitrilase 1 (normalized for nitrilase content). The reaction was conducted under N₂ (g) atmosphere on a rotating platform shaker. Reaction progress was monitored by withdrawing aliquots for HPLC analysis. After 3 h incubation, the reaction mixture was acidified to pH 2 with 1 N HCl and extracted with diethyl ether (4 x 50 ml). Organic fractions were concentrated *in vacuo* and then the residue was taken up in 10% sodium bicarbonate solution. This aqueous solutions was then washed with diethyl ether (3 x 50 ml) and then acidified to pH 2 with 1 N HCl and extracted with diethyl ether (3 x 50 ml). Organic fractions were combined, washed with brine, dried over MgSO₄, filtered and then concentrated *in vacuo*. (R)-(-)-Mandelic acid (933 mg, 6.22 mmol) was isolated as a colorless powder in 86 % yield. ¹H NMR (DMSO-d₆, 500 MHz) δ 12.6 (br, s, 1H) 7.41 (m, 2H), 7.34 (m, 2H), 7.28 (m, 1H), 5.015 (s, 1H). ¹³C NMR DMSO-d₆, 125 MHz) δ 174.083, 140.216, 128.113, 127.628, 126.628, 72.359. MS calc'd for [C₈H₈O₃] 150.07, found 150.9 (ESI +); *ee* = 98 % [HPLC]. [α]₅₉₈²⁰ = -134.6 (*c* = 0.5, methanol).

[000370] (-)-2-chloromandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.75 (m, 1H), 7.44 (m, 1H), 7.34 (m, 2H), 5.34 (s, 1H). ¹³C NMR (DMSO, 298K, 125MHz) δ 173.070, 137.985, 132.105, 129.399, 129.158, 128.705, 127.235. MS calc'd for [C₈H₇ClO₃] 186.0, found 185.0 (LC-MS -). *ee* = 96 % [HPLC]. 92 % yield. [α]₅₉₈²⁰ = -137.6 (*c* = 0.5, ethanol).

[000371] (-)-2-bromomandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.60 (d, *J* = 7.93, 1H), 7.48 (m, 1H), 7.40 (m, 1H), 7.25 (m, 1H), 5.30 (s, 1H). ¹³C NMR DMSO-d₆, 125 MHz) δ 172.994, 139.61, 132.355, 129.652, 128.753, 127.752, 122.681, 71.644. MS calc'd for [C₈H₇BrO₃] 230.0, found 230.9. *ee* = 96% [HPLC]. 92% yield. [α]₅₉₈²⁰ = -116.4 (*c* = 0.5, ethanol).

[000372] (-)-2-methylmandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 11.78 (bs, 1H) 7.38 (m, 1H), 7.16-7.38 (m, 3H), 5.18 (s, 1H), 2.35 (s, 3H). ¹³C NMR DMSO-d₆, 125 MHz) δ 174.229, 138.623, 135.649, 130.129, 127.491, 126.990, 125.698, 125.698, 69.733, 18.899. MS calc'd for [C₉H₁₀O₃] 166.1, found 165.2. *ee* = 91 % [HPLC]. 86 % yield. [α]₅₉₈²⁰ = -164.4 (*c* = 0.5, ethanol).

[000373] (-)-3-chloromandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.46 (s, 1H), 7.36 (m, 3H), 5.07 (s, 1H). ¹³C NMR (DMSO, 298K, 125MHz) δ 173.554, 142.685, 132.813, 130.069, 127.568, 126.355, 125.289, 71.659. MS calc'd for [C₈H₇ClO₃] 186.0, found 185.34 (MALDI TOF -). *ee* = 98 % [HPLC]. 70 % yield. [α]₅₉₈²⁰ = -120.4 8 (*c* = 0.5, methanol).

- [000374] (-)-3-bromomandelic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.60 (s, 1H), 7.49 (m, 1H), 7.42 (m, 1H), 7.31 (m, 1H), 5.06 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.551, 142.917, 130.468, 130.379, 129.237, 125.687, 121.404, 71.605. MS calc'd for $[\text{C}_8\text{H}_7\text{BrO}_3]$ 229.98, found 229.1 (LC-MS). $ee = 98\%$ [HPLC]. 82 % yield. $[\alpha]^{20}_{598} = -84.8$ ($c = 0.5$, ethanol).
- [000375] (-)-4-fluoromandelic acid ^1H NMR (DMSO, 298K, 500MHz) δ 12.65 (s, 1H), 7.44 (m, 2H), 7.17 (m, 2H), 5.91 (s, 1H), 5.03 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.93, 162.57, 136.47, 128.61, 128.55, 114.96, 114.80, 71.61. MS calc'd for $[\text{C}_8\text{H}_7\text{FO}_3]$ 170.0, found 168.8. $ee = 99\%$ [HPLC]. 81% yield. $[\alpha]^{20}_{598} = -152.8$ ($c = 0.5$, methanol).
- [000376] (-)-1-naphthylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.28-8.26 (m, 1H), 7.87-7.93 (m, 2H), 7.47-7.58 (m, 4H), 5.66 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 174.288, 136.284, 133.423, 130.654, 128.353, 128.192, 125.926, 125.694, 125.613, 125.266, 124.558, 70.940. MS calc'd for $[\text{C}_{12}\text{H}_{10}\text{O}_3]$: 202.21 found 201.37 (MALDI TOF -). $ee = 95\%$ [HPLC]. 90 % yield $[\alpha]^{20}_{598} = -115.4$ ($c = 0.5$, ethanol).
- [000377] (-)-2-naphthylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 12.6 (bm, 1H), 7.88-7.93 (m, 4H), 7.48-7.56 (m, 3H), 5.20 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 174.005, 137.760, 132.644, 132.498, 127.811, 127.658, 127.506, 127.209, 125.993, 125.334, 124.761, 72.472. MS calc'd for $[\text{C}_{12}\text{H}_{10}\text{O}_3]$ 202.21, found 201.37 (MALDI TOF). $ee = 98\%$ [HPLC]. 68% yield. $[\alpha]^{20}_{598} = -115.4$ ($c = 0.5$, ethanol).
- [000378] (-)-3-pyridylglycolic acid This Reaction was performed in 100 mM ammonium formate buffer at pH 8. To isolate the product, the reaction mixture was filtered through a 10,000 MWCO membrane to remove enzyme and then concentrated *in vacuo*. ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.56 (s, 1H), 8.36 (d, $J = 4.57$ Hz, 1H), 8.25 (s, 1H), 7.71 (m, 1H), 7.25 (dd, $J = 4.98, 4.80$ Hz 1H), 5.45 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 165.911, 147.862, 147.251, 139.118, 133.381, 122.746, 71.508. MS calc'd for $[\text{C}_7\text{H}_7\text{NO}_3]$ 153.04, found 154.0 ((MALDI TOF). $ee = 92\%$ [HPLC], 84% yield, $[\alpha]^{20}_{598} = -65.2$ ($c = 0.5$, H_2O).
- [000379] (-)-3-thienylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.48 (m, 1H), 7.45 (d, $J = 2.81$, 1H), 7.10 (m, 1H), 5.09 (s, 1H), 3.33 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.704, 141.109, 126.446, 126.042, 122.247, 68.915 MS calc'd for $[\text{C}_6\text{H}_6\text{O}_3\text{S}]$ 158.00, found 157.224 (MALDI TOF). $ee = 95\%$ [HPLC]. 70 % yield. $[\alpha]^{20}_{598} = -123.2$ ($c = 0.5$, methanol).

- [000380] (S)-(-)-phenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.28(m, 5H), 4.17(dd, $J = 4.5$ Hz, $J = 8.3$ Hz, 1H), 2.98(dd, $J = 4.5$ Hz, $J = 13.7$ Hz, 1H), 2.79 (dd, $J = 8.3$ Hz, $J = 13.7$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.16, 133.4, 129.27, 128.6, 127.3, 70.45, 44.12. $ee = 97\%$ [HPLC], 84 % yield. $[\alpha]^{20}_{598} = -17.8$ ($c = 0.5$, methanol).
- 5 [000381] (-)-2-methylphenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.16 (m, 4H), 4.47 (dd, $J = 3.9$ Hz, $J = 8.8$ Hz, 1H), 3.25(dd, $J = 3.9$ Hz, 14.3 Hz, 1H), 2.94 (dd, $J = 8.8$ Hz, $J = 14.3$ Hz), 2.35(s, 3H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.61, 137.08, 134.74, 130.80, 130.25, 127.44, 126.34, 70.93, 37.67, 19.79. MS calc'd $[\text{C}_{10}\text{H}_{12}\text{O}_3]$ 180.08, found 180.0 (ESI +). 86 % yield. $ee = 95\%$ [HPLC]. $[\alpha]^{20}_{598} = -13.2$ ($c = 0.5$, methanol).
- 10 [000382] (-)-2-bromophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.28 (m, 4H), 4.60(dd, $J = 4.0$ Hz, $J = 9.1$ Hz, 1H), 3.45(dd, $J = 4.0$ Hz, $J = 14.1$ Hz, 1H), 3.04(dd, $J = 8.0$ Hz, $J = 14.1$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.70, 136.05, 133.21, 132.10, 128.99, 127.72, 125.0, 70.04, 40.76. MS calc'd for $[\text{C}_9\text{H}_9\text{BrO}_3]$ 243.9, found 243.3 (ESI +). 91 % yield. $ee = 93\%$ [HPLC], $[\alpha]^{20}_{598} = -17.6$ ($c = 0.5$, methanol)
- 15 [000383] (-)-2-fluorophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.10 (m, 4H), 4.64 (t, $J = 6.8$ Hz, 1H), 3.11(d, $J = 6.8$ Hz, 2H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 132.18, 131.52, 129.66, 129.03, 128.07, 124.05, 115.8, 63.02, 44.79. MS calc'd for $[\text{C}_9\text{H}_8\text{FNO}]$: 165.06, found 164.2 (ESI +). 91 % yield. $ee = 88\%$ [HPLC]. $[\alpha]^{20}_{598} = -14.0$ ($c = 0.5$, methanol).
- 20 [000384] (-)-3-methylphenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.18 (m, 1H), 7.02 (m, 3H), 4.54 (dd, $J = 4.6$ Hz, $J = 8.0$ Hz, 1H), 3.06(dd, $J = 4.54$ Hz, $J = 14.4$ Hz, 1H), 2.83(dd, $J = 8.0$ Hz, $J = 14.4$ Hz, 1H), 2.36 (s, 3H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 175.88, 163.80, 130.33, 130.09, 125.7, 116.68, 113.75, 71.31, 34.28. MS calc'd for $[\text{C}_{10}\text{H}_{11}\text{NO}]$ 161.08, found 162.2 (ESI +). 80 % yield. $ee = 98\%$ [HPLC]. $[\alpha]^{20}_{598} = -2.4$ ($c = 0.5$, methanol).
- 25 [000385] (-)-3-fluorophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.2 (m, 1H), 6.9 (m, 3H), 4.56 (dd, 4.5 Hz, $J = 7.9$ Hz, 1H), 3.09(dd, $J = 4.5$ Hz, $J = 14.1$ Hz, 1H), 2.86 (dd, $J = 7.9$ Hz, $J = 14.1$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 175.88, 163.80, 130.33, 130.09, 125.7, 116.68, 113.75, 71.31, 34.28. MS calc'd for $[\text{C}_9\text{H}_9\text{O}_3\text{F}]$ 184.05, found 184.1 (ESI +). 82 % yield. $ee = 97\%$ [HPLC]. $[\alpha]^{20}_{598} = -5.2$ ($c = 0.5$, methanol).
- 30 [000386] (-)-1-naphyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.57 (m, 1H), 8.21(m, 1H), 8.08 (m, 1H), 7.61 (m, 4H), 4.64 (dd, 3.5 Hz, 8.5 Hz, 1H), 3.84 (dd, $J = 3.5$ Hz, $J = 14.5$

Hz, 1H), 3.38 (dd, $J = 8.5$ Hz, $J = 14.5$ Hz, 1H) ^{13}C NMR (DMSO, 298K, 125MHz) δ 177.7, 140.31, 129.74, 129.24, 128.92, 128.26, 127.84, 125.63, 124.53, 124.05, 123.42, 70.58, 38.0. MS calc'd for $[\text{C}_{13}\text{H}_{11}\text{NO}]$ 197.08, found 197.1 (ESI +). 87 % yield. $ee = 94$ % [HPLC]. $[\alpha]^{20}_{598} = -16.2$ ($c = 0.5$, methanol).

- 5 **[000387]** (-)-2-pyridyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.49 (m, 1H), 7.62 (m, 1H), 7.21 (m, 2H), 4.50 (t, $J = 5.0$ Hz, 1H), 3.01 (d, $J = 5.0$ Hz, 2H). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 178.8, 159.79, 148.84, 136.89, 124.35, 121.75, 71.14, 44.09. MS calc'd for $[\text{C}_8\text{H}_9\text{NO}_3]$: 167.06, found 167.0. (ESI +). 62 % yield. $ee = 94$ % [HPLC], $[\alpha]^{20}_{598} = -3.6$ ($c = 0.5$, methanol).
- 10 **[000388]** (-)-3-pyridyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.43(m, 2H), 7.62(m, 1H), 7.28(m, 1H), 4.57(t, 5.37Hz, 1H), 2.85(d, 5.37Hz, 2H). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 176.6, 150.03, 147.12, 136.41, 129.45, 123.26, 61.56, 31.46 MS calc'd for $[\text{C}_8\text{H}_9\text{NO}_3]$ 167.06, found 167.0 (ESI +). 59 % yield. $ee = 94$ % [HPLC]. $[\alpha]^{20}_{598} = -4.0$ ($c = 0.5$, methanol).
- 15 **[000389]** (-)-2-thienyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.18(m, 1H), 6.94(m, 1H), 6.90 (m, 1H), 4.49 (dd, $J = 4.1$ Hz, $J = 6.25$ Hz, 1H), 3.36 (dd, $J = 4.1$ Hz, $J = 15.0$ Hz, 1H), 3.26(dd, $J = 6.25$ Hz, $J = 15.0$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 127.68, 127.41, 125.58, 124.60, 118.70, 63.25, 44.84. MS calc'd for $[\text{C}_7\text{H}_7\text{NOS}]$ 153.02, found 153.0 (ESI +). 85 % yield. $ee = 95$ % [HPLC]. $[\alpha]^{20}_{598} = -13.0$ ($c = 0.5$, methanol).
- 20 **[000390]** (-)-3-thienyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.30(m, 1H), 7.13(m, 1H), 7.01(m, 1H), 4.50 (dd, $J = 4.25$ Hz, $J = 6.5$ Hz, 1H), 3.21(dd, $J = 4.25$ Hz, $J = 15.0$ Hz, 1H), 3.10 (dd, $J = 6.5$ Hz, $J = 15.0$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 127.50, 136.09, 128.83, 126.24, 123.32, 70.65, 34.84. MS calc'd for $[\text{C}_7\text{H}_8\text{O}_3\text{S}]$ 172.02, found 172.1 (ESI +). 81 % yield. $ee = 96$ % [HPLC]. $[\alpha]^{20}_{598} = -18.8$ ($c = 0.5$, methanol).

25 Enzymatic Hydrolysis of 3-Hydroxyglutarylnitrile:

- [000391]** 3-Hydroxyglutarylnitrile (1.0 g, 9.0 mmol, 240 mM) was suspended in N_2 (g) sparged sodium phosphate buffer (37.5 mL, pH 7, 100 mM) at room temperature. Cell lysate (30 mg, normalized for nitrilase content) was added to bring the concentration to 0.8 mg/ml enzyme and the reaction was at shaken at 100 rpm, room temperature. Reaction progress was
- 30 monitored by TLC (1:1 EtOAc:Hexanes, $R_f = 0.32$, nitrile; $R_f = 0.0$, acid) After 22 h, the reaction was acidified with 1M HCl. The reaction mixture was continuously extracted with diethyl ether. The acid product was isolated as a yellow oil (1.15 g, 98 % yield). ^1H NMR

(DMSO, 298K, 500MHz) δ 12.32 (s, 1H), 5.52 (s, 1H), 4.10 (m, 1H), 2.70 (dd, 1H, $J = 16.8, 4.1$ Hz), 2.61 (dd, 1H, $J = 16.9, 6.3$ Hz), 2.44 (dd, 1H, $J = 15.4, 5.3$ Hz), 2.37 (dd, 1H, $J = 15.6, 7.8$ Hz). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 171.9, 118.7, 63.4, 41.2, 25.2 MS calc'd for $[\text{C}_5\text{H}_7\text{NO}_3]$: 129.0, found 130.0 $[\text{M}+\text{H}^+]$, (ESI +).

5 Preparation of (R)-(-)-Methyl (3-O-[benzoyl]-4-cyano)-butanoate

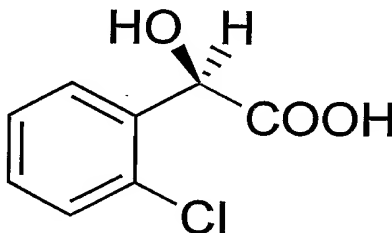
[000392] Benzoyl chloride (0.068 ml, 0.752 mmol) was added to a stirred solution of (R)-methyl-(3-hydroxy-4-cyano)-butanoate (71.7 mg, 0.501mmol) in pyridine (2.0 ml), at room temperature. After 19 hours, add an additional 0.5 equivalent of benzoyl chloride (0.023ml, 0.251mmol). Reaction was complete at 23 h, as determined by TLC. Add 1ml H_2O , extract
10 with ether (3 x 10ml). Wash with brine (2 x 10ml). Dry combined aqueous extracts with MgSO_4 . Filter off drying agent and remove solvent by rotary evaporation. Purify by column chromatography (hexane:ethyl acetate [2:1]). Rotary evaporation of fractions yielded the product as a yellow oil (46 mg, 0.186 mmol, 37%). ^1H NMR (DMSO, 298K, 500MHz) δ 7.96 (d, 2H, $J = 7.8$), 7.70 (t, 1H, $J = 7.25$), 7.56 (t, 2H, $J = 7.8$), 5.55 (m, 1H), 3.59 (s, 3H),
15 3.13 (m, 2H), 2.90 (m, 2H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 169.6, 164.5, 133.8, 129.3, 128.9, 128.5, 117.3, 66.0, 51.8, 37.5, 22.2 MS calc'd for $[\text{C}_{13}\text{H}_{13}\text{NO}_4]$: 247.25, found 270.3 $[\text{M}+\text{Na}^+]$ $ee = 95\%$ [HPLC]. $[\alpha]_D^{20} -32.4$ ($c = 0.5$, CHCl_3).

Synthesis of (R)-Ethyl-(3-hydroxy-4cyano)-butanoate

[000393] A 0.2 M solution of (R)-3-hydroxy-4-cyano-butanoic acid (50 mg, 0.387 mmol) in
20 anhydrous ethanol (1.94 mL) was prepared. The ethanol solution was added dropwise to 1.0 ml of a 50:50 (v/v) mixture of anhydrous 1 M HCl ethereal solution and anhydrous ethanol over sieves. The reaction was stirred overnight at room temperature under N_2 (g) atmosphere. The reaction was monitored by TLC, (1:1 EtOAc:Hexanes, $R_f = 0.45$, ester; $R_f = 0.0$, acid, stained with p-anisaldehyde). After 30 hrs, solvent was removed by rotary evaporation. The
25 crude product was taken up in 25 mL ether, washed with 5 mL saturated bicarbonate and then 5 mL brine. The organic extract was dried over MgSO_4 , filtered and then concentrated *in vacuo*, yielding the product as a clear oil. ^1H NMR (DMSO, 298K, 500MHz) δ 5.60 (d, 1H, $J = 5.58$ Hz), 4.12 (m, 1H), 4.07 (q, 2H, $J = 7.1$), 2.66 (m, 2H), 2.47 (m, 2H), 1.87 (t, 3H, $J = 7.0$). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 170.21, 118.60, 63.40, 59.98, 41.10, 25.14,
30 14.02. MS calc'd for $[\text{C}_7\text{H}_{11}\text{NO}_3]$: 157.1, found 158.2. $[\text{M}+\text{H}^+]$

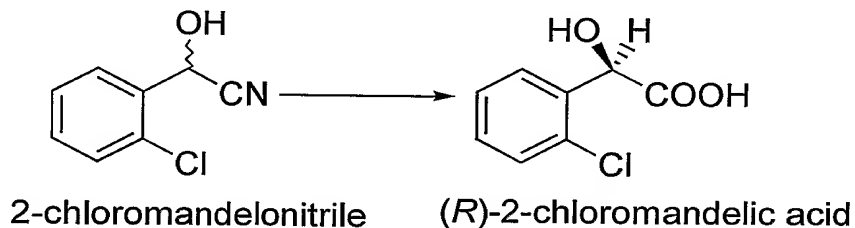
Example 13: Optimization Of Nitrilases For The Enantioselective Production Of
(R)-2-Chloromandelic Acid

[000394] Chloromandelic acid has the structure:



5

[000395] Nitrilases were identified which selectively produced (*R*)-2-chloromandelic acid from (*R,S*)-2-chloromandelonitrile. Nitrilases were identified which were useful to improve the enantioselectivity of the enzymes and establishing the effects of process conditions on the enzymes. An examination of the reaction conditions for the enzymatic nitrile hydrolysis was carried out in order to improve the enantiomeric excess of the product. Additionally, further investigation into the effects of process conditions on the enzyme was performed.



[000396] In this aspect, the enantioselective production of (*R*)-2-chloromandelic acid was the target. One enzyme, SEQ ID NOS:385, 386, was selected for further confirmation of its enantioselectivity on 2-chloromandelonitrile. SEQ ID NOS:385, 386 was shown to be stable to process components, with a half-life of 8 hours. The enzyme was inhibited by 2-chlorobenzaldehyde and a contaminant in the cyanohydrin substrate, 2-chlorobenzoic acid. The enzymatic reaction was scaled up to a substrate concentration of 45 mM 2-chloromandelonitrile. Over 90% conversion was obtained, with *ee* of 97%. The chiral HPLC method was improved, to remove a contaminating peak that was present in the substrate. Improved accuracy in the determination of enantioselectivity was obtained using this method.

[000397] Nitrilases were screened against 2-chloromandelonitrile, with 31 nitrilases exhibiting activity on this substrate. High enantioselectivities were shown by 9 enzymes. The optimization of 5 of these enzymes was undertaken and one of them was identified as a candidate for the next stage of development.

5 [000398] In an effort to improve the enantioselectivity of the selected enzymes for (*R*)-2-chloromandelic acid, a number of factors that are known to affect this property, together with the activity of the enzymes, were investigated. These included pH, temperature, buffer strength and addition of solvents to the reaction. Initially, 5 nitrilases were selected for these studies, based on the high enantioselectivities obtained by these enzymes. These enzymes
10 were: SEQ ID NOS:385, 386, SEQ ID NOS:197, 198, SEQ ID NOS:217, 218, SEQ ID NOS:55, 56, and SEQ ID NOS:167, 168.

Effect of pH

[000399] The enzymatic reactions were run at a range of pH values, from pH 5 to pH 9. An increase in both activity and enantioselectivity with increasing pH was observed for all of
15 the enzymes. With the exception of SEQ ID NOS:385, 386, pH 9 (0.1 M Tris-HCl buffer) was determined as the optimum for activity and enantioselectivity. The optimum pH for SEQ ID NOS:385, 386 was pH 8 (0.1 M sodium phosphate buffer).

Effect of temperature

[000400] The enzymes exhibited similar temperature profiles, with the highest activities
20 being measured at 37°C and 45°C. Although the latter temperature resulted in higher conversions, the enantioselectivity of most of the enzymes showed a clear preference for the lower temperatures, with ee values being 10-20% lower when the temperature was raised above 37°C. In the case of SEQ ID NOS:385, 386 a slight optimum for enantioselectivity was evident at 37°C. Therefore, this temperature was established as the optimum for
25 hydrolysis of 2-chloromandelonitrile by these enzymes.

Effect of enzyme concentration

[000401] During the concurrent investigation into the enantioselective hydrolysis of phenylacetaldehyde cyanohydrin to L-phenyllactic acid, the concentration of the enzyme in the reaction was found to have a significant effect on the enantioselectivity of the reaction.
30 This provided an indication that the enzymatic hydrolysis rate was faster than the rate of racemization of the remaining cyanohydrin in the reaction. On this basis, the effect of enzyme concentration on the enantioselectivity of the enzymes towards (*R*)-2-chloromandelonitrile was investigated. Enzymatic reactions were performed with the

standard concentration of enzyme (0.6 mg protein/ml), half the standard concentration and one-tenth of the standard concentration.

[000402] The following Table indicates the highest conversions achieved for the reactions, with the corresponding ee. With the exception of SEQ ID NOS:385, 386, it appears that very little, if any, increased enantioselectivity is observed. Therefore, it appears that the rate of racemization of the remaining chloromandelonitrile is not a limiting factor to obtaining higher enantioselectivities.

Investigation of other positive enzymes

[000403] In addition to the enzymes in the above Table, a number of other nitrilases were screened for their enantioselectivities on 2-chloromandelonitrile. Some of these enzymes were newly discovered enzymes. Some were reinvestigated under conditions that have since been found to be optimal for these enzymes (pH 8 and 37°C). The results of this screening are shown below in the Table.

Effect of co-solvent concentration

[000404] The addition of methanol as a cosolvent in the enzymatic reactions was shown to enhance the ee. In order to establish the lowest level of methanol that could be added to the reactions, the enzyme reactions were performed at varying concentrations of methanol, ranging from 0-20% (v/v). No significant differences in enantioselectivity were evident between the various methanol concentrations. However, the ee in these reactions was 97-98%, while that of the control reaction, with no added methanol was 95-96%. While this difference in ee is small, the effect of the methanol was shown in more than one set of experiments during the course of this investigation and is therefore regarded as significant.

Effect of reaction components on activity of SEQ ID NOS:385, 386

[000405] A vital part of an investigation into process optimization of an enzyme involves the determination of the effects of any compounds which could be present in the enzymatic reaction. For SEQ ID NOS:385, 386, these components were established as the starting material and equilibrium product of the cyanohydrin, 2-chlorobenzaldehyde; the product, 2-chloromandelic acid and the contaminant detected in the substrate, 2-chlorobenzoic acid. The addition of cyanide to the reaction was found to have no effect on the enzyme activity. The presence of trace amounts of triethylamine was also found to be tolerable to the enzyme.

[000406] The effect of the various reaction components on the activity of SEQ ID NOS:385, 386 was assessed by addition of various levels of possible inhibitors to the enzyme reaction. From these experiments, it appeared that both the aldehyde and its oxidation product, 2-chlorobenzoic acid were detrimental to enzyme activity. Approximately 70% and 40% of the activity of SEQ ID NOS:385, 386 was lost upon addition of 5 mM 2-chlorobenzaldehyde or 5 mM 2-chlorobenzoic acid to the reaction, respectively.

Scale-up hydrolysis of 2-chloromandelonitrile

[000407] In order to confirm the conversion and enantioselectivity obtained by SEQ ID NOS:385, 386 for the production of (R)-2-chloromandelic acid, a larger scale reaction was performed and the product isolated from the aqueous mixture. The reaction was performed in a 20 ml reaction volume, with a substrate concentration of 45 mM 2-chloromandelonitrile. Complete conversion of the cyanohydrin was obtained, with 30 mM product formed. The ee of the product was 97% and the specific activity of the enzyme was 0.13 mmol product/mg nitrilase/h.

[000408] It is evident from this experiment, together with the other experiments performed, that the formation of product does not account for the complete loss of substrate. In all experiments, a nitrile-containing control sample was run, in order to determine the extent of breakdown of the cyanohydrin. Overall, it appears that approximately 50% of the substrate is lost over a period of 4 hours at 37°C. It is expected that this breakdown would be to its equilibrium products, cyanide and 2-chlorobenzaldehyde, which could undergo further oxidation. A larger scale reaction was also run at a substrate concentration of 90 mM 2-chloromandelonitrile. However, no product was detected in this reaction. At higher substrate concentrations, it is expected that the concentration of the equilibrium product, 2-chlorobenzaldehyde and the contaminant, 2-chlorobenzoic acid will be present in higher amounts. Based on the results above, it is possible that the enzyme will be completely inhibited under such conditions.

Reactions under biphasic conditions

[000409] The use of biphasic systems can facilitate product recovery following the enzymatic reaction step. These systems can be also be used for the removal of products or by-products which are inhibitory to the enzyme. The nitrilases were shown to be active under biphasic conditions using a variety of solvents. Following the low conversions obtained at the higher substrate concentration above, further investigation of a biphasic system was performed with the hit enzyme, SEQ ID NOS:385, 386. It was important to ascertain

whether any inhibitory factors could be removed by the solvent phase and whether any process advantages could be gained by the use of a biphasic system.

[000410] Promising results were obtained with hexane as the organic phase. Therefore, further investigations involved the use of this solvent at two different levels: 100% and 70% of the volume of the aqueous phase, with increasing substrate concentrations, up to 90 mM. The substrate was dissolved in the organic phase. The level of hexane did not appear to affect the level of product formation, particularly at the higher concentrations of 2-chloromandelonitrile.

[000411] Once again, high conversion was observed in a biphasic system, with a 76% yield of product being observed after 5 hours. The rate of product formation appeared to be slightly lower than in the corresponding monophasic system, where the reaction is complete within 1 hour. Lower enantioselectivity was observed in the biphasic system. Some possibilities which may account for these results are (i) the mass transfer rate is lower than the rate of enzyme activity or (ii) the non-polar solvent directly affects the enzyme.

[000412] At a higher substrate concentration, a very low conversion was observed, with 7 mM 2-chloromandelic acid being formed from 90 mM 2-chloromandelonitrile. This level of conversion, albeit low, was higher than that observed in the monophasic system with the same substrate concentration. These results suggest that some of the inhibitory 2-chlorobenzaldehyde or 2-chlorobenzoic acid is retained in the non-polar organic solvent.

Standard assay conditions:

[000413] The following solutions were prepared:

- Substrate stock solution: 50 mM of the cyanohydrin substrate in 0.1 M phosphate buffer (pH 8).
- Enzyme stock solution: 3.33 ml of 0.1 M phosphate buffer (pH 8) to each vial of 20 mg of lyophilized cell lysate (final concentration 6 mg protein/ml)

[000414] The reaction volumes varied between the different experiments, depending on the number of time points taken. Unless otherwise noted, all reactions consisted of 25 mM 2-chloromandelonitrile and 10% (v/v) of the enzyme stock solution (final concentration 0.6 mg protein/ml). The reactions were run at 37°C, unless otherwise stated. Controls to monitor the nitrile degradation were run with every experiment. These consisted of 25 mM 2-chloromandelonitrile in 0.1 M phosphate buffer (pH 8).

[000415] Sampling of reactions: The reactions were sampled by removing an aliquot from each reaction and diluting these samples by a factor of 8. Duplicate samples were taken for

analysis by chiral and achiral HPLC methods. The reactions were sampled at 0.5, 1, 1.5, 2, 3, and 4 hours, unless otherwise shown in the figures above.

HPLC methods

The achiral HPLC method was run on a SYNERGI-RP™ column (4 µm; 50 x 2 mm) with a mobile phase of 10 mM Na phosphate buffer (pH 2.5). A gradient of methanol was introduced at 3.5 min and increased to 50% over 1.5 min, following which the methanol was decreased to 0%. Elution times for 2-chloromandelic acid and 2-chloromandelonitrile were 2.5 and 6.1 minutes, with another peak appearing with the nitrile at 5.9 minutes.

[000416] As described above, the chiral HPLC method was optimized during the course of the investigation, to improve the separation between 2-chlorobenzoic acid and (S)-2-chloromandelic acid. The optimized method was used during the latter half of the investigation and was run on a CHIROBIOTIC-R™ column. The mobile phase was 80% Acetonitrile:20% of 0.5% (v/v) acetic acid. Elution times for (S)-2-chloromandelic acid and (R)-2-chloromandelic acid were 2.4 and 3.5 minutes respectively. A peak for 2-chlorobenzoic acid eluted at 1.9 minutes. For each experiment, a standard curve of the product was included in the HPLC run. The concentration of product in the samples was calculated from the slope of these curves.

Effect of pH

[000417] The effect of pH on the enzyme activity and enantioselectivity was studied by performance of the standard assay in a range of different buffers: 0.1 M Citrate Phosphate pH 5; 0.1 M Citrate Phosphate pH 6; 0.1 M Sodium Phosphate pH 6; 0.1 M Sodium Phosphate pH 7; 0.1 M Sodium Phosphate pH 8; 0.1 M Tris-HCl pH 8; and 0.1 M Tris-HCl pH 9. The standard enzyme concentration was used for all enzymes, with the exception of SEQ ID NOS:385, 386, where half the standard concentration was used (5% v/v of the enzyme stock solution).

Effect of temperature

[000418] The effect of temperature on the activity and enantioselectivity was investigated by performing the standard assay at a range of different temperatures: room temperature, 37°C, 45°C, 50°C and 60°C. The standard enzyme concentration was used for all enzymes, with the exception of SEQ ID NOS:385, 386, where half the standard concentration was used (5% v/v of the enzyme stock solution).

Effect of enzyme concentration

[000419] Reactions were run under standard conditions, with varying enzyme concentrations: 1%, 5% and 10% (v/v) of the enzyme stock solution. The reaction volume was normalized with the appropriate buffer.

5 Addition of solvents

[000420] The enzyme reactions were performed in the presence of methanol as a cosolvent. Methanol was added to the standard reaction mixture at the following levels: 0, 5, 10, 15 and 20% (v/v).

10 [000421] Biphasic reactions with hexane were also investigated. The aqueous phase contained 10% (v/v) of the enzyme stock solution in 0.1 M phosphate buffer (pH 8). The cyanohydrin was dissolved in the hexane, prior to addition to the reaction. Two levels of organic phase were used: 1 equivalent and 0.7 equivalents of the aqueous phase volume. In addition, a range of nitrile concentrations was investigated: 25, 45 and 90 mM. These reactions were run at room temperature.

15 [000422] Samples from these reactions were taken both from the aqueous and the solvent phase. The hexane was evaporated by centrifugation under vacuum and redissolved in a 50:50 mixture of methanol and water, so that the samples were at the same dilution as the aqueous samples. Analysis of the samples was performed by non-chiral and chiral HPLC.

Effect of process components

20 [000423] (i) Activity: The effect of the process components on the activity of the enzymes was established by addition of the individual components, 2-chlorobenzaldehyde, 2-chlorobenzoic acid or 2-chloromandelic acid, to the enzymatic reaction. The enzymatic reactions were carried out under standard conditions, in the presence of one of the 2 possible inhibitors as follows: 5, 10, 20 and 25 mM 2-chlorobenzaldehyde; 1.5 and 5 mM 2-chlorobenzoic acid; and 10, 20, 40 and 80 mM 2-chloromandelic acid. Control reactions
25 were performed under standard conditions, with no additive. At each of the sampling times, the samples were diluted to a level of 1 in 10. Control samples containing the reaction components without enzyme were used and diluted to the same level. The samples were analysed by non-chiral HPLC.

30 [000424] (ii) Stability: The stability of the enzymes to process conditions was monitored by incubation of the enzymes in the presence of the reaction components, 2-chlorobenzaldehyde and 2-chloromandelic acid for predetermined time periods, prior to assay of the enzyme activity under standard conditions. In these experiments, the enzymes were

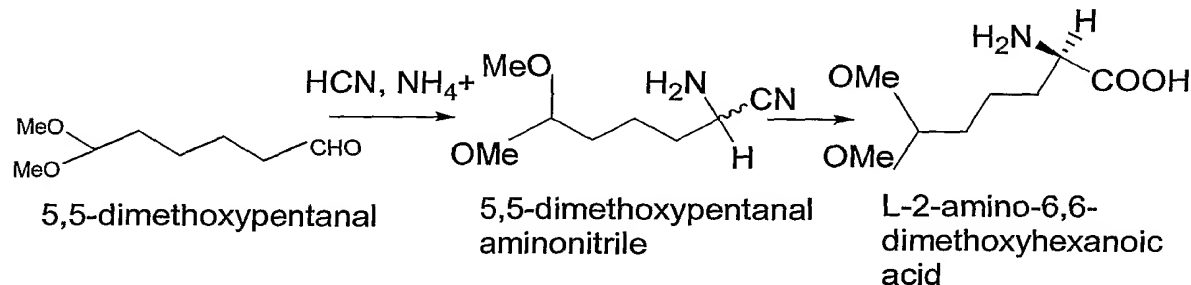
incubated at a concentration of 3 mg protein/ml in the presence of each of the following reaction components: 5, 10, 20 and 25 mM 2-chlorobenzaldehyde; and 10, 20, 40 and 80 mM 2-chloromandelic acid. Control reactions were performed by incubation of the enzyme in buffer only.

5 [000425] Assay conditions: At 0, 4, 8 and 24 hours of incubation in the particular additive, 20 μ l of the enzyme solution was removed and added to 60 μ l of a 41.6 mM substrate stock solution and 20 μ l buffer. The enzyme activity was thus assayed under standard conditions. The reactions were sampled 90 minutes after substrate addition and analyzed using the non-chiral HPLC method.

10 Scale-up of enzymatic reaction

[000426] The enzymatic reactions were run at two difference concentrations: 45 mM and 90 mM substrate. The reactions were run under standard conditions, i.e. pH 8 (0.1 M sodium phosphate buffer), 37°C and 10% (v/v) of the enzyme stock solution. The substrate was dissolved in 10% (v/v) methanol prior to addition of the buffer. The final reaction
15 volume was 20 ml and the reactions were performed with magnetic stirring.

Example 14: Optimization Of Nitrilases For The Enantioselective Production Of L-2-amino-6,6-dimethoxyhexanoic acid



[000427] Four of the isolated enzymes were shown to hydrolyze 2-amino-6-hydroxy hexanenitrile to (S)-2-amino-6-hydroxy hexanoic acid, with selectivity towards the L-enantiomer. A new target, with a similar structure to (S)-2-amino-6-hydroxy hexanoic acid was identified. A panel of the isolated nitrilases are screened against the target, 5,5-dimethoxypentanal aminonitrile. The positive enzymes are characterized on this substrate. Laboratory evolution techniques can be used to optimize these nitrilases for improved
20 enantiospecificity towards the specified target. A primary screen is used to identify putative
25 up-mutants, which is confirmed using HPLC.

[000428] Optimization of enzymes: GSSMTM and GeneReassemblyTM can be performed on selected nitrilases, in order to improve the enantioselectivity and activity of the enzymes

for the production of L-2-amino-6,6-dimethoxyhexanoic acid. Four enzymes were identified that can hydrolyze enantioselectively 2-amino-6-hydroxy hexanenitrile to L-(S)-2-amino-6-hydroxy hexanoic acid. However, a slight structural difference is present in the new target molecule, L-2-amino-6,6-dimethoxyhexanoic acid. In order to determine whether this difference affects the activity and enantioselectivity of the enzymes, the complete spectrum of nitrilases is screened against the new target.

[000429] An enzyme exhibiting the highest combination of activity and enantioselectivity for the production of L-2-amino-6,6-dimethoxyhexanoic is selected for GSSM™. Following the mutation of the target enzyme, the resulting mutants will be screened on 5,5-dimethoxypentanal aminonitrile, using high throughput screening technology. Following confirmation of the up-mutants by HPLC analysis, the individual up-mutants will be combined in order to further enhance the properties of the mutant enzymes.

[000430] In parallel to GSSM™, a GeneReassembly™ can be performed on a combination of parent enzymes, at least one of which can be selected for activity and enantioselectivity on L-2-amino-6,6-dimethoxyhexanoic acid. At least two other nitrilases, with a high degree of homology, can be reassembled with the former enzyme(s); these enzymes will be selected in order to provide diversity to the reassembled sequences.

[000431] Crucial to the success of this evolution effort is the development of a high throughput assay for enantioselectivity. Such an assay is a novel enzyme-based enantioselectivity assay that allows for the screening of >30,000 mutants in a significantly shorter time period than the traditionally used method of HPLC.

[000432] In one aspect, a non-stochastic method, termed synthetic ligation reassembly, that is related to stochastic shuffling, except that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically, can be used to create variants. This method does not require the presence of high homology between nucleic acids to be shuffled. The ligation reassembly method can be used to non-stochastically generate libraries (or sets) of progeny molecules having at least 10^{100} or at least 10^{1000} different chimeras. The ligation reassembly method provides a non-stochastic method of producing a set of finalized chimeric nucleic acids that have an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, as assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

[000433] The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In a one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (*e.g.*, T4 DNA ligase) to achieve covalent bonding of the building pieces.

[000434] In a another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized, recombined or shuffled.

[000435] In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are nitrilase enzymes. Nucleic acids encoding the nitrilases of the invention can be mutagenized in accordance with the methods described herein.

[000436] Thus, according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates encoding nitrilases are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

[000437] Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates, and preferably at almost all of the progenitor templates. Even more preferably still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

[000438] In a one aspect, the ligation reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.*, the order of assembly of each building
5 block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic, non-random). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

[000439] In another aspect, the method provides that, the ligation reassembly process is performed systematically, for example in order to generate a systematically
10 compartmentalized library, with compartments that can be screened systematically, *e.g.*, one by one. Each compartment (or portion) holds chimeras or recombinants with known characteristics. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be
15 achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

[000440] Because of its ability to perform chimerizations in a manner that is highly
20 flexible, yet exhaustive and systematic, particularly when there is a low level of homology among the progenitor molecules, the invention described herein provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the ligation reassembly method, the progeny molecules generated preferably comprise a library of finalized chimeric nucleic acid molecules having an overall
25 assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

[000441] In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that
30 can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

[000442] The synthetic ligation reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which preferably has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (i.e. each having an overhang of zero nucleotides), or preferably one blunt end and one overhang, or more preferably still two overhangs. On a double-stranded nucleic acid, a useful overhang can be a 3' overhang, or a 5' overhang. A nucleic acid building block can have a 3' overhang, a 5' overhang, two 3' overhangs, or two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design (*e.g.*, by designing sticky ends between building block nucleic acids based on the sequence of the 5' and 3' overhangs) and is not random.

[000443] According to one preferred aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos) and contacting them together under hybridization conditions so as to allow them to anneal to form a double-stranded nucleic acid building block. A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Preferred sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other preferred size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between), and upper limits of from 2 bp to 100, 000 bp (including every integer value in between).

[000444] According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. Preferably the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,GIT cassettes or alternatively using one or more N,N,N cassettes.

Example 15: Assays for Evaluation of Nitrilase Activity and Enantioselectivity

[000445] An assay method amenable to high throughput automation to increase the screening throughput both of the discovery and evolution efforts for nitrilases is described. The ideal assay is one that permits quantification of both product formation or substrate conversion and also enantiomeric excess. Two achiral and two chiral colorimetric assays that
5 are amenable to high throughput screening were developed.

Achiral Colorimetric Assays Developed:

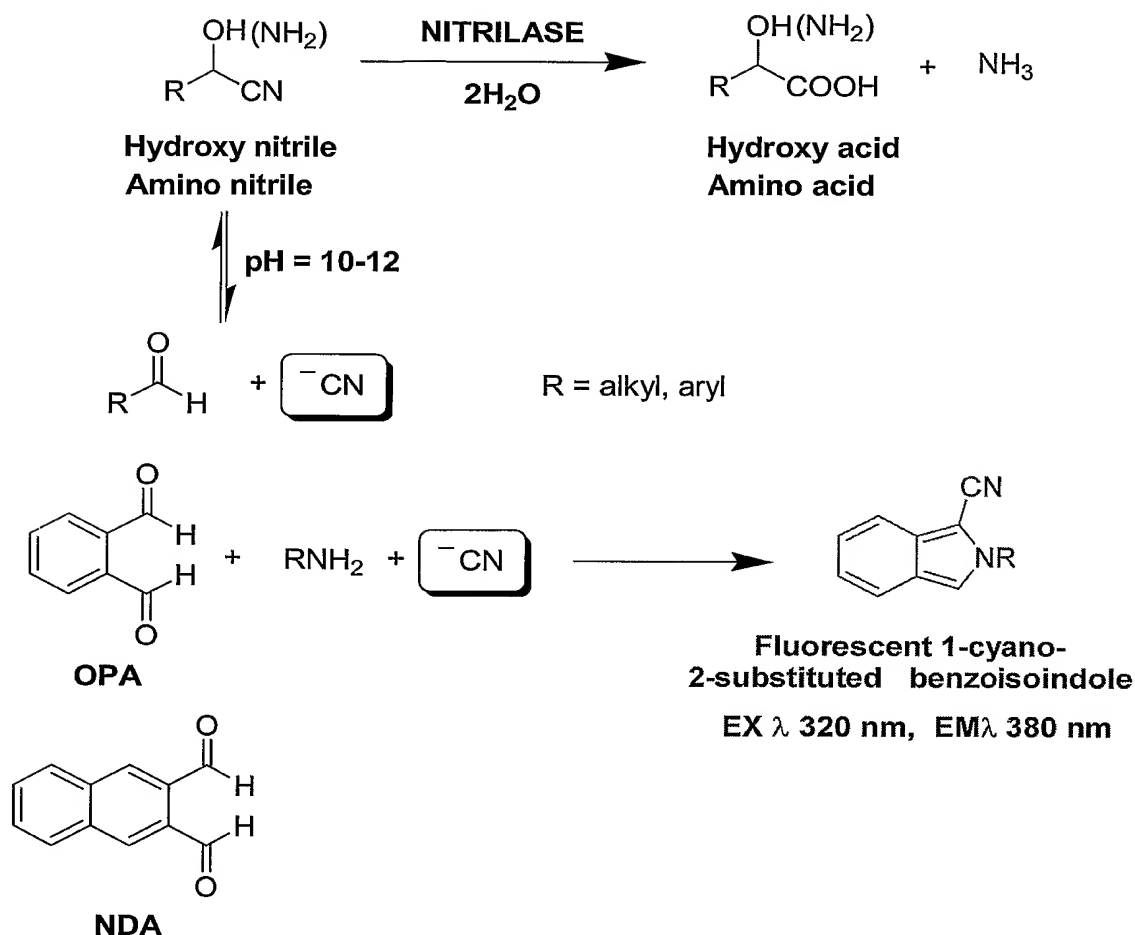
[000446] OPA assay for residual substrate. The OPA assay is Applicable to α -amino or α -hydroxy nitrile substrates. The lysis of whole cells is not necessary. These results were corroborated by HPLC for 2-chloromandelonitrile and phenyl acetaldehyde cyanohydrin.
10 The assay works best with aromatic nitriles. Aliphatic compounds exhibit a linear standard curve, fluorescence is reduced, reducing the efficacy of the assay.

[000447] LDH Assay for quantification and *ee* determination of hydroxyacid formed. The LDH assay is applicable to phenyl lactic acid but not to 2-chloromandelic acid. Use of a resazurin detection system increases sensitivity and reduces background. Background
15 fluorescence of whole cells was overcome either by centrifugation or heat inactivation prior to performing assay.

[000448] AAO Assay for quantification and *ee* determination of aminoacid formed. The AAO assay is applicable to phenylalanine and (S)-2-amino-6-hydroxy hexanoic acid. The use of the Amplex Red detection system increases sensitivity. Cell lysis was shown not be
20 necessary. Cells are grown in defined media in order to prevent background fluorescence.

OPA Assay

[000449] The *o*-phthalaldehyde (OPA) fluorescence based nitrilase assay is used to quantify the amount of α -hydroxynitrile substrate remaining. OPA reacts with the cyanide released from the pH controlled decomposition of α -hydroxynitriles to the corresponding
25 aldehyde and cyanide to yield a fluorescent, quantifiable product. OPA reacts with the cyanide released from the pH controlled decomposition of α -hydroxynitriles to the corresponding aldehyde and cyanide to yield the fluorescent 1-cyano-2-R benzoisindole.



[000450] Standard curves were established for the following substrates: 2-Chloromandelonitrile (CMN, 0.998), Cyclohexylmandelonitrile (CHMN, 0.99),

5 Acetophenone aminonitrile (APA, 0.99), and Phenylacetaldehyde cyanohydrin (PAC, 0.97), (Figure 5), (R^2 values in parentheses). A standard curve for Phenylglycine (PGN, 0.93) was also established. Three of the substrates tested, Dimethylbutanal aminonitrile (DMB) (2-amino-4,4-dimethyl pentanenitrile), Hydroxypivaldehyde aminonitrile (HPA) and Pivaldehyde aminonitrile (PAH), gave very low fluorescence readings and unreliable results

10 under the original assay conditions. For these compounds a number of parameters were adjusted, however the fluorescent signal strength of these compounds was not increased by these manipulations.

[000451] In an attempt to increase the fluorescent signal of these three compounds, naphthalene dicarboxaldehyde (NDA) was substituted for OPA. Standard curves for PAH,

15 HPA and DMB with either OPA or NDA were constructed. To determine sensitivity and background fluorescence, a lyophilized nitrilase lysate (SEQ ID NOS:189, 190) with

suspected catalytic activity on each of the substrates was added. Hydrolysis was detected in three out of four of the compounds. NDA sharply boosted the signal, often by an order of magnitude, though this reduced linearity is presumably due to signal saturation.

[000452] NDA was established as an alternative detection reagent for the aliphatic compounds. However, it is desirable for the assay to utilize the same detection system for all of the substrates since this would facilitate the automated evaluation of multiple nitrilase substrates. The current OPA based assay is effective for the analysis of PAC, CMN, CHMN, APA, MN and PGN. While standard curves have been developed for the aliphatic compounds PAH, HPA, and DMB.

10 Whole cell optimization

[000453] The effect of addition of lyophilized nitrilase lysate to the assay components, either untreated or heat inactivated, was evaluated. Interfering background fluorescence was not observed in either case. The OPA assay was next evaluated and optimized for nitrilase activity detection in a whole cell format. Both nitrilase expressing whole cells and *in-situ* lysed cells were evaluated. Lyophilized cell lysates were evaluated alongside their respective whole cell clones as controls. For this optimization study, mandelonitrile (MN) was chosen as a model substrate.

[000454] The lyophilized cell lysate of SEQ ID NOS:187, 188 was evaluated alongside whole cells expressing SEQ ID NOS:187, 188 and *in situ lysed* cells expressing SEQ ID NOS:187, 188. The addition of whole cells did not affect fluorescence nor result in fluorescence quenching. Addition of any of the three cell lysis solutions improved permeability (and therefore conversion) of mandelonitrile in the whole cell systems. Three cell lysing solutions were evaluated: B-PER (Pierce), BugBuster (Novagen) and CellLytic B-II (Sigma) and were found not to have a deleterious affect on the OPA assay. The addition of product α -hydroxyacid or α -aminoacid did not affect detection by the OPA assay.

[000455] The assay was modified from its original format, which required several liquid transfer steps, into a one plate process, where cell growth, nitrile hydrolysis and OPA assay reaction occurred in the same microtiter plate. Mandelonitrile was tested using this single well format. In this case, the *E. coli*. Gene site-saturation mutagenesis (GSSMTM) cell host was evaluated. Three clones were tested: SEQ ID NOS:101, 102, SEQ ID NOS:187, 188, and an empty vector, which was used as a control. Hydrolysis was evaluated at four timepoints, at 10 and 20 mM, and also with a 0 mM control. In an earlier experiment, clone

SEQ ID NOS:187, 188 was evaluated against the phenylacetaldehyde cyanohydrin substrate (for which this enzyme does not exhibit activity), and no activity was observed.

[000456] The OPA assay was found to detect the presence of both α -hydroxy and α -amino nitrile substrate. Aromatic compounds were readily detectable with the assay, while aliphatic compounds posed some detection challenges. No background issues were evident when using lyophilized cell lysates, *in-situ* lysed whole cells or unlysed whole cells. The assay is amenable to one-plate analysis, where cells are grown, incubated with the substrate, and assayed on the same plate: no liquid transfers are required, easing automation. While all nitriles tested produced a linear response, aliphatic compounds gave a low fluorescent response.

Chiral LDH Assay

[000457] A spectroscopic system based on lactate dehydrogenase (L-LDH) was developed for the analysis of the chiral α -hydroxy acids which are generated by the nitrilase catalyzed hydrolysis of cyanohydrins. The hydroxynitrile substrate is not metabolized by the secondary or detection enzyme and thus starting material does not interfere. Cell lysate which is not heat treated results in background activity for the LDH system; however, heat inactivation or pelleting of the cell lysates eliminates the background activity. (See Figure 4.)

[000458] The activity and enantiomeric specificity of commercially available D- and L-lactate dehydrogenases against the nitrilases disclosed herein was evaluated. An LDH was identified which is suitable to both D- and L-phenyl lactic acid analysis. An enzyme suitable for 2-Chloromandelic acid analysis was not found. The chosen LDH enzymes exhibited virtually absolute stereoselectivity. The viability of the assay to detect D- and L-LDH produced from PAC using lyophilized cell lysate was established.

[000459] Originally, three colorimetric dyes were evaluated, all of which are tetrazolium salts: NBT (3,3'-dimethoxy-4,4'-biphenylene)bis[2,(4-nitrophenyl)-5-phenyl-2H]-, chloride) MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) INT (2-(4-Iodophenyl)-3-(4-nitrophenyl)-5-phenyl-2H-tetrazolium chloride). The insolubility of the product of these detection system posed an analytical challenge. To address this, another tetrazolium salt with a reportedly soluble product, XTT (2,3-Bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide, was evaluated. While XTT yielded a soluble bright red product, the substrate was insoluble which thus effected the same analytical challenges. As an alternative to the tetrazolium family of dyes, the dual

colorimetric/fluorometric dye resazurin was evaluated. Oxidation of resazurin produces resourfin. Both substrate and product are soluble, and the color change can be quantified colorimetrically or fluorimetrically, increasing accuracy. Due to the sensitivity of resazurin, 0.05 mM of lactic acid can be quantified. Optimal results were obtained when using the dye in the same range as the substrate, e.g. 0.5 mM resazurin can quantify a range of lactic (and analogs) from 0.05 to 0.5, though the best linearity is at the lower end of this scale. Resourfin was stable over 28 hours, and had a linear fluorescent response.

[000460] In the presence of the LDH assay components, lyophilized enzyme gave background fluorescence/absorption. To address this problem the lysate was boiled for 10 minutes and then centrifuged. This resulted in a 90% decrease in background signal. Interestingly, both centrifugation alone (5 minutes @ 14.1 rcf) or boiling followed by centrifugation (5 minutes @ 100°C) reduced the fluorescence to background levels. In a high-throughput format such as 1536 well plates, spinning would be preferable to boiling, as boiling would increase evaporation (8 µl well size) and potentially volatilize the nitrile substrates. No background signal resulting from growth media (LB and TB and M9) or cell lytic solutions (B-PER, CellLytic and BugBuster) was noted.

Chiral AAO Assay

[000461] A spectroscopic system based on amino acid oxidase (AAO) was developed for the analysis of the chiral α -amino acids which are generated by the nitrilase catalyzed hydrolysis of amino nitriles.

Assay Development and Validation

[000462] The initial assay validation utilized the 2,2'-azino-di-{3-ethylbenzothiazoline-6-sulfonic acid (ABTS) detection system as outlined above. However, since the color was not stable further investigations utilized the phenol amino antipyrine (PAAP) detection system which is analyzed at λ max 510nm. Enzymes with suitable activity were found for each enantiomer of 4-methyl-leucine, phenylalanine, (S)-2-amino-6-hydroxy hexanoic acid, and *tert*-leucine. The assay is not applicable to methylphenylglycine and does not work well with phenylglycine.

[000463] Standard curves were generated for phenylalanine from 0-15 mM. The curve is much more linear when the concentrations remained below 1 mM. The color remains stable for several days as long as it is kept in the dark. Three cell lysing solutions Bug Buster

(BB), Bacterial Protein Extracting Reagent (BPER), and Cell Lytic Reagent (CLR) were added to the standard curve and shown to have no affect on color development. The addition of cell lysate (cl) did not exhibit background color formation. Addition of the phenylacetaldehyde aminonitrile sulfate (PAS) starting material also showed no effect on color formation.

[000464] The AAO system exhibits greater linearity at up to 1 mM substrate. The concentration of the AAO enzymes and of the acid substrate were adjusted to try to move the intersection of the L-AAO and D-AAO curves closer to the middle of the graph. Premixing the PAAP, the HRP, and the AAO was demonstrated to be effective and caused no change in observed activity establishing that the assay components may be added to the assay in a cocktail format.

[000465] A high level of background was observed for the AAO assay of whole cells and this was attributed to the L-amino acids present in the TB and LB growth media. Washing and resuspension of the cells in M9 media eliminated background. For all future experiments cells were grown in M9 media with 0.2% glucose. The lysed cells gave only a slightly better response than unlysed cells. Therefore, cell lysis is not necessary. SEQ ID NOS:187, 188 demonstrated activity on HPA in primary screening based on HPLC analysis.

[000466] The use of a fluorescent detection system which would permits implementation of the assay in ultra high throughput fashion such as 1536 well or gigamatrix format was investigated. The fluorescent reagent most applicable to our system is Amplex Red from Molecular Probes which produces the highly fluorescent resorufin (λ_{ex} 545 nm; λ_{em} 590nm) Standard curves for phenylalanine and (S)-2-amino-6-hydroxy hexanoic acid were established (0-100 μM).

[000467] In preparation for assay automation, nitrilase expressing cells were added into microtiter plate containing M9 0.2% glucose, 0.25 mM IPTG media by fluorescence activated cell sorting (FACS). Three nitrilase expressing subclones, and the empty vector control were evaluated: SEQ ID NOS:101, 102, SEQ ID NOS:187, 188, SEQ ID NOS:29, 30 and the empty vector. The viability of the cells following cell sorting proved to be inconsistent. Thus colony picking is currently being evaluated as an alternative method to add cells into microtiter plates. The evaporative loss from an uncovered 1536-well microtiter plate is approximately 30% per day in the robot incubator (incubator conditions: 37°C at 85% relative humidity (RH)). Incubation in the 95% RH incubator reduced evaporative loss to 1% per day.

[000468] The ability of the three subclones to grow in the presence of up to 3.5 mM of nitrile was established using HPA nitrile. Growth rates were only slightly retarded (less than 30%). Subclones grown in the presence of HPA were shown to express a nitrilase that catalyzes the formation of hydroxy norleucine (HNL) as established using the Amplex Red detection system. Only *S* was evaluated as the enzymes are *S*-selective. The reaction plate was read at 10 minute intervals, with 40 minutes showing the best linearity. While cell growth is significantly inhibited above 5 mM of HPA when the cells were grown at pH 7, growth was inhibited above 0.1 mM HPA for cells grown at pH 8.

[000469] In order to verify the AAO results by HPLC, a reaction was performed using high concentrations of HPA, up to 40 mM (due to HPLC detection challenges for (S)-2-amino-6-hydroxy hexanoic acid) and lyophilized cell lysate SEQ ID NOS:187, 188.

Comparison AAO and HPLC data for HNL

[HNL] mM	%ee		%conversion	
	AAO	HPLC	AAO	HPLC
40	89%	100%	17%	18%
30	89%	97%	29%	36%
20	86%	97%	21%	34%
10	78%	98%	13%	35%

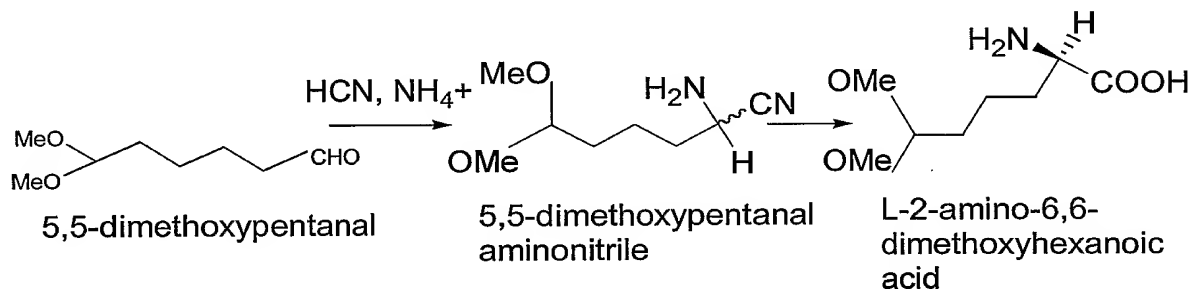
[000470] In order to determine if conducting the screen at a lower concentration introduces a bias in the results compared to the 20 mM substrate range that was used for HPLC based screens, an experiment was performed with SEQ ID NOS:187, 188 using three concentration ranges. Each experiment was done in triplicate in order to remove any nonsystematic error.

[000471] The AAO assay can be run on 384 or 1536 well format with cells sorted into an M9 0.2% glucose, 0.25 mM IPTG media. Cells can be grown in the presence of nitrile (in this case HPA), or the cells can be allowed to reach a certain density and the nitrile can then be added. Though cell lytic reagents do not interfere with the assay, when HPA was assayed, addition of the lytic reagents was found to be unnecessary. Either pre- or post- nitrile addition, the mother plate will have to be split into daughter plates, which are then assayed for the respective L- and D- enantiomer content. Incubation times with the AAO/Amplex Red reagents can be adjusted so that the D- and L- plate are read at separate times.

Example 16: Identification, Development and Production of Robust, Novel Enzymes
Targeted for a Series of High-Value Enantioselective Bioprocesses

[000472] The invention provides for the development of nitrilases, through directed evolution, which provide significant technical and commercial advantages for the process manufacturing of the following chemical target:

L-2-amino-6,6-dimethoxyhexanoic acid



[000473]

Nitrilase enzymes were shown to hydrolyze 2-amino-6-hydroxy hexanenitrile to (S)-2-amino-6-hydroxy hexanoic acid, with selectivity towards the L-enantiomer. The panel of nitrilases was screened against the target, 5,5-dimethoxypentanal aminonitrile. The positive enzymes were characterized on this substrate. A primary screen is used to identify putative up-mutants, which is then confirmed using HPLC.

[000474] GSSM™ and GeneReassembly™ are performed on selected nitrilases, in order to improve the enantioselectivity and activity of the enzymes for the production of L-2-amino-6,6-dimethoxyhexanoic acid. Nitrilases were identified for the enantioselective hydrolysis of 2-amino-6-hydroxy hexanenitrile to L-(S)-2-amino-6-hydroxy hexanoic acid. However, a slight structural difference is presented by the new target molecule, L-2-amino-6,6-dimethoxyhexanoic acid. In order to determine whether this difference affects the activity and enantioselectivity of the enzymes, the complete spectrum of nitrilases was screened against the new target.

[000475] First, identification of the correct target gene for GSSM through more detailed characterization of the hit enzymes for the production of L-2-amino-6,6-dimethoxyhexanoic acid was carried out. This effort involves a more extensive investigation of the effects of pH

and temperature on activity and enantioselectivity and a more in-depth analysis of the stability of the enzyme to process conditions. Prior to initiation of the screening, the synthesis of a single enantiomer of an alkyl aminonitrile is done; the racemization of this nitrile is studied, in an effort to understand the relationship between this factor and

5 enantioselectivity of the enzymes.

An enzyme exhibiting the highest combination of activity and enantioselectivity for the production of L-2-amino-6,6-dimethoxyhexanoic acid is selected for GSSM. Following the mutation of the target enzyme, the resulting mutants are screened on 5,5-dimethoxypentanal aminonitrile, using high throughput screening technology. Following

10 confirmation of the up-mutants by HPLC analysis a decision point is reached, in order to evaluate the results of the GSSM on the target.

[000476] In parallel to GSSM™, a GeneReassembly™ is performed on a combination of parent enzymes, at least one of which is selected for activity and enantioselectivity on L-2-amino-6,6-dimethoxyhexanoic acid. At least two other nitrilases are reassembled with the

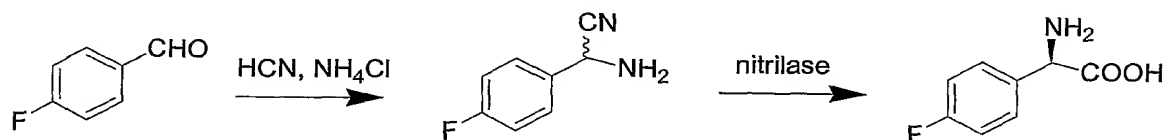
15 former enzyme(s); these enzymes are selected in order to provide diversity to the reassembled sequences.

[000477] The present invention provides for development of racemization conditions for the original substrate aminonitriles. In addition, the present invention provides for the identification of enzymes capable of the conversion of these aminonitriles to the target α-amino acids by dynamic kinetic resolution. The present invention also provides for

20 screening and development of a nitrilase-catalyzed kinetic resolution process for (R)-2-amino-6,6-dimethoxy hexanoic acid (allysine) production. (S)-2-amino-6-hydroxy hexanoic acid will be used as a model substrate for development of the kinetic resolution.

The target α-amino acid products are shown below:

25 (i) D-4-Fluorophenylglycine

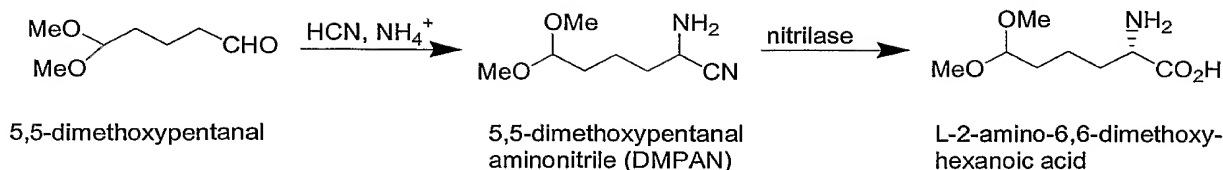


4-fluorobenzaldehyde

4-fluorophenylglycinonitrile (FPGN)

D-4-fluorophenylglycine

(ii) L-2-Amino-6,6-dimethoxyhexanoic acid (Allysine)



[000478] Conditions are developed for the racemization of the aminonitrile substrates for the nitrilase-catalyzed production of D-4-fluorophenylglycine and 2-amino-4,4-dimethyl pentanenitrile (allysine). Two model substrates, phenylglycinonitrile and pentanal aminonitrile are used initially, and racemization is studied in the absence of the enzyme. Concurrently determination of the performance of one or more available nitrilases under a variety of possible racemization conditions is carried out. In addition, the nitrilases are screened against hydroxypentanal aminonitrile for the production of (S)-2-amino-6-hydroxy hexanoic acid, and the promising enzymes are optimized. Once racemization conditions are established, the nitrilases are screened for activity. Further optimization for a kinetic resolution of the product is performed.

[000479] A number of enantioselective nitrilases were identified for the hydrolysis of α -aminonitriles to α -amino acids. While these enzymes were shown to have a preference for the required enantiomer of certain aminonitriles, a limiting factor in the further screening, development and comparison of candidate nitrilases is the rate of racemization of the aminonitrile substrates under the reaction conditions.

Aromatic aminonitrile racemization

[000480] The first step is to establish conditions under which aromatic aminonitrile racemization occurs, using the model substrate, phenylglycinonitrile. Racemization strategies include, but are not limited to the list below. Options are roughly prioritized according to their commercial applicability.

(1) Manipulation of the pH of the reaction. Since it has been shown that racemization is rapid at high pH, this approach requires the discovery and optimization of nitrilases which are active and selective at $\text{pH} > 10$.

(2) Addition of known chemical racemizing agents, such as aldehydes, ketones, weak bases, resins, metal ions, Lewis acids etc., which can enhance racemization at lower pH.

(3) Synthesis of N-acylated aminonitrile derivatives, *e.g.* N-acetyl phenylglycinonitrile, which may be more easily racemized. In the case of N-acetyl phenylglycinonitrile, a selective D-acylase which removes the acetyl group would enhance the optical purity of the nitrilase product.

(4) Use of a biphasic system in which base-catalyzed racemization occurs in the hydrophobic organic phase and enzymatic hydrolysis in the aqueous phase.

(5) Use of a 2-enzyme system comprised of a nitrilase and an aminonitrile racemase. One amino acid racemase is commercially available at present, and will be tested for activity against phenyl- and fluorophenylglycinonitrile. Gene libraries will be searched for genes showing homology to known amino acid amide racemases, hydantoin racemases or any other racemases which can be identified.

5 [000481] Once conditions for this racemization have been established, they provide the basis for development of conditions for racemization of the target aromatic substrate, 4-fluorophenylglycinonitrile (FPGN). The FPGN is expected to be less stable than the model substrate; thus, it may racemize more quickly, but degradation reactions may be faster as well. The ability of sample enzyme(s) to tolerate and/or function well under them is
10 evaluated. Final optimization of screening methods include the target substrates, sample nitrilases, and substrate racemization conditions.

[000482] Investigations carried out have shown that phenylglycinonitrile is easily racemized at pH 10.8. However, it does not appear that any of the existing enzymes can tolerate such harsh conditions of pH. Samples from highly alkaline environments are
15 screened for the presence of nitrilases which are tolerant to such conditions. Once discovered, the enzymes are sequenced and subcloned, and the enzymes are produced as lyophilized cell lysates ready for screening.

Aliphatic aminonitrile racemization

[000483] A model aliphatic aminonitrile, pentanal aminonitrile, is synthesized in its
20 racemic form. However optically enriched samples are prepared using one the following approaches: (i) preparative chiral HPLC; (ii) diastereomeric salt resolution; (iii) diastereomeric derivatization or column chromatography; (iv) synthesis from L-N-BOC norleucine. An HPLC assay is used for the detection of these compounds.

HPLC Assay

25 [000484] An HPLC assay for the detection of the (S)-2-amino-6-hydroxy hexanoic acid is used. An assay involving pre-column derivatization is used.

Screening/Characterization:

[000485] Nitrilases are screened against 2-amino-6-hydroxy hexanenitrile. For enzymes capable of performing well at greater than 25 mM substrate, scale up reactions are performed.

30 The substrate/product tolerance and stability profiles of the other enzymes are investigated.

[000486] The nitrilases are screened, and hits are characterized, focusing on pH and temperature optimum, enantioselectivity and stability under the reaction conditions.

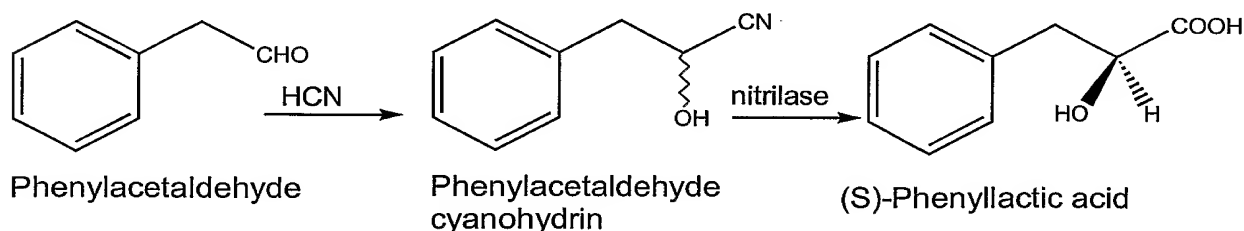
Enzyme Evolution

[000487] A target enzyme exhibiting the desired properties is selected for GSSM™. Following the mutation of the target enzyme, the resulting mutants are screened on the substrate using high throughput screening technology. Once the up-mutants have been confirmed by HPLC analysis, the individual mutations responsible for increased performance may be combined and evaluated for possible additive or synergistic effects.

[000488] In addition, a GeneReassembly™ will be performed on a combination of lead enzymes, which are selected for their desirable characteristics, including activity, enantioselectivity and stability in the reaction.

Example 17: Optimization of Nitrilases for the Enantioselective Production of (S)-Phenyllactic Acid

[000489] Nitrilases were identified for the enantioselective hydrolysis of 5 different nitrile substrates. These nitrilases were isolated and optimized for selected targets. The optimization involves process optimization and directed evolution. In particular, enzymes specific for the production of (S)-phenyllactic acid were characterized and optimized. This was aimed primarily at improving the activity of the enzymes, while maintaining a high enantioselectivity. An investigation into the effects of process conditions on the enzymes was also performed.



[000490] The development of high throughput assays for screening of mutants from potential directed evolution efforts was accomplished. Two achiral and two chiral colorimetric assays that are amenable to high throughput screening were developed and used for nitrilase directed evolution.

[000491] SEQ ID NOS:103, 104 was identified as a highly enantioselective nitrilase for the production of (S)-phenyllactic acid. Characterization of SEQ ID NOS:103, 104 shows the optimum reaction pH and temperature to be pH 8 and 37°C, respectively; the reaction starting material, phenylacetaldehyde, and the product, phenyllactic acid showed no effect on

the enzyme activity up to levels of 5 mM and 30 mM, respectively. The scaled-up enzymatic reaction with an enantiomeric excess (*ee*) of 95%.

Example 18: Directed Evolution of a nucleic acid encoding a nitrilase enzyme.

[000492] The *nitB* gene (GenBank Accession No. AX025996, from *Alcaligenes*
5 *faecalis*) was subjected to Gene Site Saturated Mutagenesis™ or GSSM™ to generate a library of single amino acid substitution mutants covering the entire enzyme. The sequence of the "parental" *nitB* gene used in the directed evolution is SEQ ID NO: 103, 104. A *nitB* mutant library was generated from carrying out GSSM™. This *nitB* mutant library was then screened for clones with increased whole cell hydroxymethylthiobutyronitrile (HMTBN,
10 which is a nitrilase substrate) activity. The product of the nitrilase reaction on that substrate is hydroxymethylthiobutyric acid (HMTBA).

[000493] Assays were run at 35°C with 100mM HMTBN and 100mM K₃PO₄, pH 7 to approximately 30-40% conversion. Two methods were used to quantitate HMTBN conversion, one being direct measurement of HMTBS produced by HPLC analysis and the
15 other being indirect detection of residual HMTBN using the fluorescent cyanide assay, which has previously been described.

[000494] Putative *nitB* up mutants were subjected to a secondary assay to confirm the increased activity. In the secondary assay, up mutants and the wild type control were induced in expression medium in shake flasks. Shake flask cultures are then washed with 100mM
20 K₃PO₄, pH7 and resuspended to the same optical density at 660nm. Kinetic assays were then performed with the normalized cell resuspensions under the same conditions used in the initial assays. Putative up mutants confirmed to have increased HMTBN activity were sequenced and tested for increased activity after transformation back into the same expression strain to ensure that increases in activity are not due to host mutations.

25 [000495] A confirmed *nitB* GSSM™ up-mutant is *nitB* G46P, which contains a glycine (GGT) to proline (CCG) substitution at amino acid 46. The whole cell HMTBN activity of this mutant is approximately 50% greater than that of wild type *NitB* at both 25°C and 35°C. Upon identification of the beneficial G46P mutation, GSSM™ was used again to generate a pool of double mutants using the *nitB* G46P template. These mutants all contain the G46P
30 mutation and an additional single amino acid substitution at a random site. The double mutants were assayed for HMTBN activity greater than that of *nitB* G46P. Double, triple and quadruple mutants were created in order to speed up the mutation process and identify beneficial mutations more quickly. After the first few beneficial mutations were identified

and isolated, they were combined to generate double mutants, the best of which was DM18. DM18 was used as a template to generate triple mutants. The most active triple mutant was TM3 and that was used as a template to generate quadruple mutants. The most active quadruple mutant was QM2. The table summarizes these mutations.

mutant	mutation 1	mutation 2	mutation 3	mutation 4
DM18	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)		
TM3	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)	L(ctt) 170 T(act)	
QM2	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)	L(ctt) 170 T(act)	A(gcg) 197 N9(aat)

[000496] The mutants were characterized first by studying their whole cell HMTBN activity. At 100 mM HMTBN, the HMTBS production rate of QM2 is 1.2 times greater than that of the parental gene. However, at 200 mM HMTBN, the rate of QM2 is 3.6 times that of the parental gene. The productivity of these mutants is increased considerably when the HMTBN concentration is raised from 100 mM to 300 mM. As to conversion rates, TM3 completely converted the substrate after 270 minutes and both DM18 and SM show greater than 75% conversion after this time. To further address the issue of HMTBN concentration effects on activity/productivity of NitB, several mutants were assayed at both 400 mM and 528 mM HMTBN. NitB is essentially inactive at these substrate concentrations, however the mutants retain significant activity at these concentrations. In particular, the activity at these high concentrations were essentially the same as their activity at 200 mM substrate. Therefore, the mutants can be used over a wide substrate concentration range and provide much more flexibility in utility than the NitB parental gene.

[000497] The mutants were shown to have higher expression levels than the parental gene and it also appeared that the QM2 and TM3 mutants contained a greater proportion of soluble enzyme than the wild type as seen in SDS-PAGE analysis. As to stability, all of the enzymes showed essentially the same stability pattern at both 25°C and 35°C.

[000498] Finally, the mutants were subjected to codon-optimization. The approach was to optimize the codons and therefore increase the expression levels in the particular host cell. That would, in turn, increase the activity per cell of the enzyme. This resulted in increased whole cell activity in the codon-optimized mutants as compared to controls. The increase in activity was approximately double the activity. An *E. coli* expression system was used.

Example 19: Selected Examples of Compounds Produced From a Nitrilase-Catalyzed Reaction

[000499] The compounds listed in Figure 15 are selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[000500] In addition, the following are potential products which can be made via the nitrilase Strecker format. More than 100 amino acids and many new drugs can be produced from their respective aldehydes or ketones utilizing the nitrilase enzymes of the invention.

For example, large market drugs which can be synthesized using nitrilases of the invention include homophenylalanine, VASOTECT™, VASOTERIC™, TECZEM™, PRINIVIL™, PRINZIDE™, ZESTRIL™, ZESTORETIC™, RAMACE™, TARKA™, MAVIK™, TRANDOAPRIL™, TRANDOLAPRILAT™, ALTACE™, ODRIK™, UNIRETIC™, LOTENSIN™, LOTREL™, CAPOTEN™, MONOPRIL™, TANATRIL™, ACECOL™, LONGEST™, SPIRAPRIL™, QUINAPRIL™, and CILAZAPRIL™. Other chiral drugs include DEMSER™ (alpha-methyl-L-Tyrosine), ALDOCHLOR™, LEVOTHROID™, SYNTHROID™, CYTOMEL™, THYOLAR™, HYCODAN™, CUPRIMINE™, DEPEND™, PRIMAXIN™, MIGRANOL™, D.H.E.-45, DIOVAN™, CEFEBID™, L-DOPA, D-DOPA, D-alpha-methyl-DOPA, L-alpha-methyl-DOPA, L-gamma-hydroxyglutamate, D-gamma-hydroxyglutamate, 3-(2-naphthyl)-L-alanine, D-homoserine, and L-homoserine.

[000501] Furthermore, the nitrilase enzymes of the invention can be useful for synthesizing the following amino acids. Many of these amino acids have pharmaceutical applications. D-phenylglycine, L-phenylglycine, D-hydroxyphenylglycine, L-hydroxyphenylglycine, L-tertiary leucine, D-tertiary leucine, D-isoleucine, L-isoleucine, D-norleucine, L-norleucine, D-norvaline, L-norvaline, D-2-thienylglycine, L-2-thienylglycine, L-2-aminobutyrate, D-2-aminobutyrate, D-cycloleucine, L-cycloleucine, D-2-methylphenylglycine, L-2-methylphenylglycine, L-thienylalanine, and D-thienylalanine.

[000502] The enzymes of the nitrilase enzymes of the invention can be useful for the synthesis of the following natural amino acids: glycine, L-alanine, L-valine, L-leucine, L-isoleucine, L-phenylalanine, L-tyrosine, L-tryptophan, L-cysteine, L-methionine, L-serine, D-serine, L-threonine, L-lysine, L-arginine, L-histidine, L-aspartate, L-glutamate, L-asparagine, L-glutamine, and L-proline. The following are examples of unnatural amino acids which can be produced using the nitrilase enzymes of the invention. D-alanine, D-valine, D-leucine, D-isoleucine, D-phenylalanine, D-tyrosine, D-tryptophan, D-cysteine, D-methionine, D-threonine, D-lysine, D-arginine, D-histidine, D-aspartate, D-glutamate, D-asparagine, D-glutamine, and D-proline.

[000503] Furthermore, nitrilase enzymes of the invention can be used in non-Strecker chemical reactions including the synthesis of more chiral drugs such as TAXOTERE™ as well as chiral drugs containing 3-hydroxy-glutaronitrile (a \$5.5B market); LIPITOR™, BAYCOL™, and LESCOT™. Chiral product targets that are not drugs include

5 PANTENOL™, L-phosphinothricin, D-phosphinothricin, D-fluorophenylalanine, and L-fluorophenylalanine. Finally, nitrilase can be used to produce unnatural amino acid compounds lacking a chiral center such as sarcosine, iminodiacetic acid, EDTA, alpha-aminobutyrate, and beta-alanine.

Figure 16 examples of substrates and products produced by the nitrilases of the invention and/or the methods of the invention. The chemical structures of the substrates and of the products are shown. The chemical reactions shown here are non-limiting examples of activities of the nitrilases of the invention.

Example 20: Exemplary Preparation Using a Polypeptide of a Variant of SEQ ID NO:210

[000504] The variant, nitrilase 1506-83-H7A, is SEQ ID NO:210 with the Ala at residue 15 190 replaced with His. At the codon level, the mutation that occurred was GCT to CAT. This variant exhibits improved enantioselectivity in the conversion of 3-hydroxyglutarylnitrile (HGN) to (R)-4-Cyano-3-hydroxybutyrate.

[000505] This variant has been demonstrated to perform this transformation in 100 mM pH 7 sodium phosphate buffer at room temperature. This mutant can perform in other buffer 20 systems and temperatures as well with the potential for providing additional altered properties. Exemplary properties include, but are not limited to, altered rates of the reaction, % ee, and stability. In particular, the altered properties can be a higher reaction rate, a higher % ee, and greater stability. Altered properties can be an increase or decrease of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% more than 25 wildtype.

[000506] This variant was shown to perform the transformation by producing products in high enantiomeric excess of 10 mM to 3 M substrate (HGN). Higher or lower substrate concentrations are also possible. Enantiomeric excess greater than or equal to 95% have been achieved. However, enantiomeric excess can be at least 25%, 30%, 35%, 40%, 45%, 50%, 30 55%, 60%, 65%, 70%, 75%, 80%, 85%, or 90% more than wildtype.

[000507] Variants of the SEQ ID NOs: of the invention, can be cloned into expression vectors. For example, variants of nucleic acid sequence SEQ ID NO:195, 205, 207, 209, OR 237, and nucleotides that encode the variants of amino acid sequence SEQ ID NO:210 can

be cloned into exemplary vectors that include, but are not limited to, pSE420 (E. coli expression vector) and pMYC (pseudomonas expression vector).

Example 21: Preparation using variants of the invention:

[000508] Add 3-Hydroxyglutaronitrile (1 g, 9 mmol) drop-wise to a stirred solution of nitrilase cell lysate (normalized for 150 mg protein content) in 2.12 mL of 100 mM pH 7 sodium phosphate buffer at room temperature, ~22 °C. Stir this 3 M reaction by magnetic stir bar for 24 hours at room temperature. Monitor the progress of the reaction by TLC (Thin Layer Chromatography) and GC (Gas Chromatography). The reaction should be complete within 24 hours.

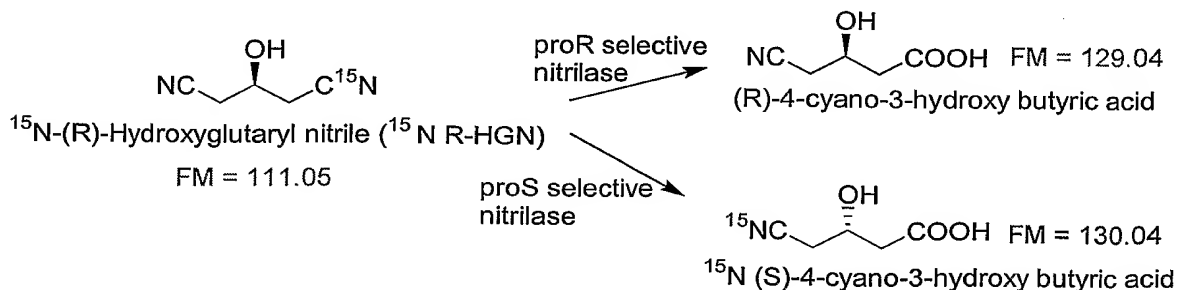
[000509] Other variants contemplated herein include, but are not limited to the following: N111S; A190H, S, Y or T; F191L, V, M, D, G, E, Y or T; M199E, orL; D222L; A55K, G, or Q; I60E, or any combination thereof.

Example 22: Screening Assay for Enantioselective Transformation

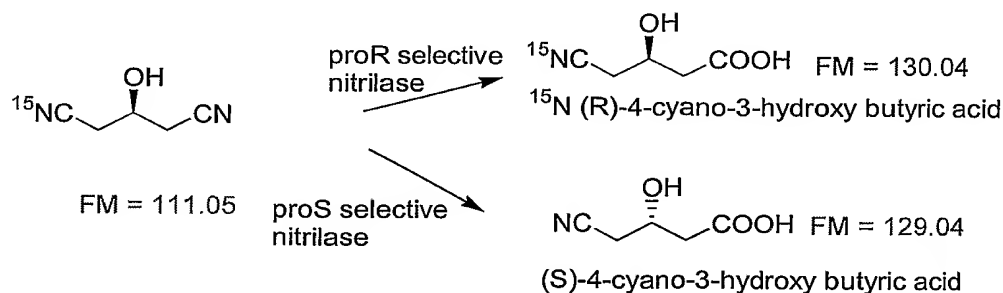
[000510] A new method to screen for enantioselective transformation, for example, of a prochiral substrate into a chiral one that affords the ability to monitor enantiomeric excess (% ee) of the resultant product is disclosed. This approach can also be applied to determine diastereomeric excess (% de).

[000511] For example, by labeling one of the two prochiral or enantiotopic moieties in a molecule, for example by the use of a heavier or lighter isotope, the modification of one of the two moieties by a selective catalyst, for example, an enzyme, can be established by mass spectroscopy (MS).

[000512] By performing the exemplary nitrilase reaction on ^{15}N -(R)-HGN (R) (as shown in Figure 17) or ^{15}N -(S)-HGN, one can determine the enantioselectivity of the enzyme by analyzing the amount of each of the two possible labeled versus unlabeled acid products which can be formed.



[000513] The screening experiment may be performed in either direction. The screening experiment can be used for both the ^{15}N -(R)- and (S)-HGN moieties. In fact, to ensure that the label does not effect any artifactual changes, at the onset, both should be investigated.

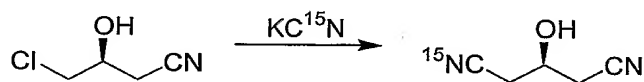


[000514] To equate the observed enantiomeric excess resulting from the nitrilase transformation, the following exemplary formula may be applied:

% ee = $\{[130] - [129]\} / \{[130] + [129]\}$, where each concentration of the light acid (129) and the heavy acid (130) are determined by correlation of the peak area on the mass spectrometer to a standard curve or by direct comparison of the areas of each of the 129 and 130 mass peaks. The actual mass units used to determine the relative amounts of each of the two enantiomers (labeled and unlabelled) are dependent on how the mass spectrometer is tuned.

[000515] In some cases, the % ee observed by mass spectrometry may differ by a factor from that observed by an alternate analytical technique such as liquid chromatography due to background or contaminating peaks resulting from natural isotopic abundance. This does not, however, affect the final outcome of the screening process. Exemplary standard curves for quantification of heavy acid and light acid are shown in Figures 14 A and B.

[000516] The following reaction is a possible synthetic route to prepare, for example, ^{15}N -(R)-HGN using chemistry techniques known in the art with commercially available starting materials.



[000517] The amount of each of the two possible stereomeric outcomes can be established by the use of MS in either positive mode, negative mode and from analysis of either of the parental mass or of any fragmentation mass.

Example 23: Stability and activity of exemplary enzymes of the inventionEnzyme stability:

Wild-type enzyme (SEQ ID NOS:209 and 210) was compared to mutant A190H of SEQ ID NOS:209 and 210. In the experiment, each enzyme was incubated at 10 mg/ml in water for 1, 25, 50, 75 and 150 hours at 4°C and at 21°C, on two different substrates: adiponitrile and hydroxyglutaryl nitrile. Both enzymes, in all conditions, were found to retain activity for 150 hours. The wild-type enzyme showed greater activity on adiponitrile, while the mutated (A190H) enzyme showed greater activity on hydroxyglutaryl nitrile, as assessed by the Nitroprusside Bertholet assay (see, e.g., Fawcett, J. K. & Scott, J. (1960); J. Clin. Path.; Vol. 13, pg 156).

GSSM TM Variant of SEQ ID NOS:209 and 210	100 mM hydroxyglutaryl nitrile ee%	2.25 mM hydroxyglutaryl nitrile ee%	Time to completion (hours)
A55G	96.5 ± 0.4	Not determined	>160
A55K	94.7 ± 0.2	Not determined	>160
I60E	96.5 ± 0.5	Not determined	>160
N111S	95.8 ± 0.5	96.1 ± 0.9	>160
A190T	96.5 ± 0.2	96.6 ± 0.4	40
A190S	96.8 ± 0.2	95.5 ± 0.7	40
A190H	97.9 ± 0.1	98.1 ± 0.1	15
F191L	97.9 ± 0.1	Not determined	>160
F191T	97.9 ± 0.1	Not determined	>160
F191M	97.9 ± 0.1	Not determined	>160
F191V	97.9 ± 0.1	Not determined	>160
M199E	97.9 ± 0.1	Not determined	160
M199L	97.9 ± 0.1	95.4 ± 0.1	>160
Wild type SEQ ID NOS:209 and 210	94.5 ± 0.1	87.8 ± 0.2	24

GSSM mutants with enhanced enantioselectivity

100 mM reactions were performed with nitrilase expressed from E. coli in whole cell format and were complete with 36 hours. 2.25 M reactions were performed with nitrilase as lyophilized clarified cell lysate. All % ee data reported are the average of three measurements, with standard deviation of the mean. The time for reaction completion was approximated by TLC.

Specifically:Nitrilase Activity Assay, 100 mM HGN:

Putative nitrilase up-mutants were assayed in triplicate. Each transformant was grown in 5 mL LB (100 µg/mL ampicillin), at 37 °C, 220 rpm for 18 h. The overnight culture was diluted 2-fold and nitrilase expression induced at 37 °C, 220 rpm with 0.1 mM IPTG for 6 h. Cells were harvested by centrifugation, washed in 100 mM pH 7 sodium phosphate buffer and then re-suspended in 1 mL of 100 mM HGN in 100 mM pH 7 sodium phosphate buffer. Reactions were allowed to proceed for at least 36 h at 22 °C with gentle agitation. Reaction progress was monitored by TLC (1:1 EtOAc:Hexanes, R_f=0.5, nitrile; R_f=0.0, acid). Cells and other debris were removed by centrifugation and the treated with one volume methanol prior to lyophilization. The lyophilizate was re-suspended in methanol and treated with TMS-diazomethane (10 equivalents, 2 M solution in hexanes) until gas evolution ceased and yellow color persisted in order to prepare the methyl ester for GC analysis. Selected nitrilase variants producing (R)-(-)-3-hydroxy-4-cyanobutyric acid of 95% ee or greater were then evaluated for performance at 2.25 M HGN.

Nitrilase Activity Assay at 2.25 M 3-HGN:

3-HGN (0.2 g, 1.8 mmol, 3 M) was suspended in sodium phosphate buffer (0.6 mL, pH 7, 100 mM) at 22 °C. Cell lysate (6 mg, normalized for nitrilase content) was added to bring the concentration to 11 mg/ml enzyme and the reaction shaken (100 rpm, 22 °C). Reaction progress was monitored by TLC (1:1 ethyl acetate:hexanes, R_f = 0.32, nitrile; R_f = 0.0, acid). The reaction mixture was treated with one part methanol prior to lyophilization. The lyophilizate was re-suspended in methanol and treated with 10 equivalents of TMS-diazomethane (10 equivalents, 2 M solution in hexanes) to prepare the methyl ester and analyzed by GC.

Description of novel high throughput LC/MS method for screening high numbers of samples:

Ultra High-throughput Primary Chiral Activity Screen:

Distinct members of the GSSM library were arrayed into 384 well plates containing 40 µL of (Luria-Bertani) LB medium (100 µg/mL ampicillin) via an automated colony picker and then incubated at 37 °C, 85% humidity. Nitrilase expression was induced with 0.1 mM IPTG at 37 °C for 24 h. Each plate was replicated and 20% glycerol stocks prepared for archival at -80 °C. To each 384 well plate was added 10 mM 15N-(R)-1 substrate. The plates were incubated at 37 °C, 85% humidity for three days. Cells and other debris were removed by centrifugation and the supernatant was diluted 17,576-fold prior to MS analysis.

LC/MS ionspray was applied for high through-put analysis in the following manner. High-throughput screening was achieved by flow injecting samples from 384-well plates using a CTCPAL autosampler (Leap Technologies, Carrboro, N.C.). An isocratic mixture of 71% acetonitrile, 29% water, with 0.1% formic acid, provided by LC-10ADvp pumps (Shimadzu, Kyoto, Japan) at 2.2 mL/min through an LC-18 cartridge (Supelco, Bellefonte, PA) was used. Samples were applied to an API 4000 TurboIon spray triple-quadrupole mass spectrometer (Applied Biosystems, Foster City, CA). Ion spray and Multiple Reaction Monitoring (MRM) were performed for analytes in the negative ion mode, and each analysis took 60 seconds.

E. coli transformed with wild type enzyme (SEQ ID NOS:209 and 210) was used as a positive activity control and *E. coli* transformed with empty vector was used as the negative activity control. The % ee of the WT enzyme positive control determined by mass spectrometry using either 15N-(R)-1 or 15N-(S)-1 were the same, thus demonstrating the absence of a significant isotope effect.

Temp (°C)	pH	Sodium phosphate buffer conc. (mM)	% ee	Std. Dev.
4	7	100	98.7	0.1 %
19	7	100	98.7	0.1 %
21	7	100	98.6	0.1 %
37	7	100	98.4	0.1 %
21	7	100	98.6	0.1 %
21	6	100	98.6	0.1 %
21	8	100	98.6	0.1 %
21	7	100	98.5	0.1 %
21	7	50	98.6	0.1 %
21	7	25	98.7	0.1 %

Effect of reaction parameters on SEQ ID NOS:209 and 210 with the A190H mutation.

Reactions were performed at 3 M HGN concentration with 150 mg/ml protein (~49 mg/ml enzyme). % ee was determined by GC analysis in triplicate runs.

[000518] While the invention has been described in detail with reference to certain preferred aspects thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

What is claimed is:

1. An isolated or recombinant nucleic acid comprising nucleotides having a sequence at least 50% identical to SEQ ID NO:195, 205, 207, 209, or 237, variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments thereof, wherein the nucleic acid or fragment encodes a polypeptide having nitrilase activity, or their complements.
2. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises nucleotides having a sequence substantially identical to the SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.
3. An isolated or recombinant nucleic acid comprising nucleotides having a sequence identical to the SEQ ID NO:195, 205, 207, 209, or 237, fragments having nitrilase activity, or their complements.
4. An isolated or recombinant nucleic acid comprising nucleotides having a sequence identical to a variant of SEQ ID NO:195, 205, 207, 209, or 237, having one or more

mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments having nitrilase activity, or their complements.

5. An isolated or recombinant nucleic acid that hybridizes to a nucleic acid of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments having nitrilase activity, or their complements.
6. The isolated or recombinant nucleic acid of claim 5, wherein the stringent conditions comprise at least 50% formamide, and about 37°C to about 42°C.
7. A nucleic acid probe comprising from about 15 nucleotides to about 50 nucleotides, wherein at least 15 consecutive nucleotides are at least 50% complementary to a nucleic acid target region within a nucleic acid sequence of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT,

CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.

5

8. A nucleic acid probe comprising at least 15 consecutive nucleotides of a nucleic acid target region within a nucleic acid sequence of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.

10

15

9. A nucleic acid vector capable of replication in a host cell, wherein the vector comprises the nucleic acid of any one of claims 1 to 6, 12, or 13.

20

10. A host cell comprising the nucleic acid of any one of claims 1 to 6, 12 or 13.

11. A host organism comprising the host cell of claim 10.

12. An isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, fragments encoding polypeptides wherein the polypeptides have nitrilase activity, or its complement.

30

13. An isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence of SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, fragments encoding a polypeptides having nitrilase activity, or its complement.
14. The isolated or recombinant nucleic acid of any one of claims 1 to 6, 12 or 13, wherein the nucleic acid is affixed to a solid support.
15. The isolated or recombinant nucleic acid of claim 14, wherein the solid support is selected from the group of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.
16. An isolated or recombinant polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or fragments thereof, wherein the polypeptide has a nitrilase activity.
17. An isolated or recombinant polypeptide comprising amino acid having SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222

leucine; or any combination thereof, or fragments thereof, wherein the polypeptide has nitrilase activity.

18. The isolated or recombinant polypeptide of any one of claims 16 or 17, wherein the
5 fragment is at least 20 amino acids in length, and wherein the fragment has nitrilase activity.

19. A peptidomimetic of the polypeptide of claim 16 or claim 17 or fragments thereof
10 having a nitrilase activity.

20. A codon-optimized polypeptide of the polypeptide of claim 16 or claim 17, or
fragments thereof, having a nitrilase activity, wherein the codon usage is optimized for
a particular organism or cell.

21. The polypeptide of claim 16 or claim 17 or fragments thereof, having a nitrilase
15 activity, or a peptidomimetic thereof having a nitrilase activity, wherein the polypeptide, fragment, or peptidomimetic is affixed to a solid support.

22. The polypeptide of claim 21, wherein the solid support is selected from the group
20 consisting of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.

23. A purified antibody that specifically binds to the polypeptide of claim 16 or claim 17 or
25 fragments thereof, having a nitrilase activity.

24. A fragment of the antibody of claim 23, wherein the fragment specifically binds to a
polypeptide having a nitrilase activity.

25. An enzyme preparation which comprises at least one of the polypeptides of any one of
30 claims 16 and 17, wherein the preparation is liquid or dry.

26. The enzyme preparation of claim 25, wherein the preparation is affixed to a solid
support.

27. A composition comprising at least one nucleic acid of claims 1 to 6, 12, or 13 or comprising at least one polypeptide of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, or any combination thereof.
28. A method for hydrolyzing a nitrile to a carboxylic acid comprising contacting the molecule with at least one polypeptide of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.
29. A method for hydrolyzing a cyanohydrin moiety or an aminonitrile moiety of a molecule, the method comprising contacting the molecule with at least one polypeptide of any one of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.
30. A method for making a chiral alpha-hydroxy acid molecule or a chiral amino acid molecule, the method comprising admixing a molecule having a cyanohydrin moiety or an aminonitrile moiety with at least one polypeptide having an amino acid sequence at least claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having enantio-selective nitrilase activity.
31. A method for making a composition or an intermediate thereof, the method comprising admixing a precursor of the composition or intermediate, wherein the precursor comprises a cyanohydrin moiety or an aminonitrile moiety, with at least one polypeptide of any one of claim 16 or claim 17 or fragments thereof or peptidomimetic thereof having nitrilase activity, hydrolyzing the cyanohydrin or the aminonitrile moiety in the precursor thereby making the composition or the intermediate thereof.
32. A method for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide encoded by a nucleic acid having a sequence of SEQ ID NO:195, 205, 207, 209, OR 237, or a variant of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions

178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or a fragment thereof encoding a polypeptide having nitrilase activity, that selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid.

33. A method for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of any one of SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

34. A method for making an (*R*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of any one of SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity.

35. A method for making an (*S*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of SEQ ID

NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity.

36. A method for making an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative, the method comprising admixing a phenyllactocyanonitrile with at least one polypeptide selected from SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity, or any active fragment or peptidomimetic thereof that selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

37. A method for making the polypeptide of claim 16 or claim 17 or fragments thereof, the method comprising

- (a) introducing a nucleic acid encoding the polypeptide into a host cell under conditions that permit production of the polypeptide by the host cell, and
- (b) recovering the polypeptide so produced.

38. A method for generating a nucleic acid variant encoding a polypeptide having nitrilase activity, wherein the variant has an altered biological activity from that which naturally occurs, the method comprising

- (a) modifying the nucleic acid of any one of claims 1 to 6, 12, or 13 by
 - (i) substituting one or more nucleotides for a different nucleotide, wherein the nucleotide comprises a natural or non-natural nucleotide;

- (ii) deleting one or more nucleotides,
- (iii) adding one or more nucleotides, or
- (iv) any combination thereof.

- 5 39. A method for making a polynucleotide from two or more nucleic acids, the method comprising:
- (a) identifying regions of identity and regions of diversity between two or more nucleic acids, wherein at least one of the nucleic acids comprises a nucleic acid of any one of claims 1 to 6, 12, or 13;
 - 10 (b) providing a set of oligonucleotides which correspond in sequence to at least two of the two or more nucleic acids; and,
 - (c) extending the oligonucleotides with a polymerase, thereby making the polynucleotide.
40. A screening assay for identifying a nitrilase, the assay comprising:
- 15 (a) providing a plurality of nucleic acids or polypeptides comprising at least one of the nucleic acids of any one of claims 1 to 6, 12, or 13, or at least one of the polypeptides of claim 16 or claim 17 or fragments thereof;
 - (b) obtaining polypeptide candidates to be tested for nitrilase activity from the plurality;
 - (c) testing the candidates for nitrilase activity; and
 - 20 (d) identifying those polypeptide candidates which are nitrilases.
41. A kit comprising (a) the nucleic acid of any one of claims 1 to 6, 12, or 13, or a fragment thereof encoding a polypeptide having nitrilase activity, or (b) the polypeptide of any one of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof
- 25 having nitrilase activity, or a combination thereof; and (c) a buffer.
42. A method for modifying a molecule comprising:
- (a) mixing a polypeptide of any one of claim 16 or claim 17 or fragments thereof, or peptidomimetic thereof having nitrilase activity, with a starting molecule to produce a
 - 30 reaction mixture;
 - (b) reacting the starting molecule with the polypeptide to produce the modified molecule.

43. A method for identifying a modified compound comprising:

(a) admixing a polypeptide of any one of claim 16 or claim 17 or fragments thereof, or peptidomimetic thereof having nitrilase activity, with a starting compound to produce a reaction mixture and thereafter a library of modified starting compounds;

(b) testing the library to determine whether a modified starting compound is present within the library which exhibits a desired activity;

(c) identifying the modified compound exhibiting the desired activity.

44. A computer readable medium having stored thereon at least one nucleotide sequence

selected from the group consisting of: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383 385, or variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384 and 386, and variants thereof.

45. A computer system comprising a processor and a data storage device, wherein the data storage device has stored thereon at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, and variants thereof.

46. A method for identifying a feature in a sequence which comprises:

(a) inputting the sequence into a computer;

(b) running a sequence feature identification program on the computer so as to identify a feature within the sequence; and

(c) identifying the feature in the sequence,

wherein the sequence comprises SEQ ID NOS:1-386, variants, or any combination thereof.

47. An assay for identifying a functional fragment of a polypeptide which comprises:

- 5 (a) obtaining a fragment of at least one polypeptide of claim 16 or claim 17;
- (b) contacting at least one fragment from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity;
- (c) measuring the amount of reaction product produced by each at least one fragment
- 10 from step (b); and
- (d) identifying the at least one fragment which is capable of producing a nitrilase reaction product; thereby identifying a functional fragment of the polypeptide.

48. An assay for identifying a functional variant of a polypeptide which comprises:

- 15 (a) obtaining at least one variant of at least one polypeptide of claim 16 or claim 17;
- (b) contacting at least one variant from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity;
- (c) measuring the amount of reaction product produced by each at least one variant from step (b); and
- 20 (d) identifying the at least one variant which is capable of producing a nitrilase reaction product; thereby identifying a functional variant of the polypeptide.

49. An assay for screening enantioselective transformation comprising:

- (a) labeling one of two prochiral or enantiotopic moieties in a molecule;
- (b) modifying at least one of the two moieties by selective catalyst to produce
- 25 products; and
- (c) determining the resultant products by mass spectroscopy.

50. The assay of claim 49, wherein the label is heavier or lighter isotope.

30 51. The assay of claim 49, wherein the selective catalyst is an enzyme.

52. The assay of claim 49, wherein the use of mass spectroscopy is by a positive mode or a negative mode.

53. The assay of claim 49, wherein the analysis is of either a parental mass or a fragmentation mass.

5 54. The assay of claim 49, wherein the assay can be used to monitor or determine % enantiomeric excess or % diastereomeric excess.

55. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having one or
10 more mutations selected from the group consisting of a mutation at residue 55 lysine, residue 55 glycine, residue 55 glutamine, residue 60 glutamic acid, residue 111 serine, residue 190, residue 190 serine, residue 190 histidine, residue 190 tyrosine, residue 190 threonine, residue 191 leucine, residue 191 valine, residue 191 methionine, residue 191 aspartic acid, residue 191 glycine, residue 191 glutamic acid, residue 191
15 tyrosine, residue 191 threonine, residue 199 glutamic acid, residue 199 leucine, residue 222 leucine, and any combination thereof.

56. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having a mutation
20 at residue 190 or equivalent, wherein alanine is replaced with a hydrogen-binding amino acid or peptidomimetic residue.

57. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having a mutation
25 at residue 190 or equivalent, wherein alanine is replaced with a hydrophobic amino acid or peptidomimetic residue.

58. An isolated or recombinant nitrilase having the equivalent of one or more mutations at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111
30 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine of SEQ ID NO:196, 206, 208, 210 or 238.

59. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a nitrilase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1, or a subsequence thereof.

5

60. The amplification primer pair of claim 59, wherein a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

10

61. A nitrilase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 59.

62. The nitrilase-encoding nucleic acid of claim 61, wherein the amplification is by polymerase chain reaction (PCR).

15

63. The nitrilase-encoding nucleic acid of claim 62, wherein the nucleic acid generated by amplification of a gene library.

20

64. The nitrilase-encoding nucleic acid of claim 63, wherein the gene library is an environmental library.

65. An isolated or recombinant nitrilase encoded by a nitrilase-encoding nucleic acid as set forth in claim 61.

Figure 1

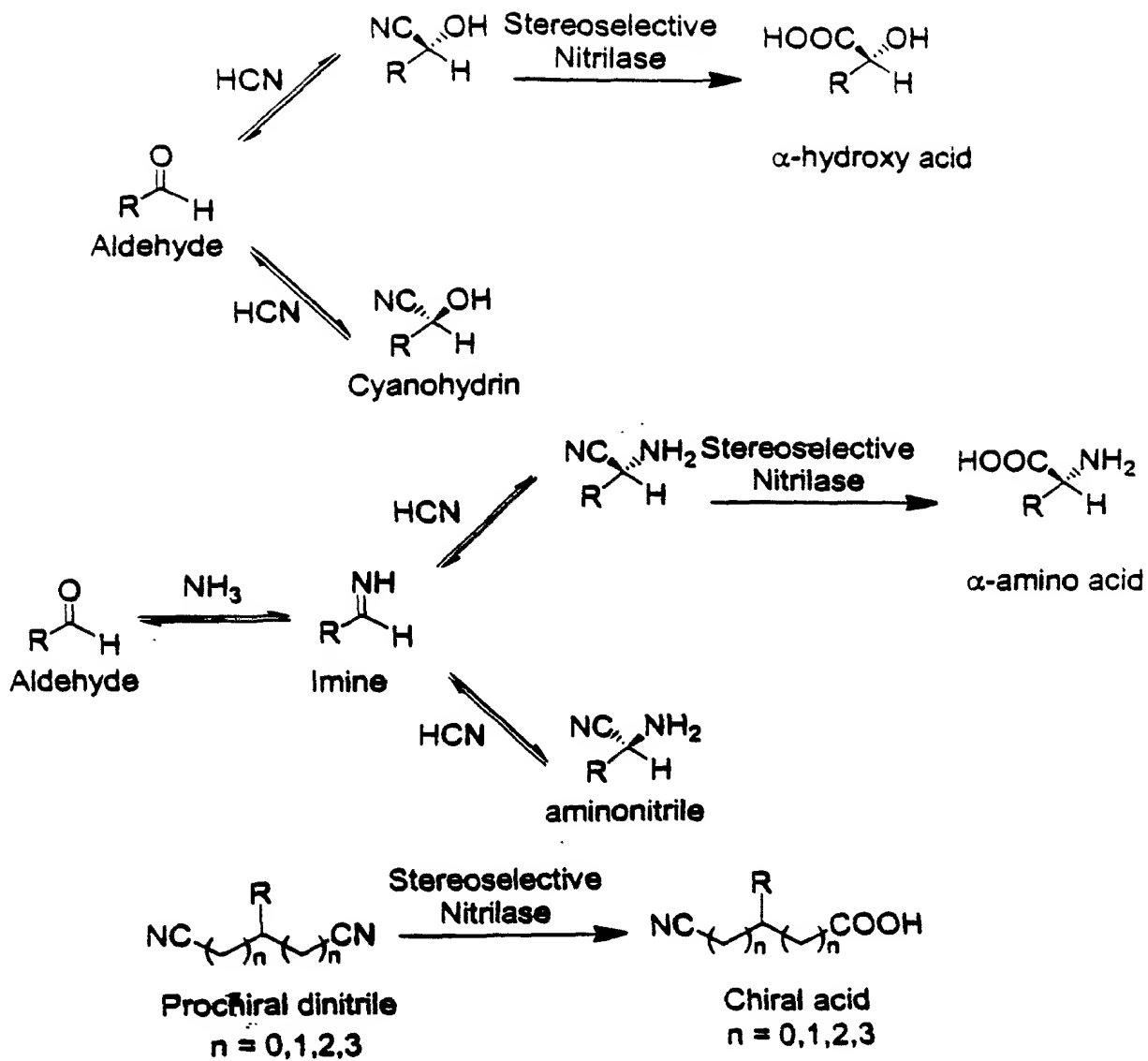


Figure 2

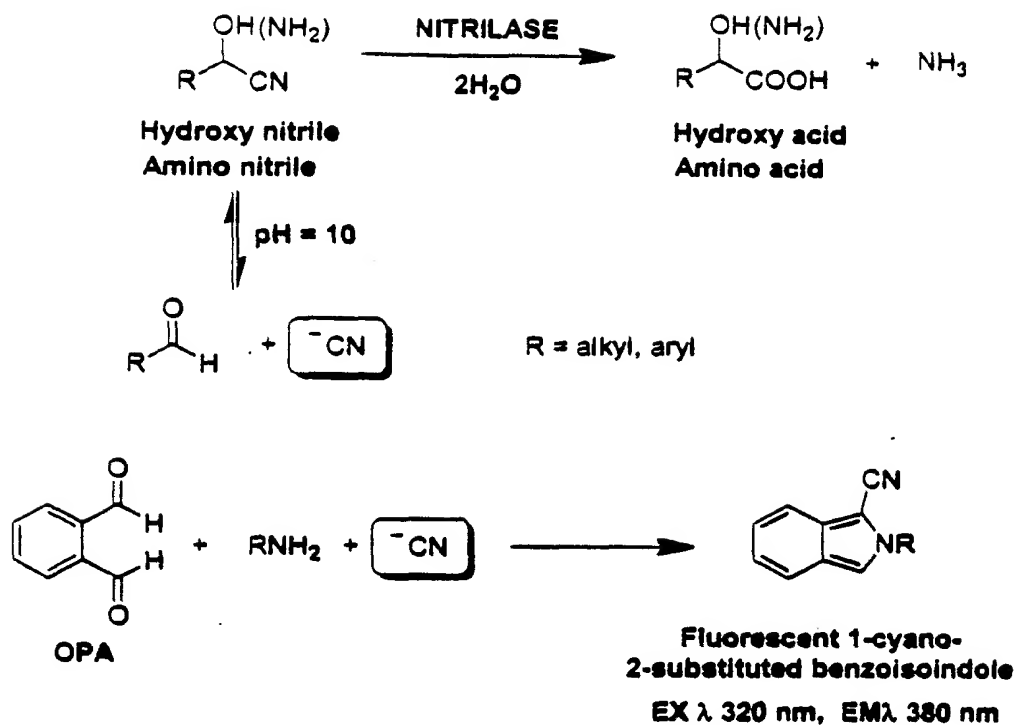


Figure 3

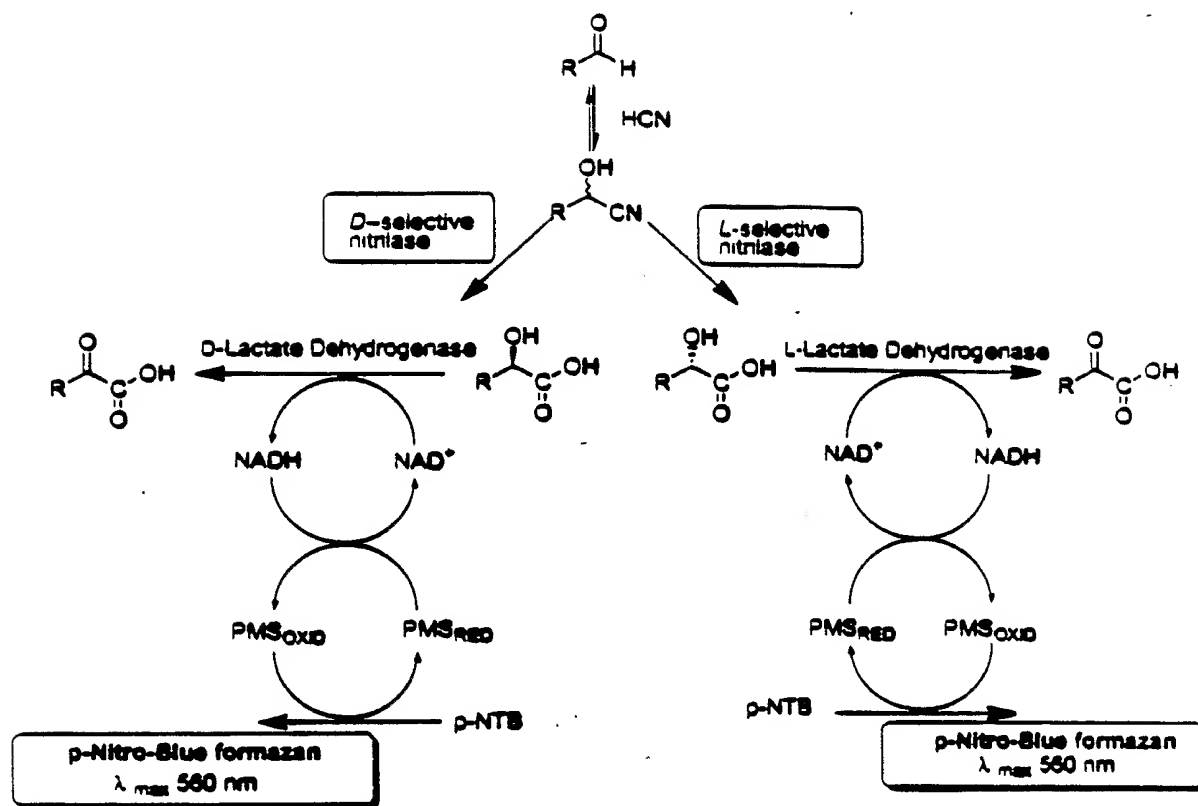
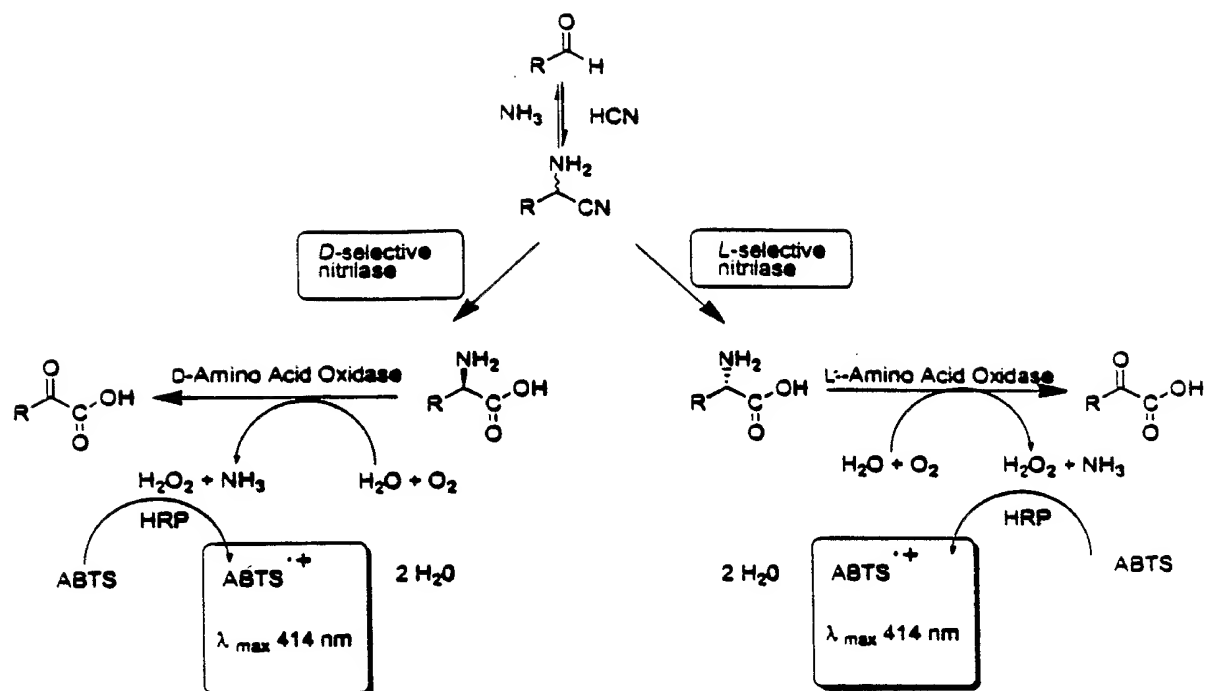


Figure 4



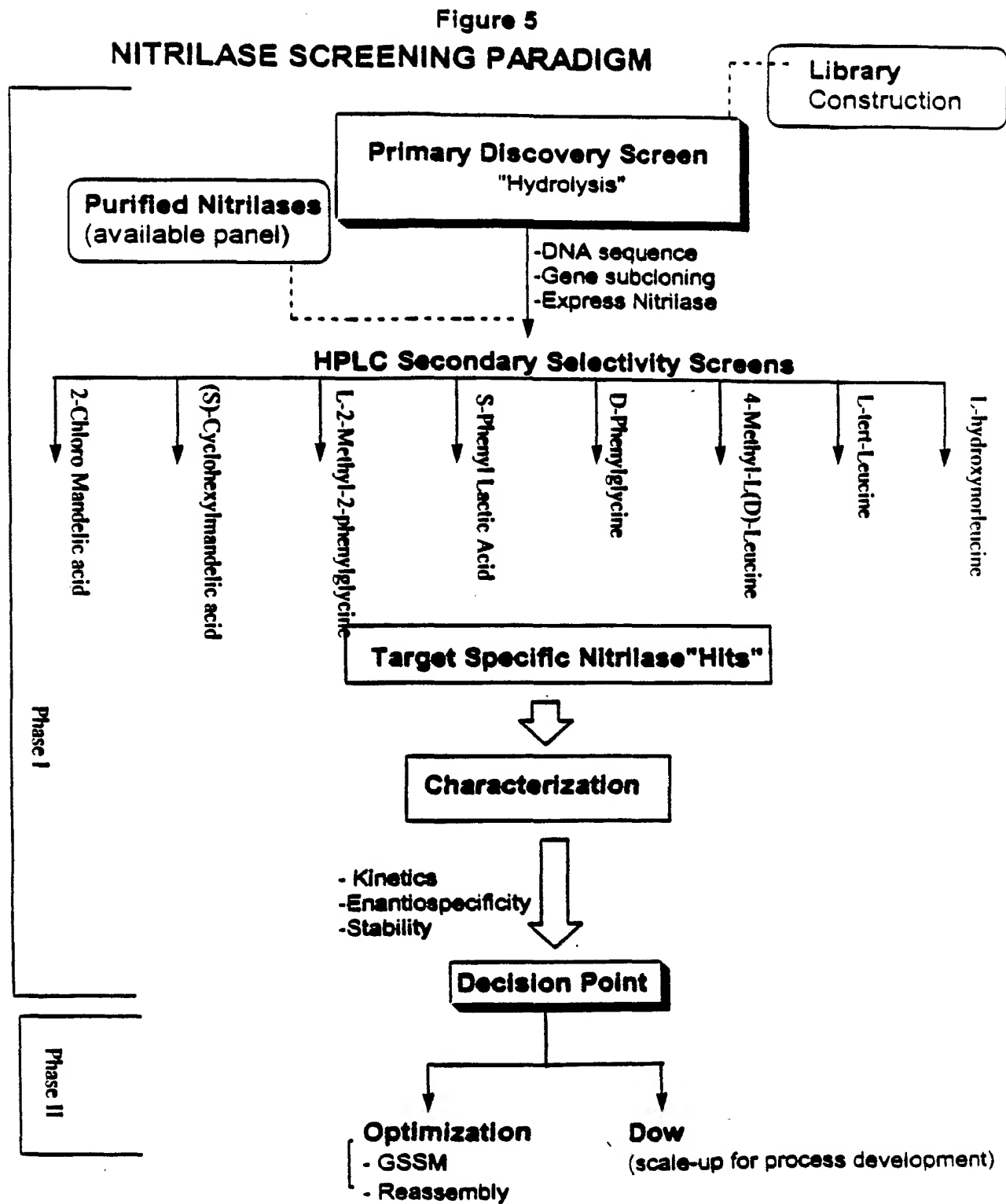


Figure 6A

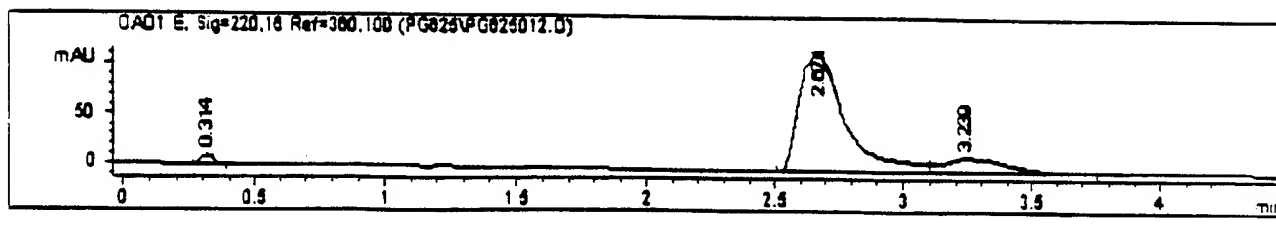


Figure 6B

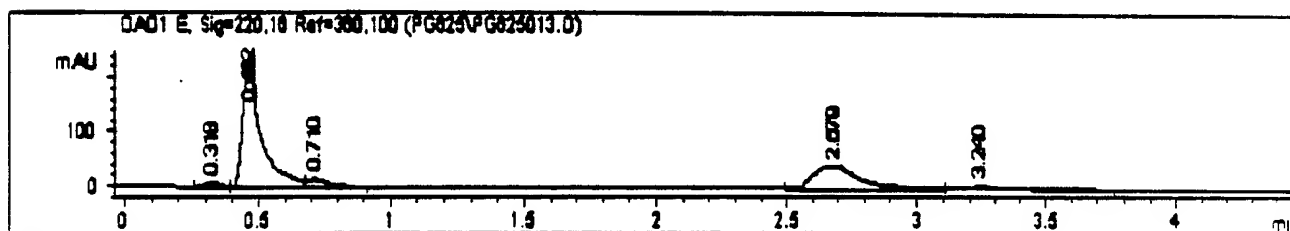
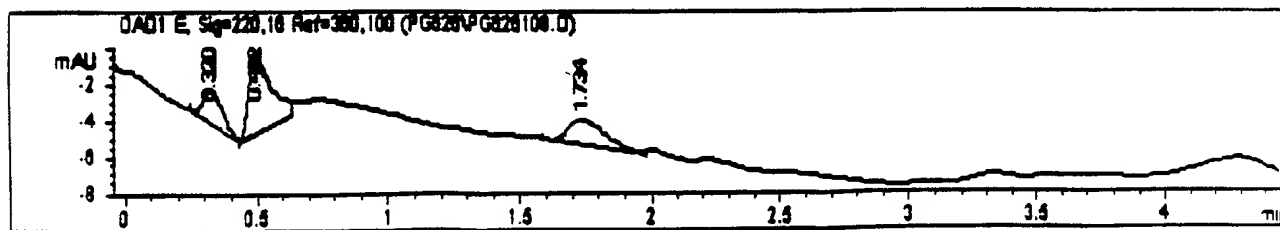


Figure 6C



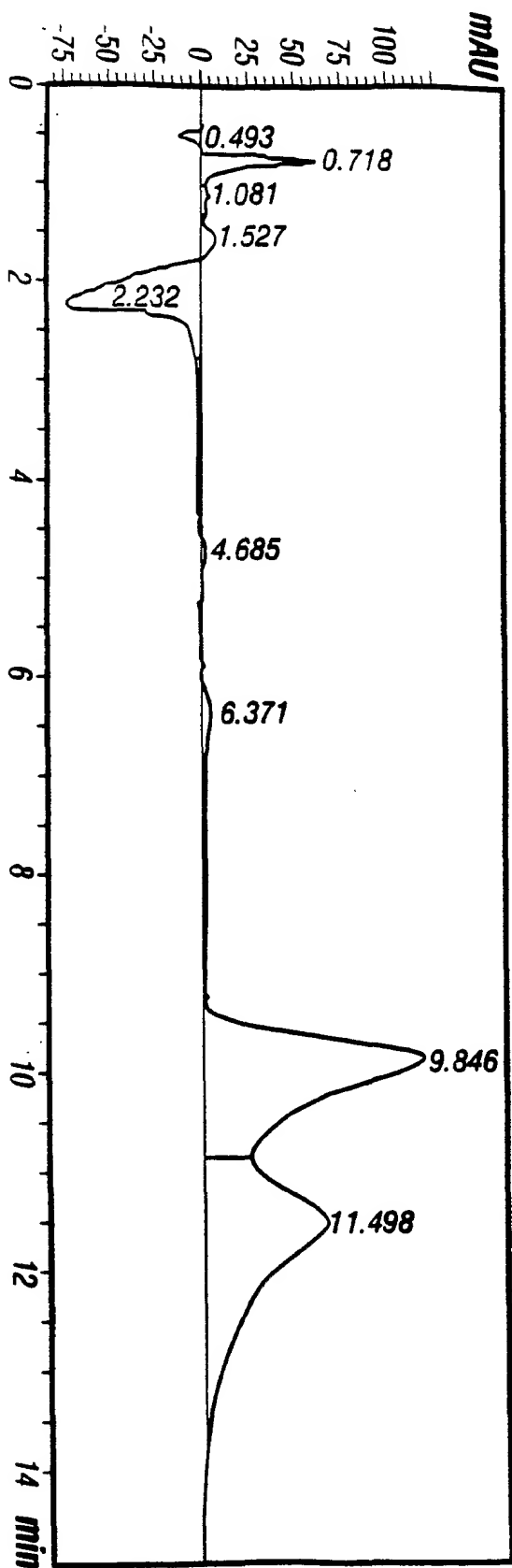


FIG. 6E

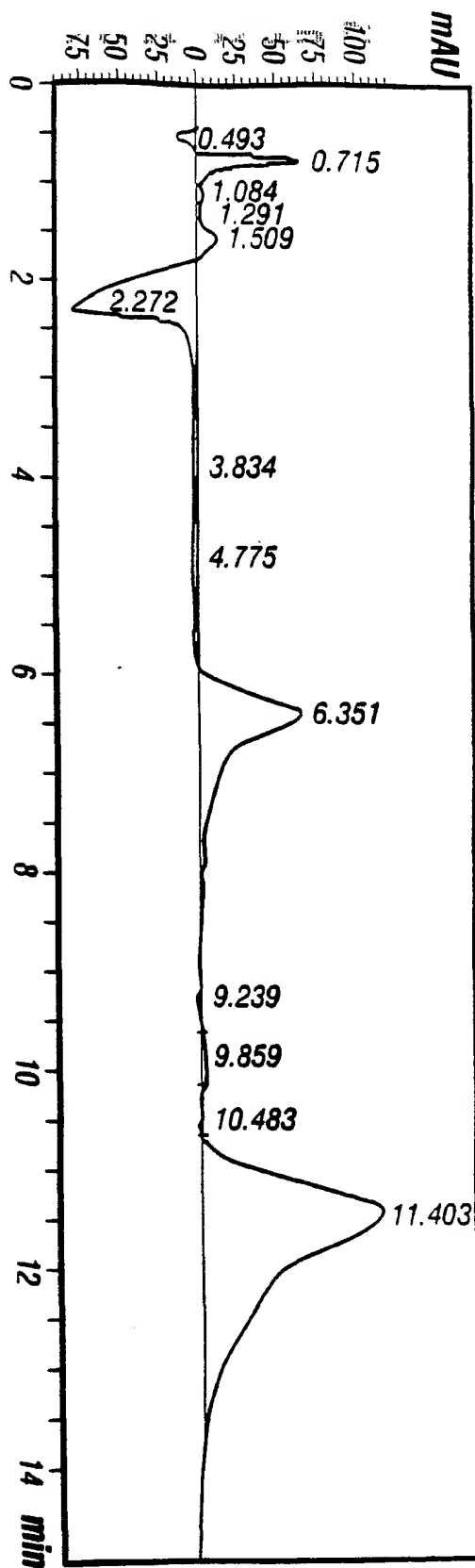
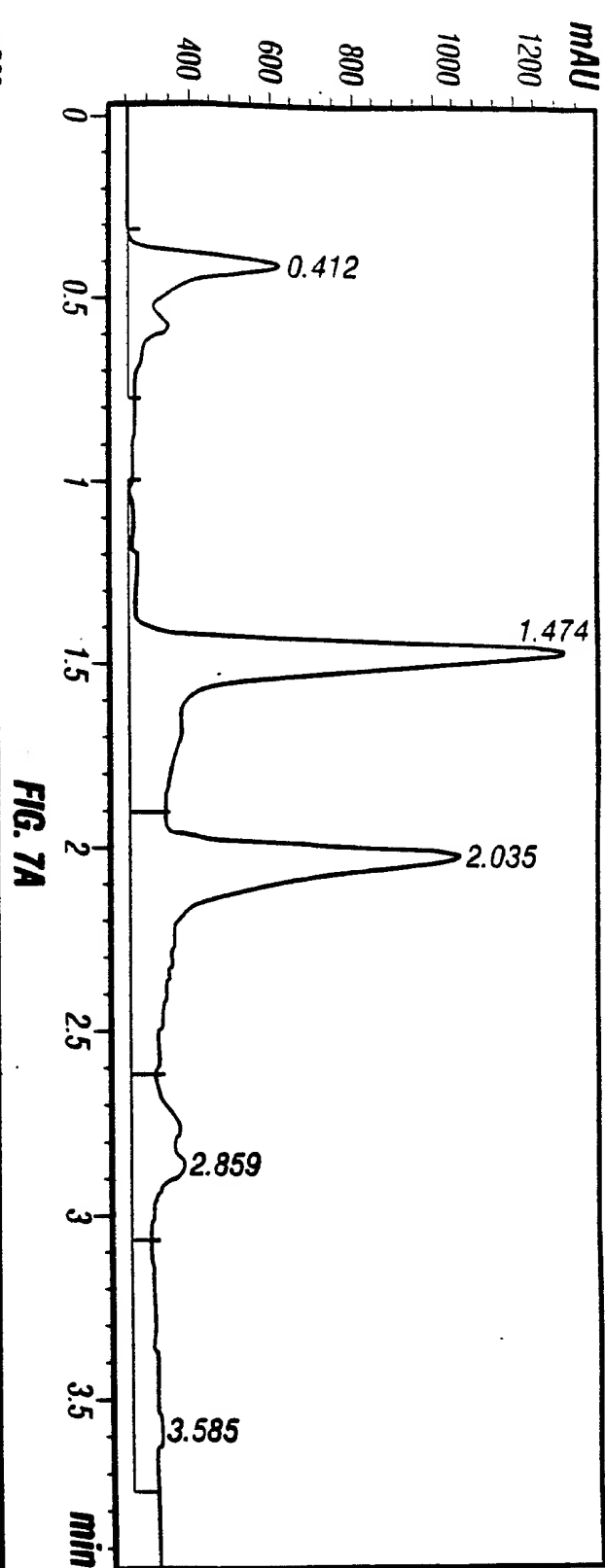
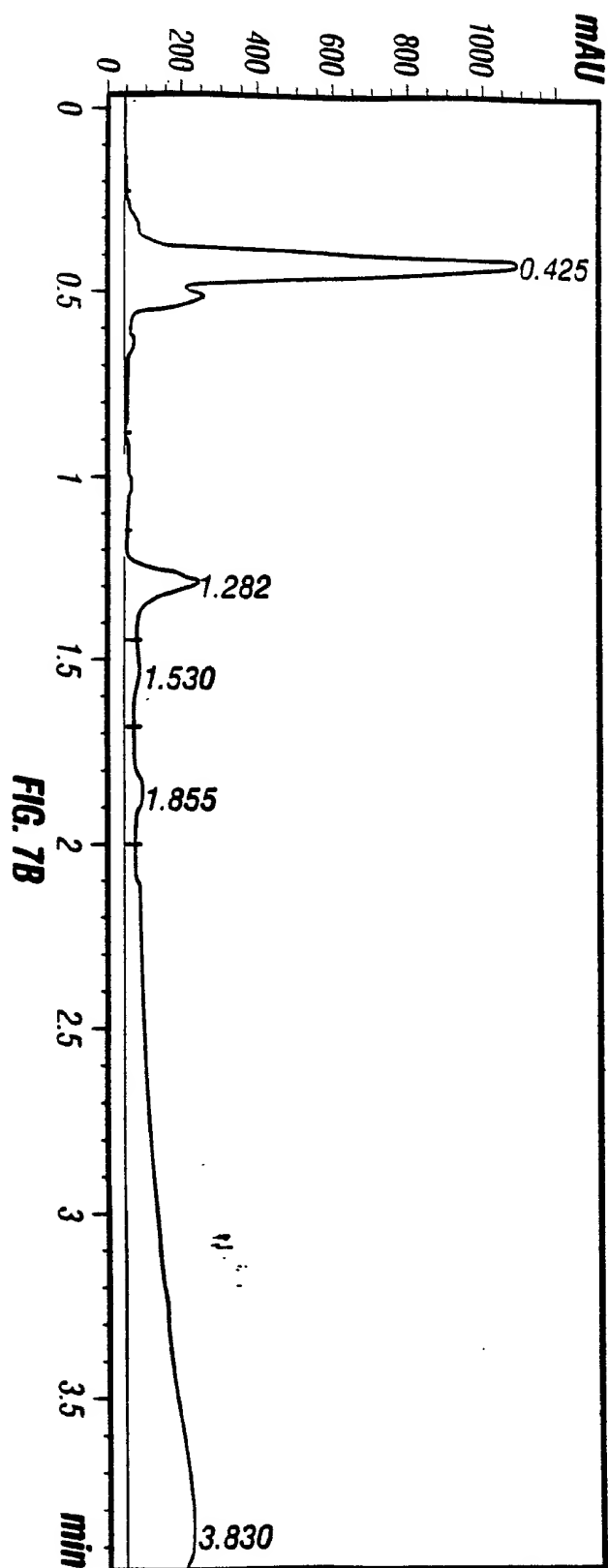
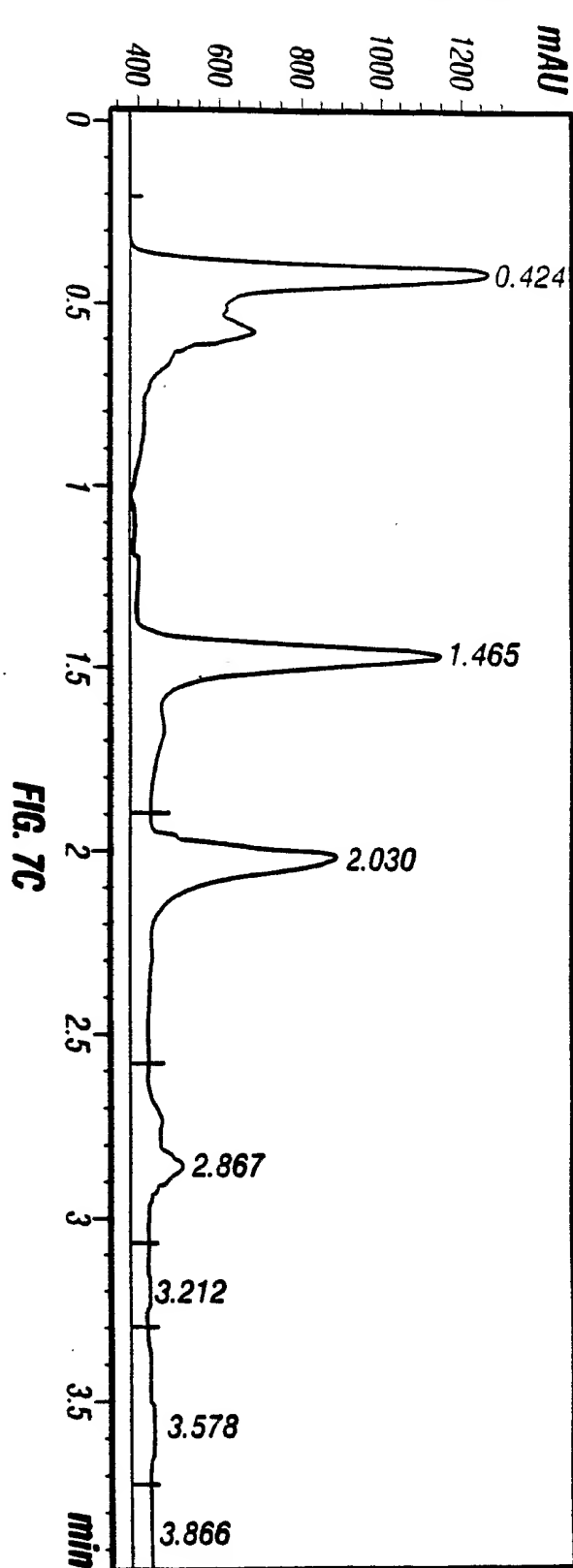
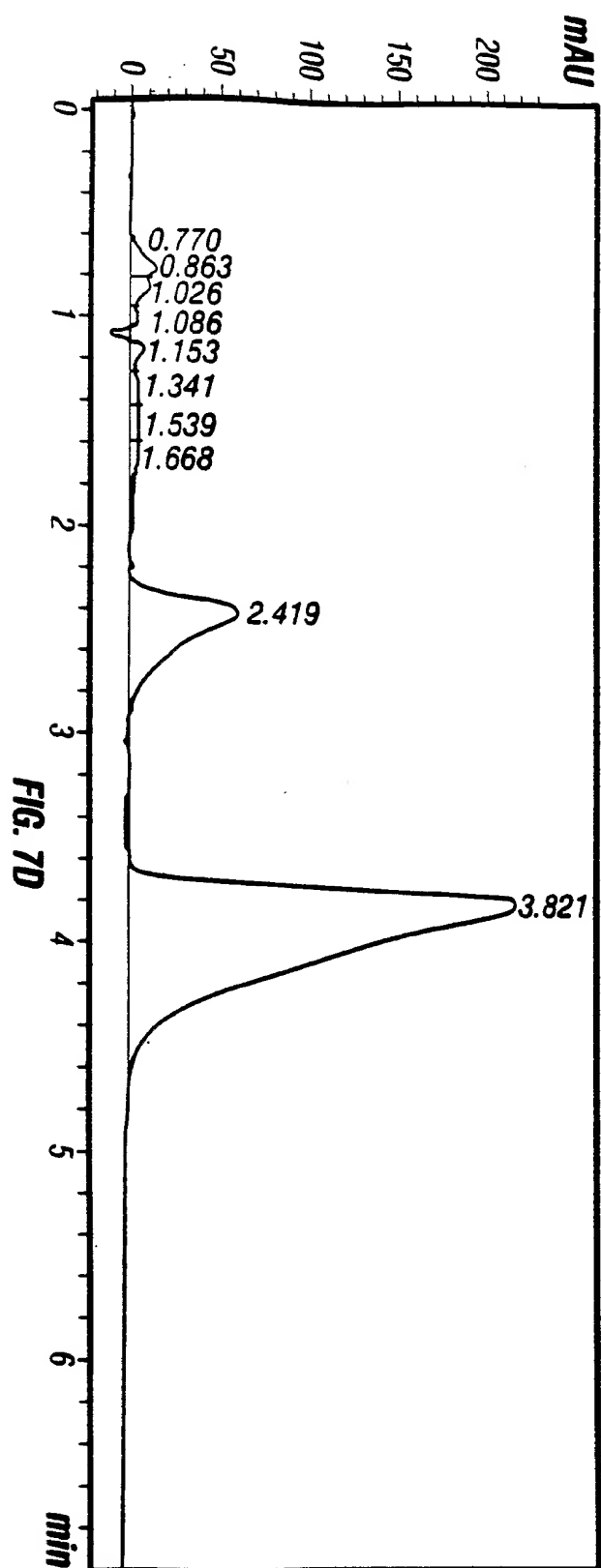
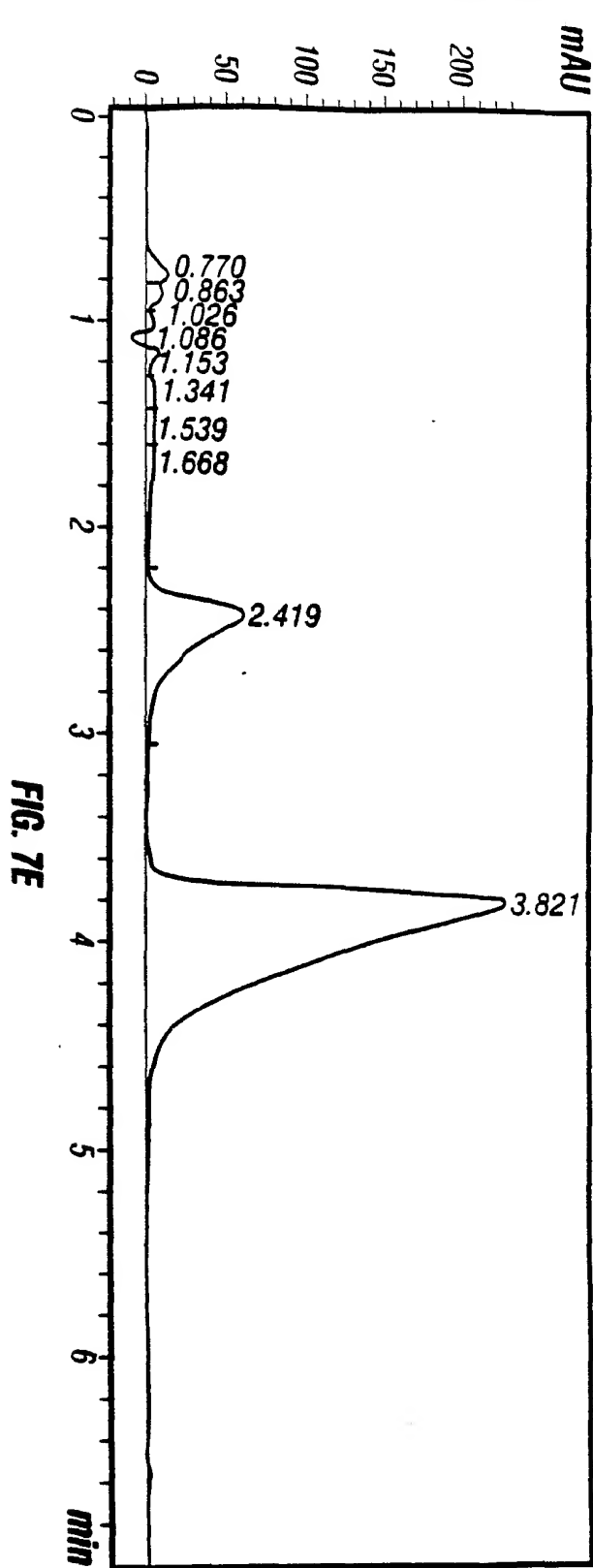
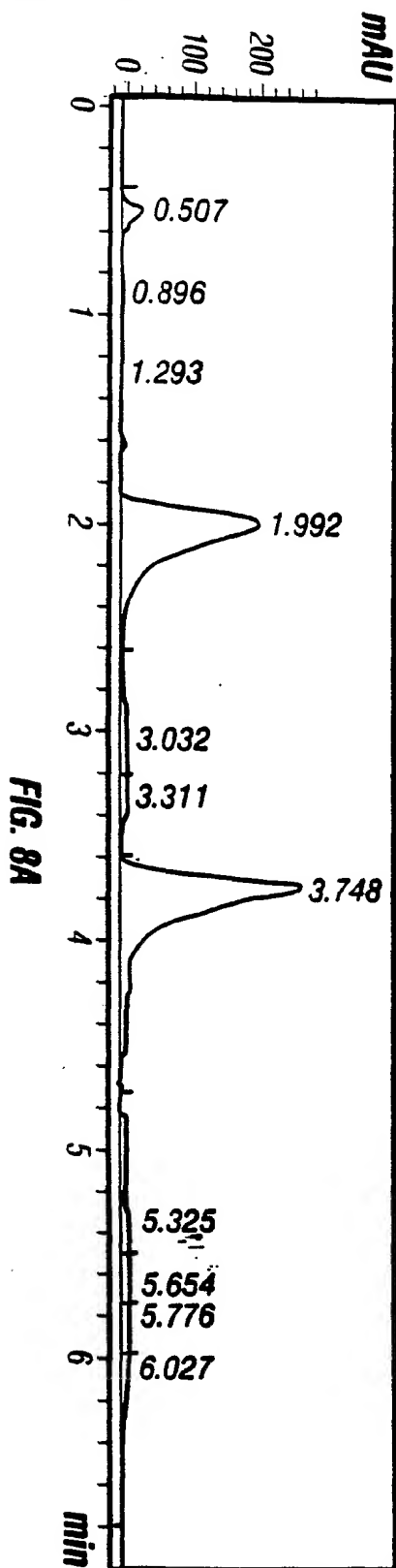
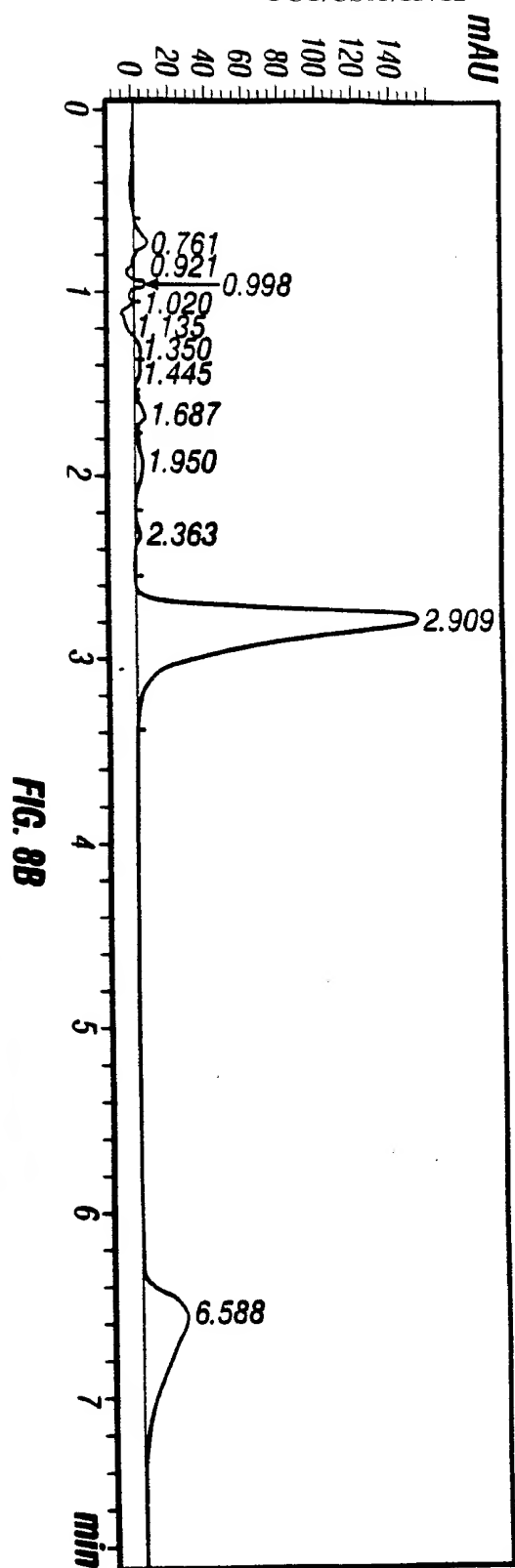
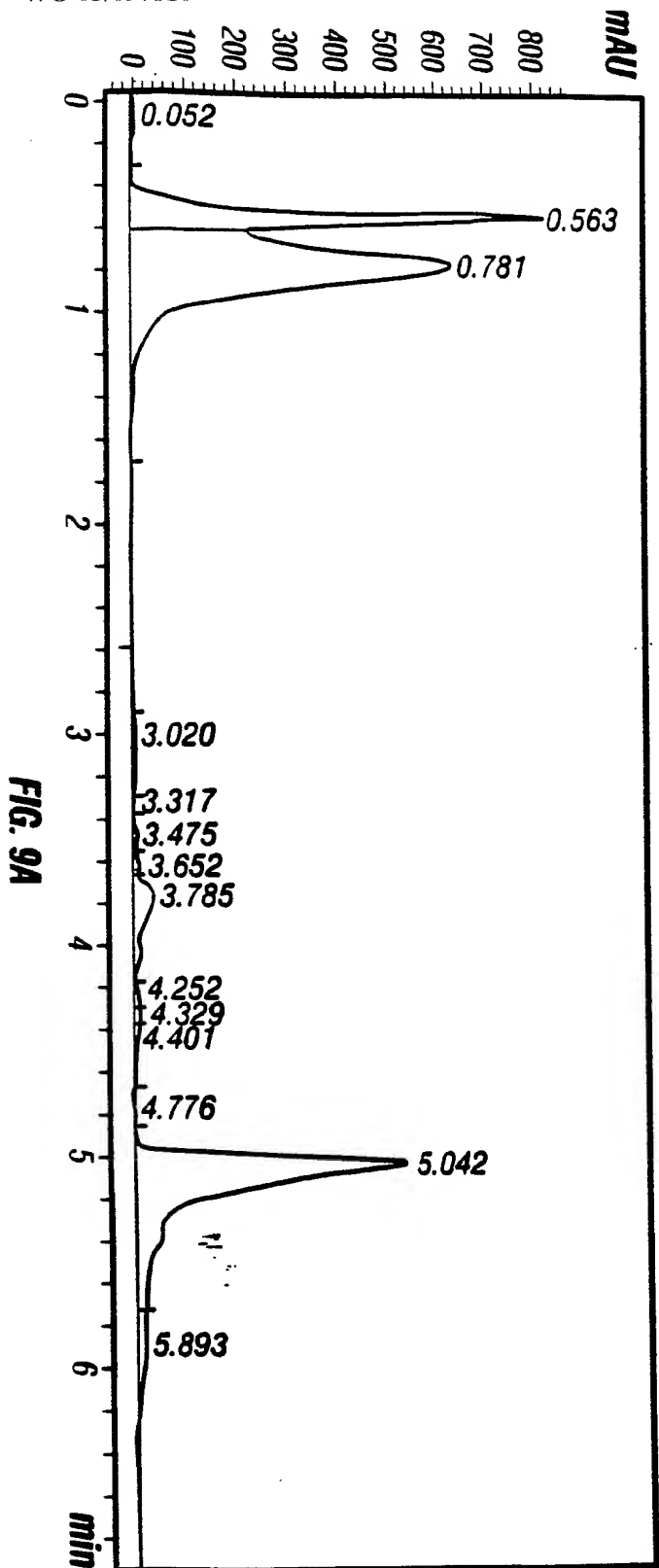


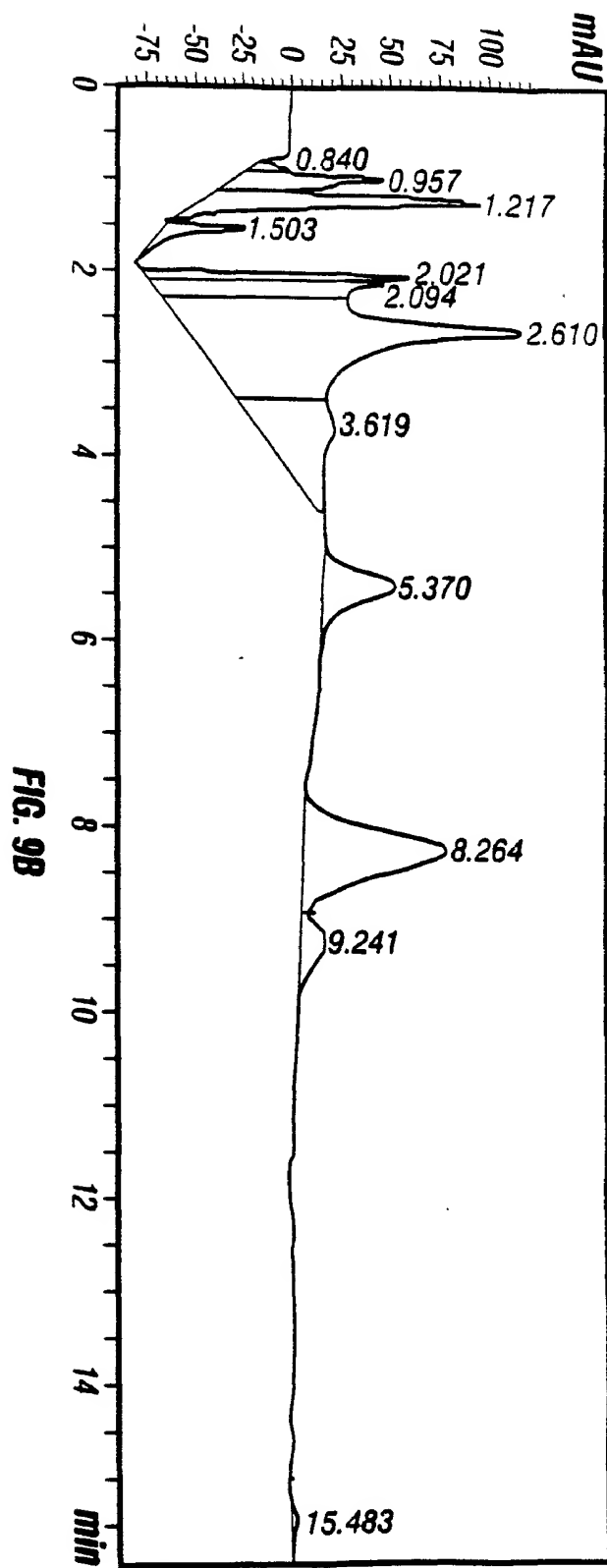
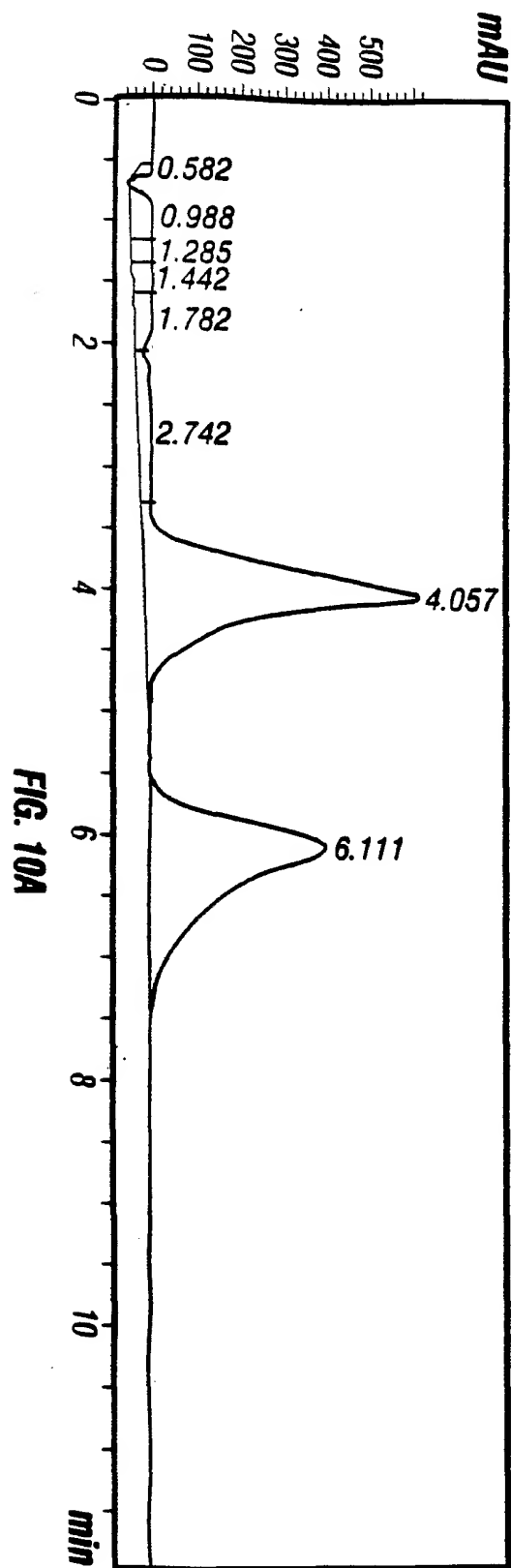
FIG. 6D

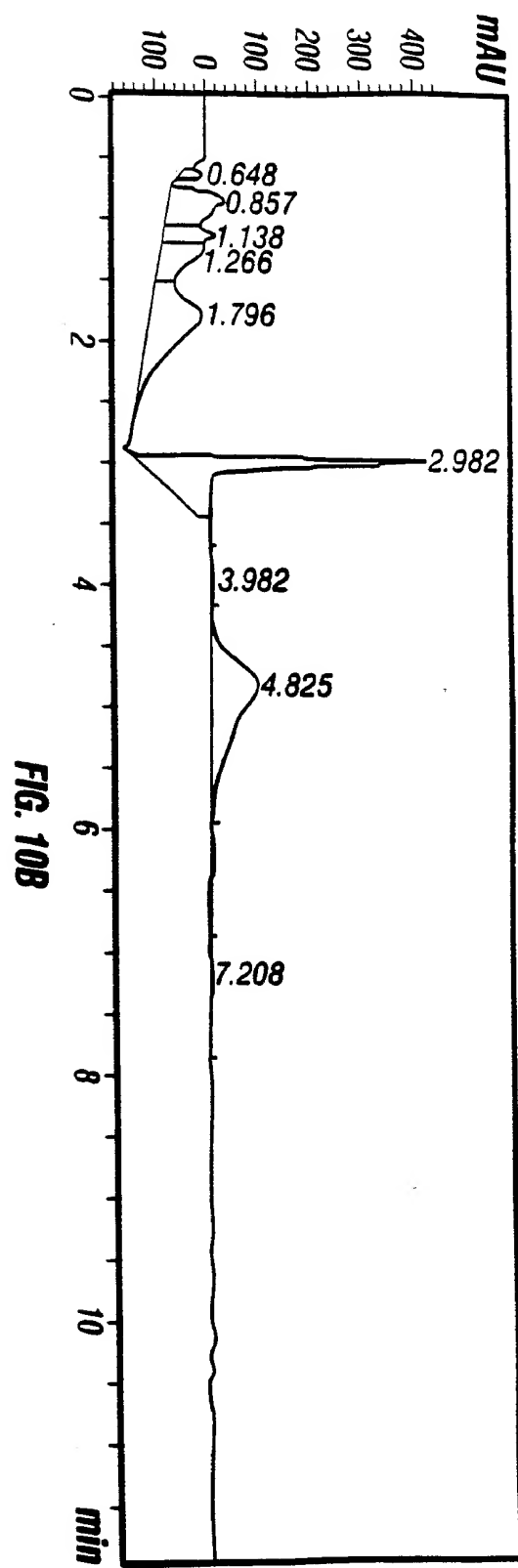
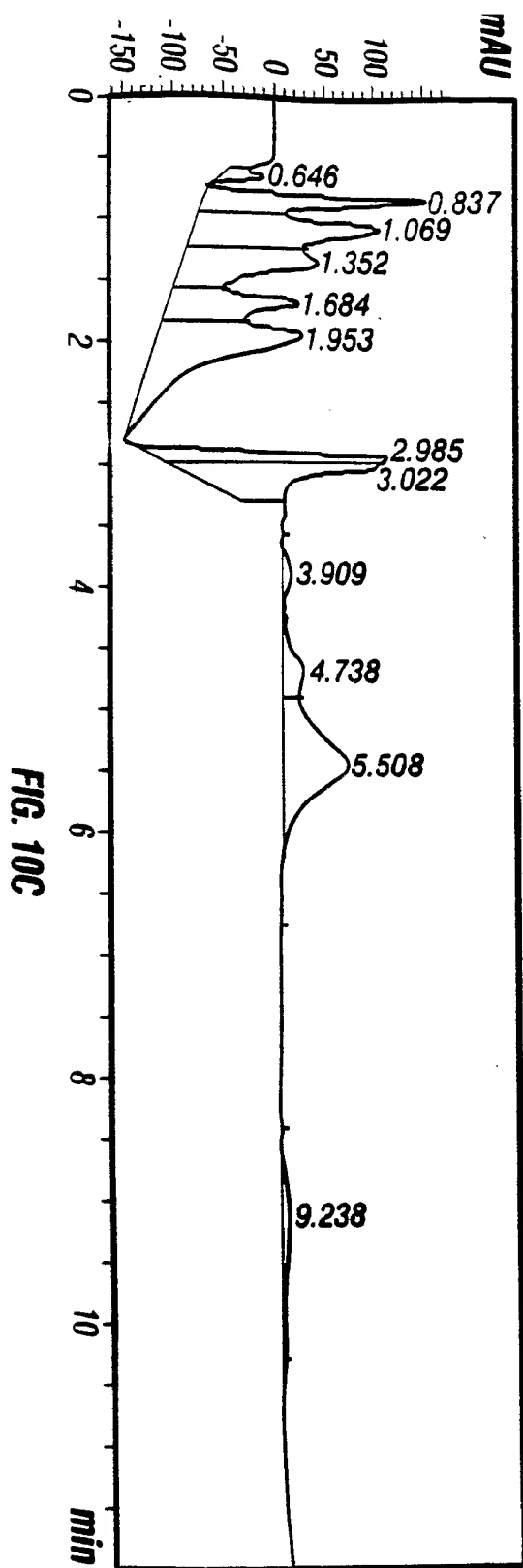


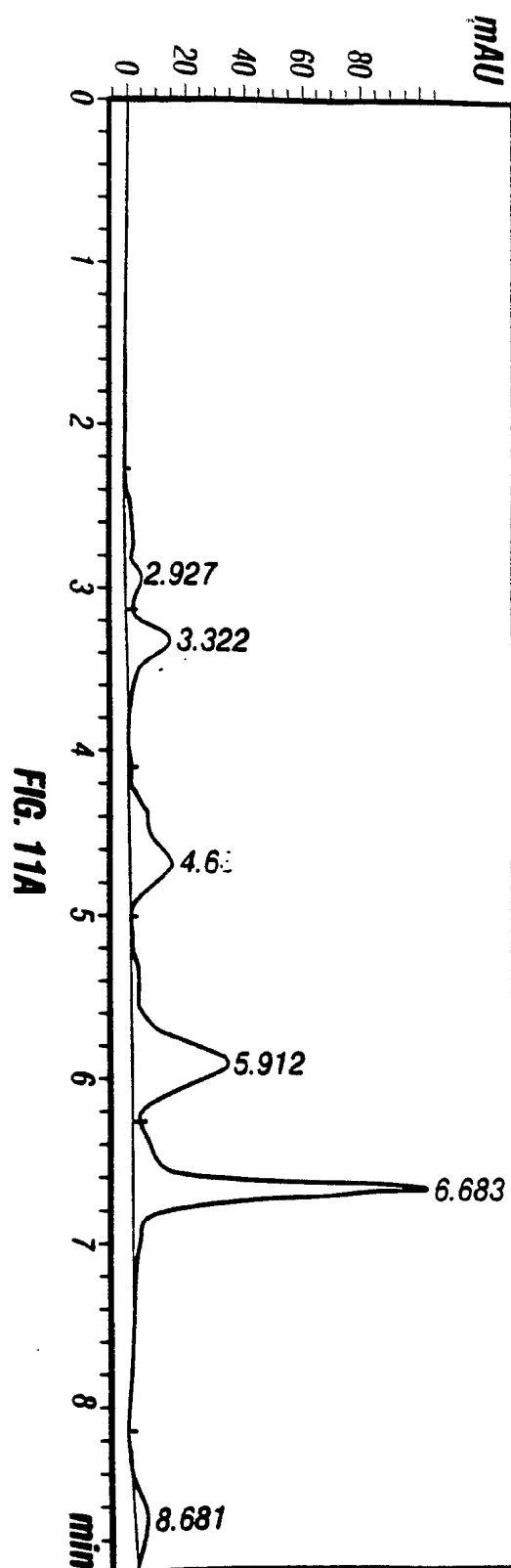
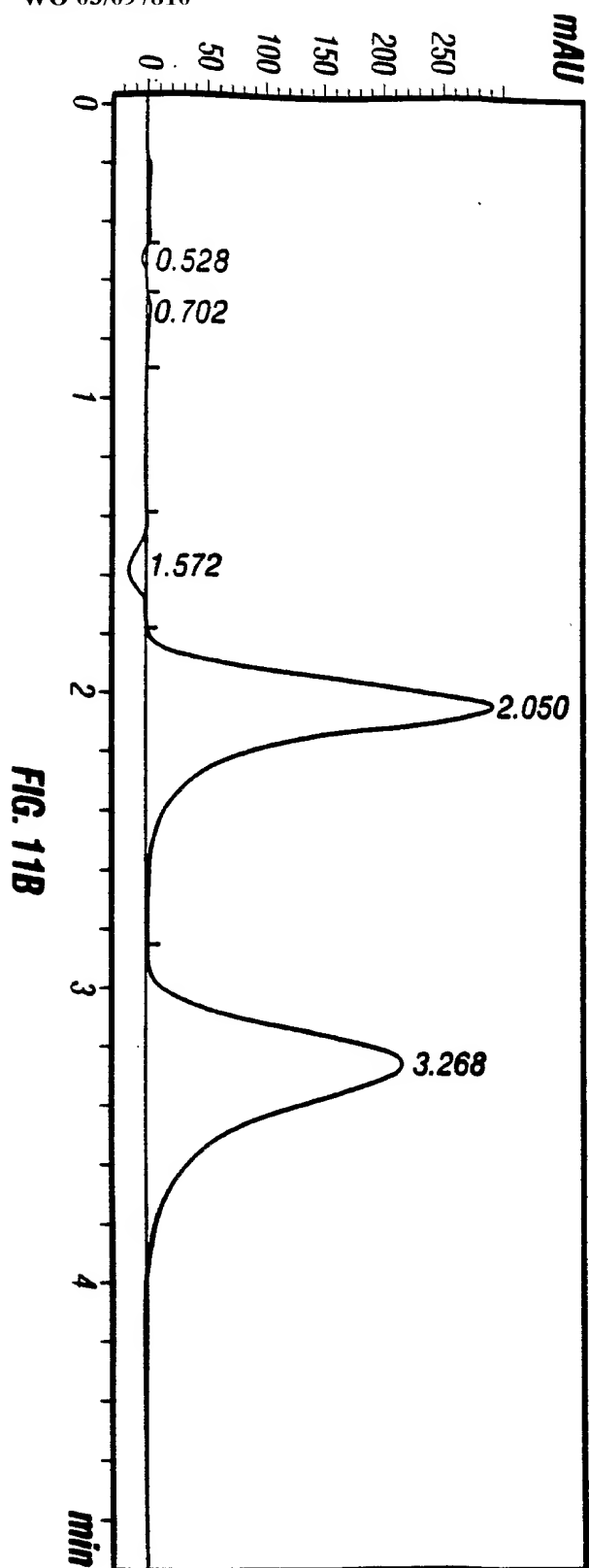












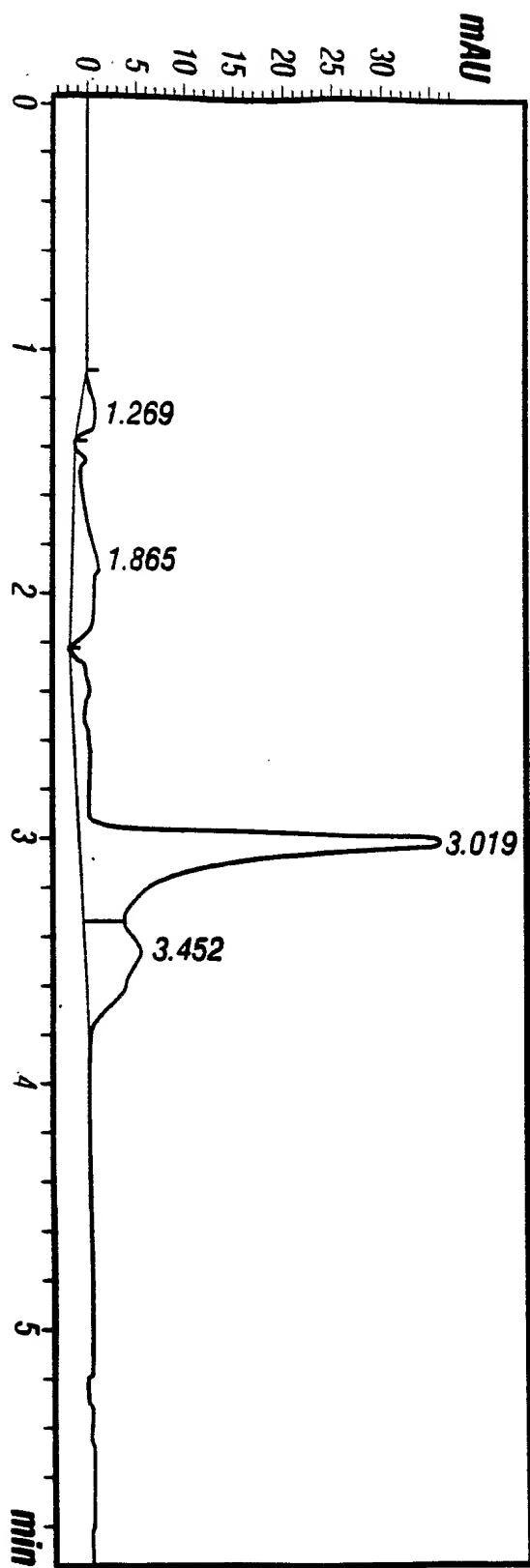


FIG. 12A

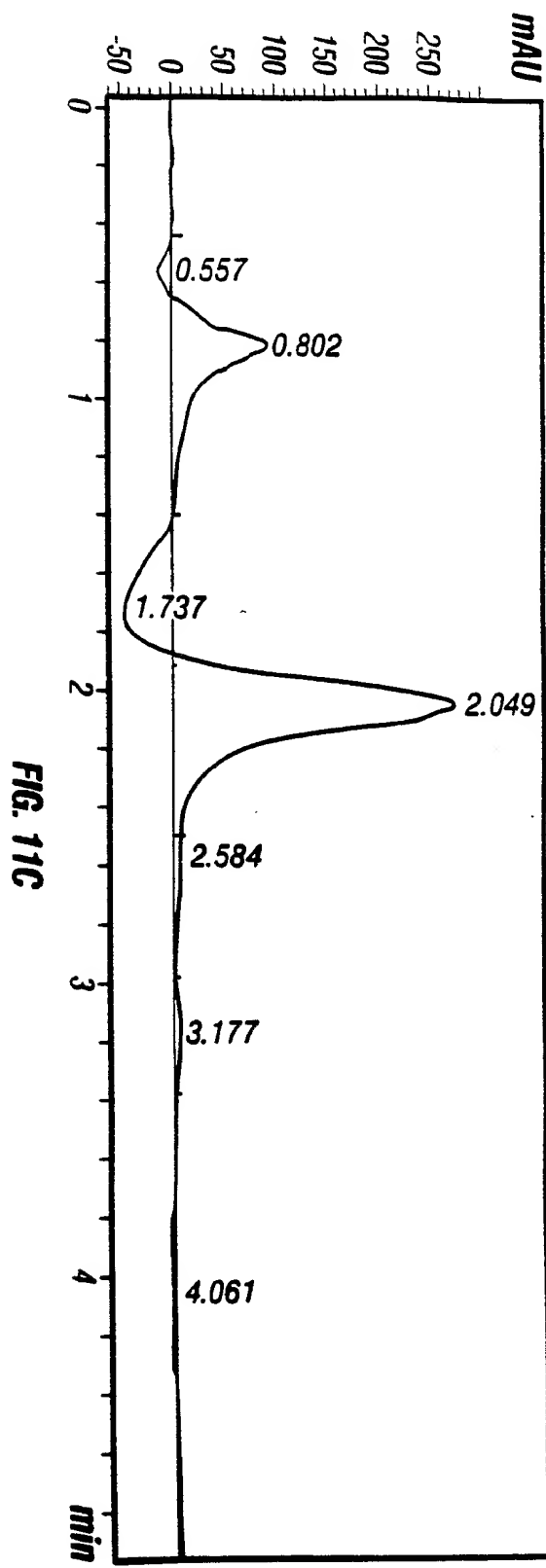
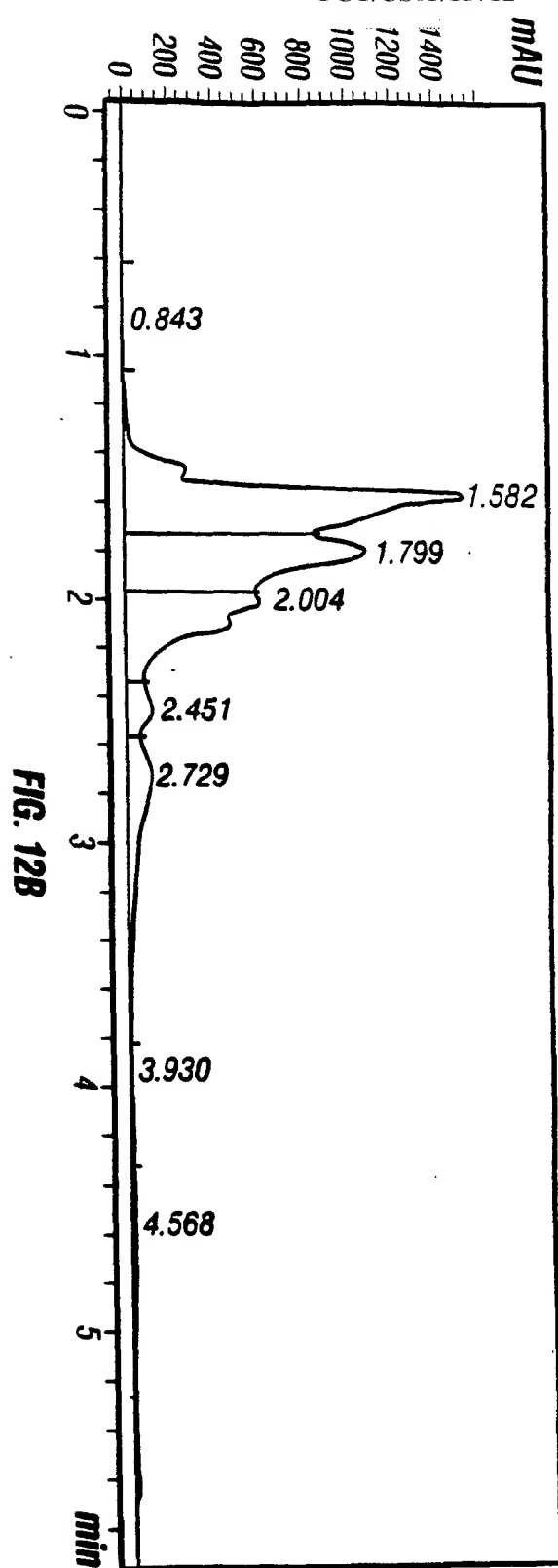
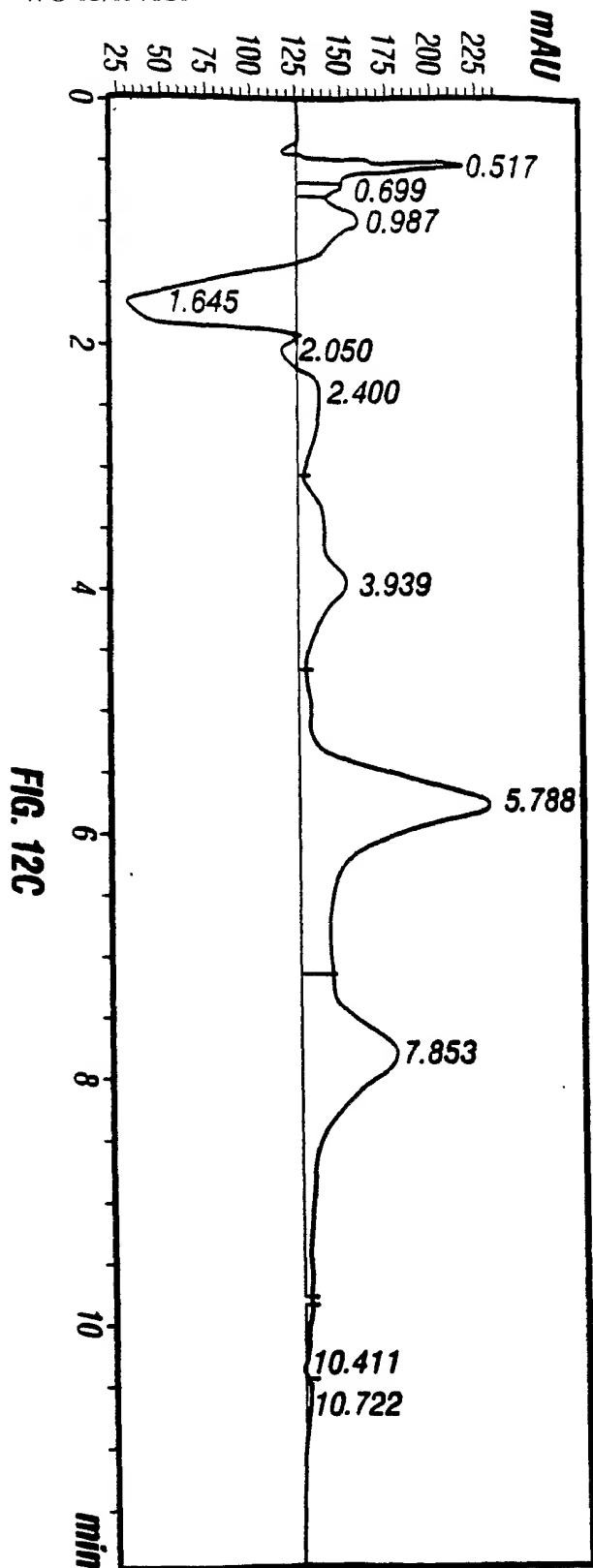


FIG. 11C



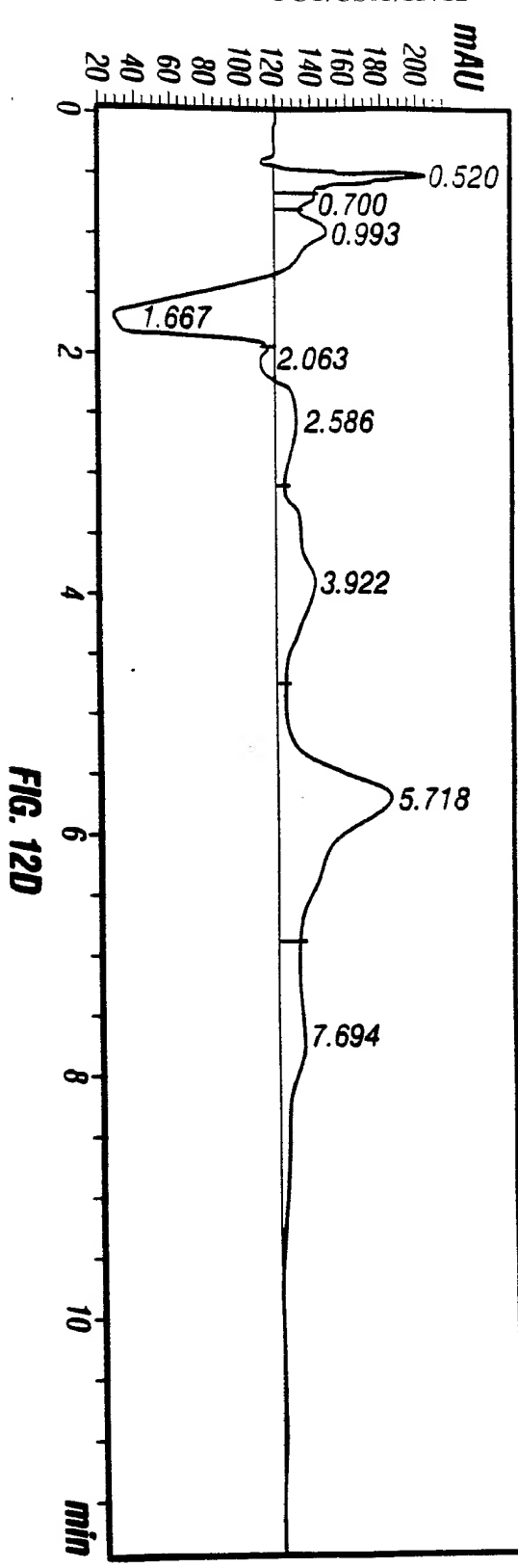
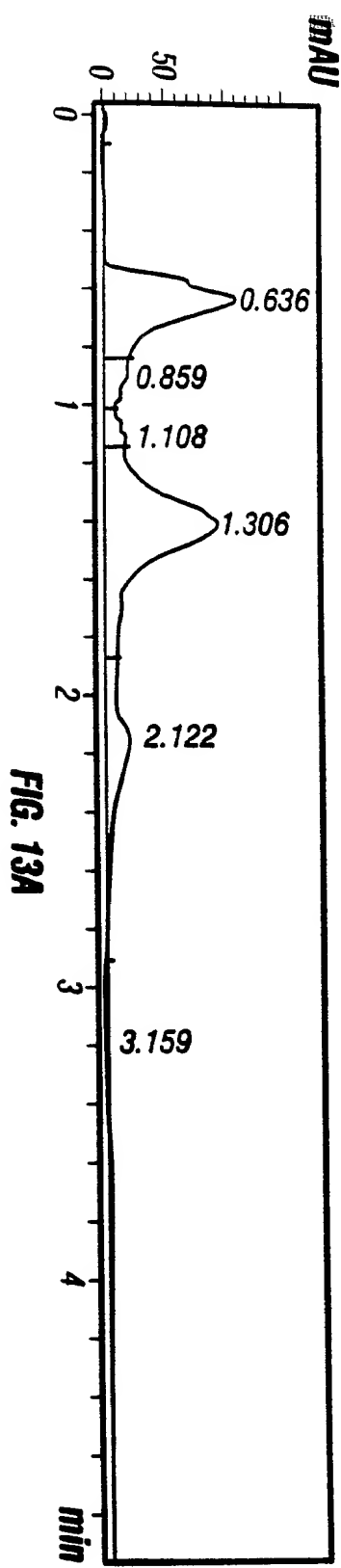
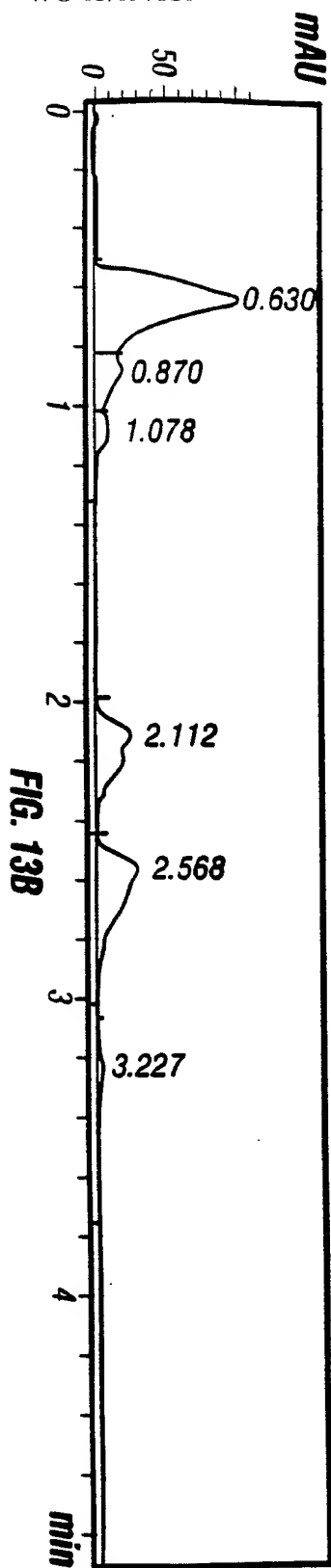


FIGURE 14A

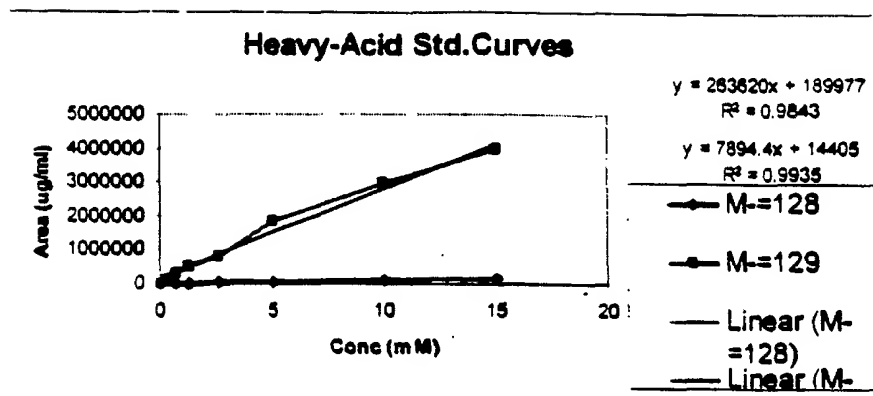


FIGURE 14B

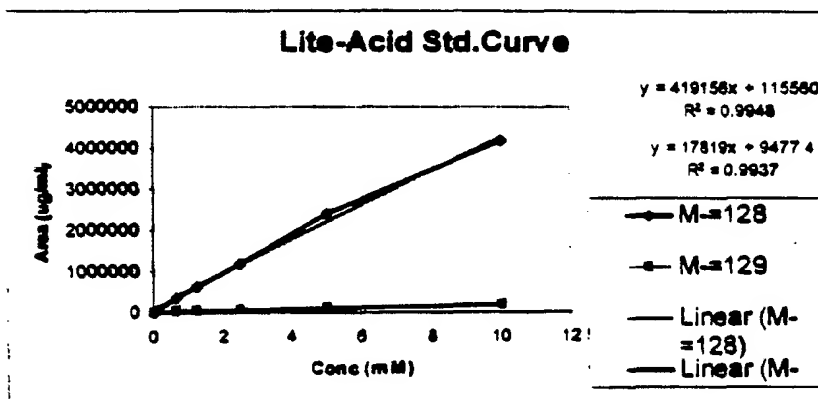


Figure 15

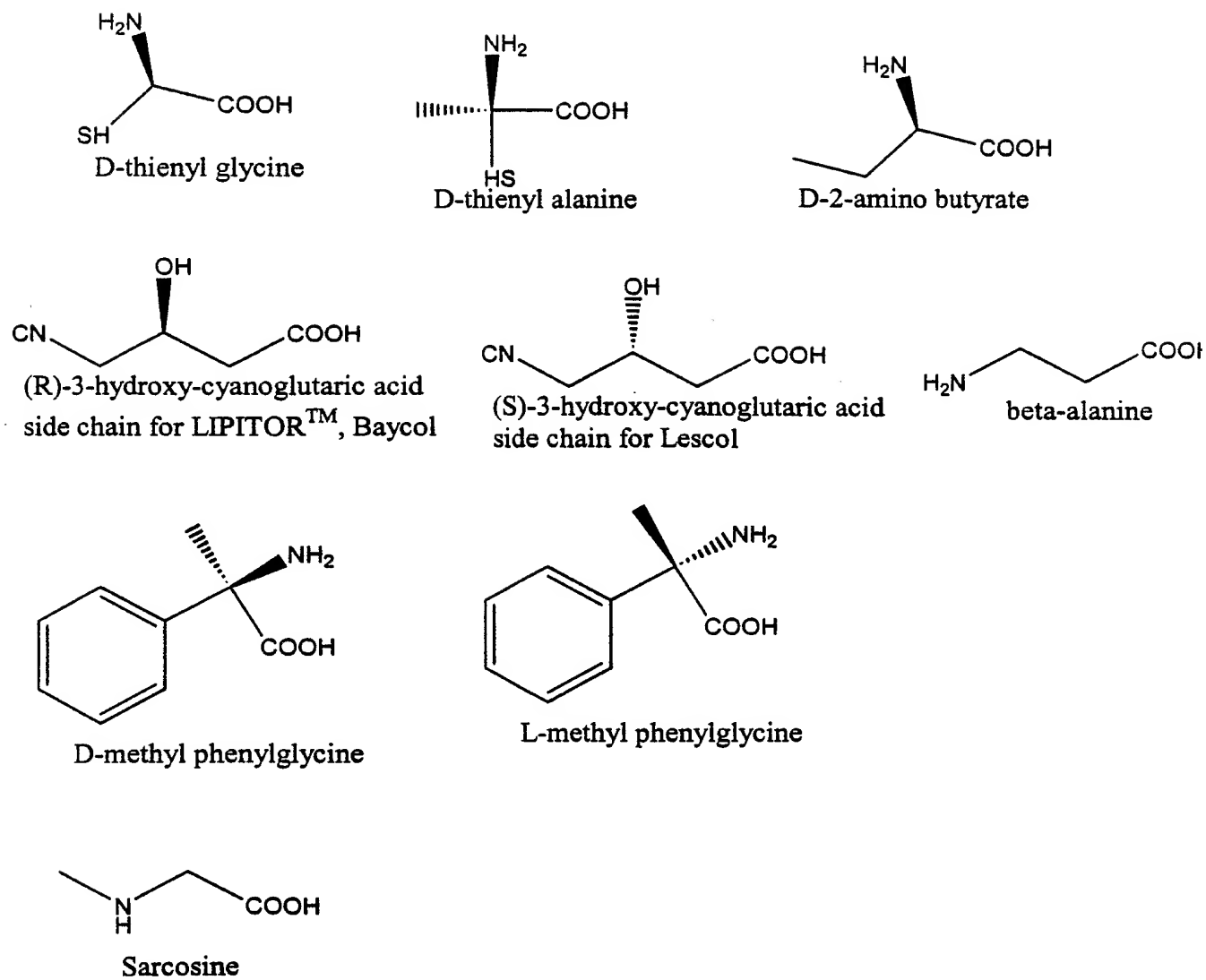


Figure 15

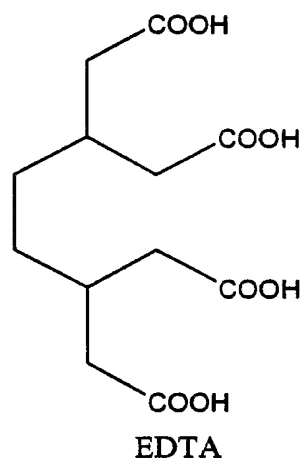
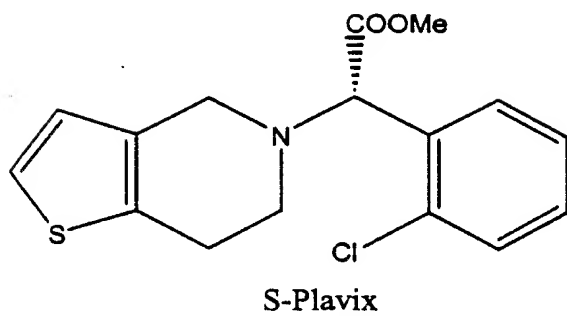
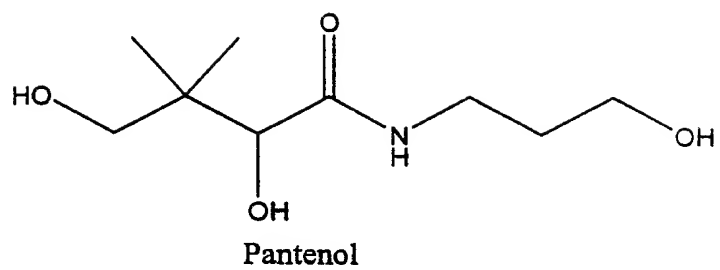
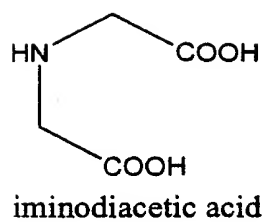


Figure 15

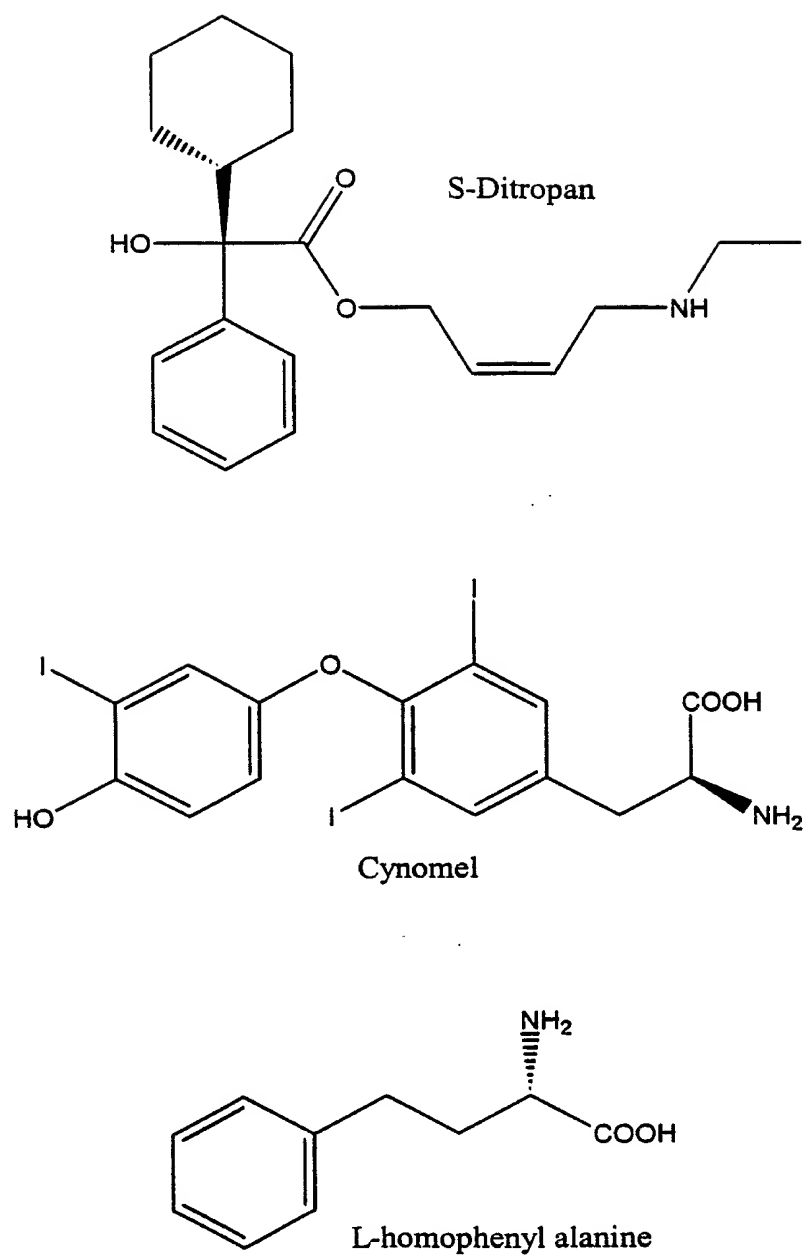
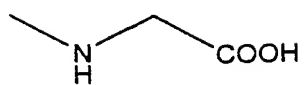
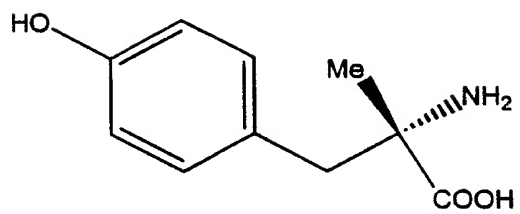


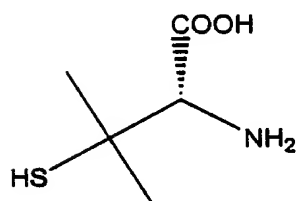
Figure 15



Sarcosine



alpha-methyl-L-tyrosine



Cuprimine/Depen

Figure 15

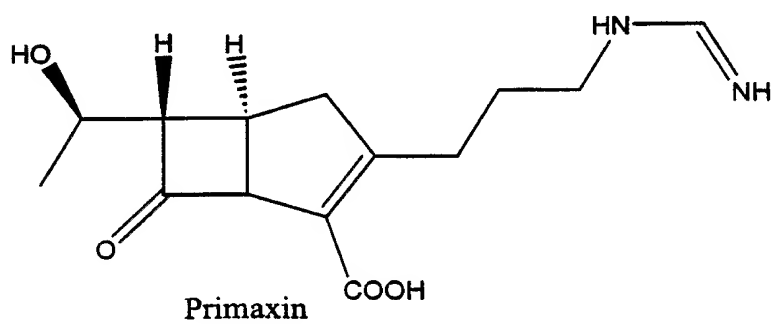
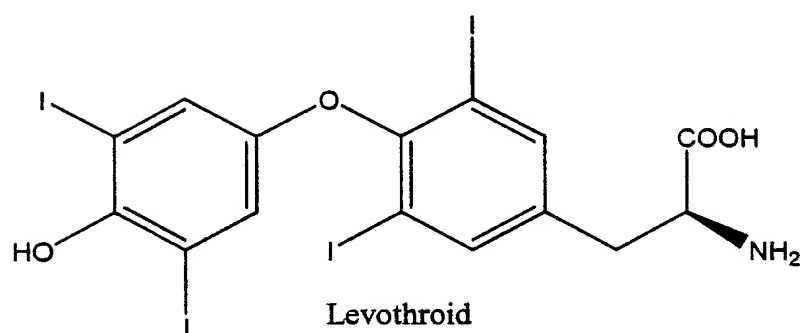
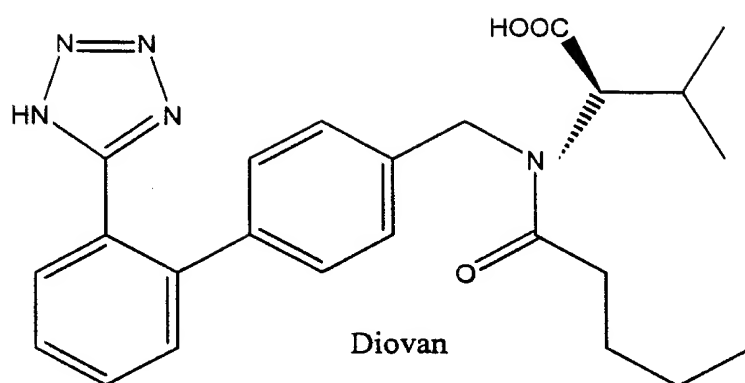


Figure 15

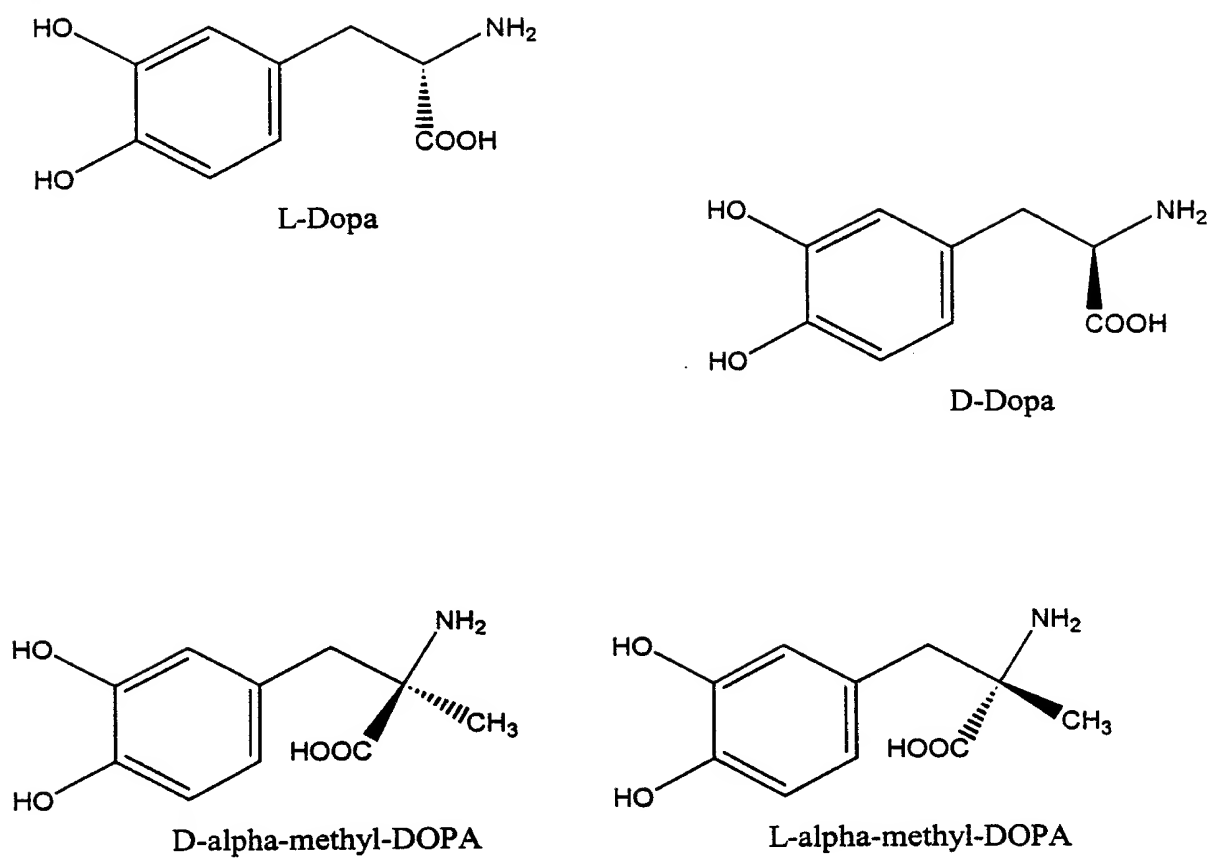
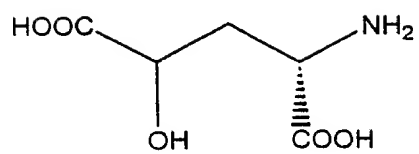
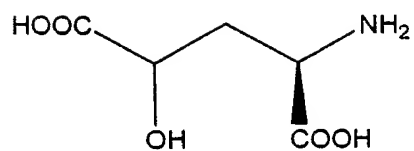


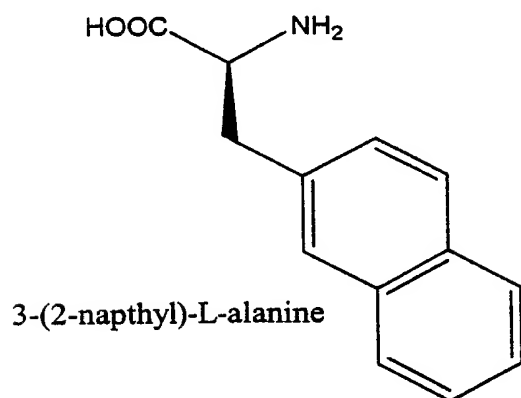
Figure 15



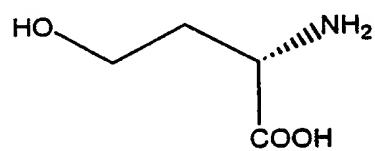
L-gamma-hydroxy glutamate



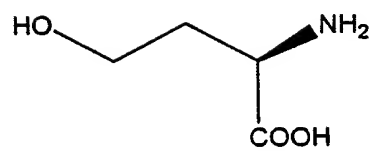
D-gamma-hydroxy glutamate



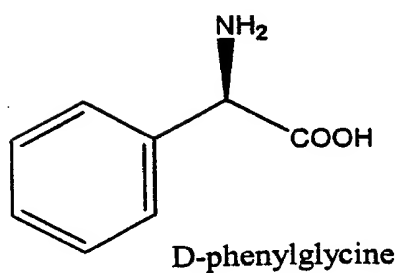
3-(2-naphthyl)-L-alanine



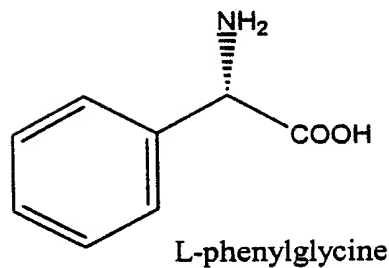
L-homoserine



D-homoserine



D-phenylglycine



L-phenylglycine

Figure 15

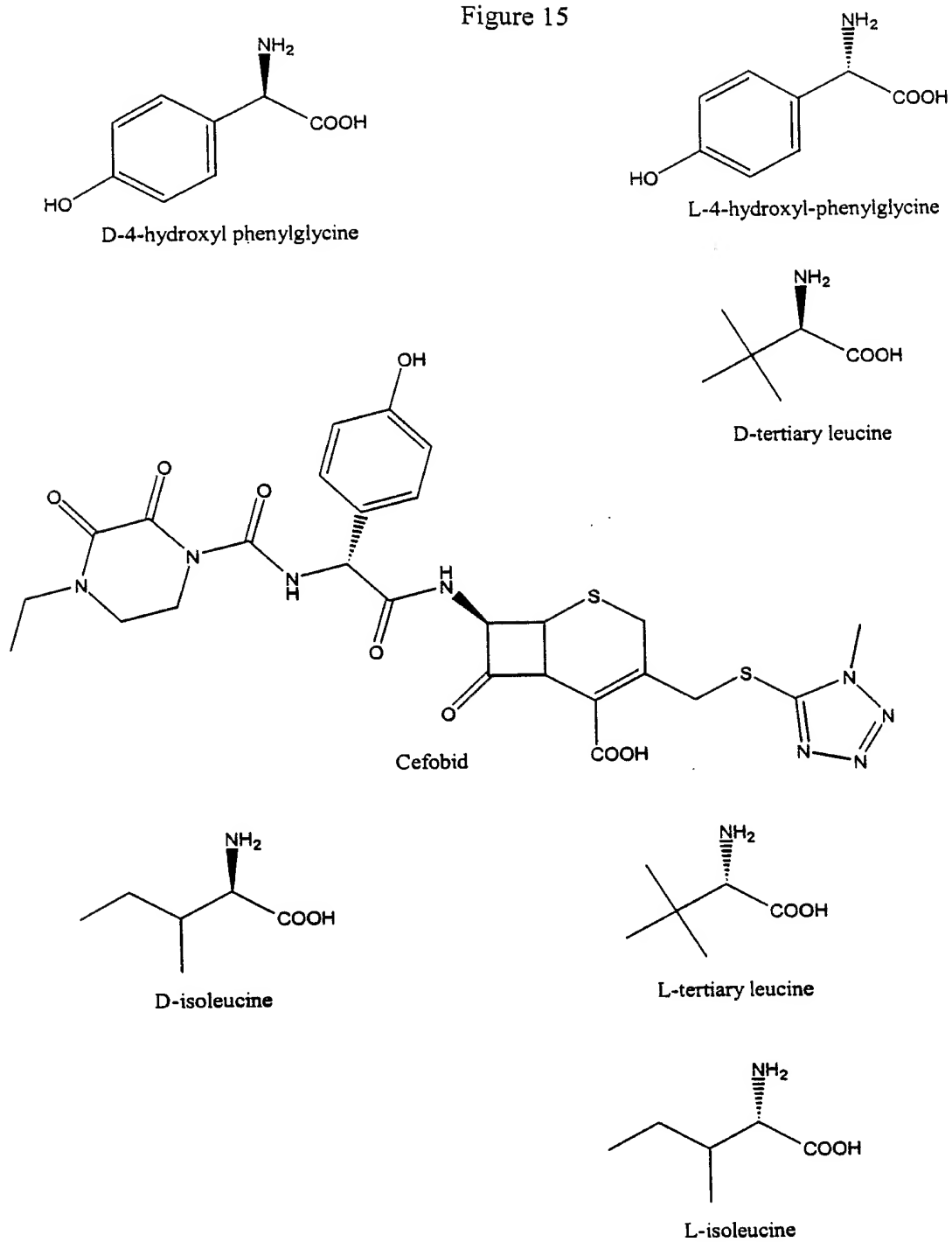
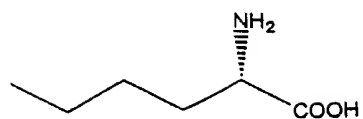
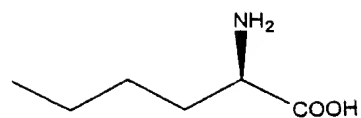


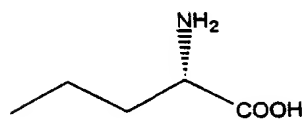
Figure 15



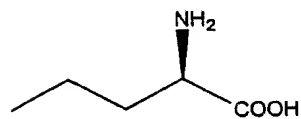
L-norleucine



D-norleucine



L-norvaline



D-norvaline

Figure 15

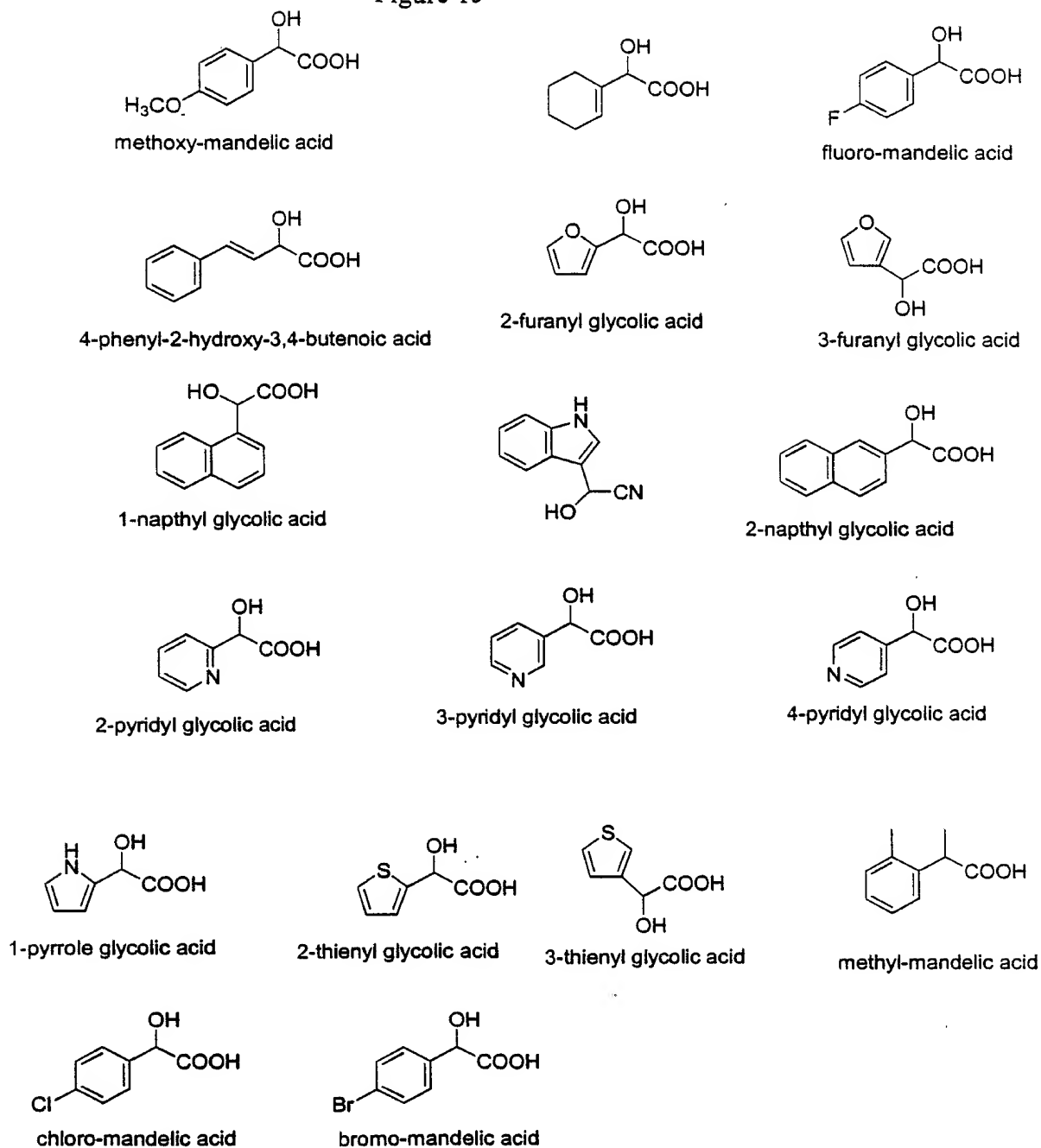


Figure 15

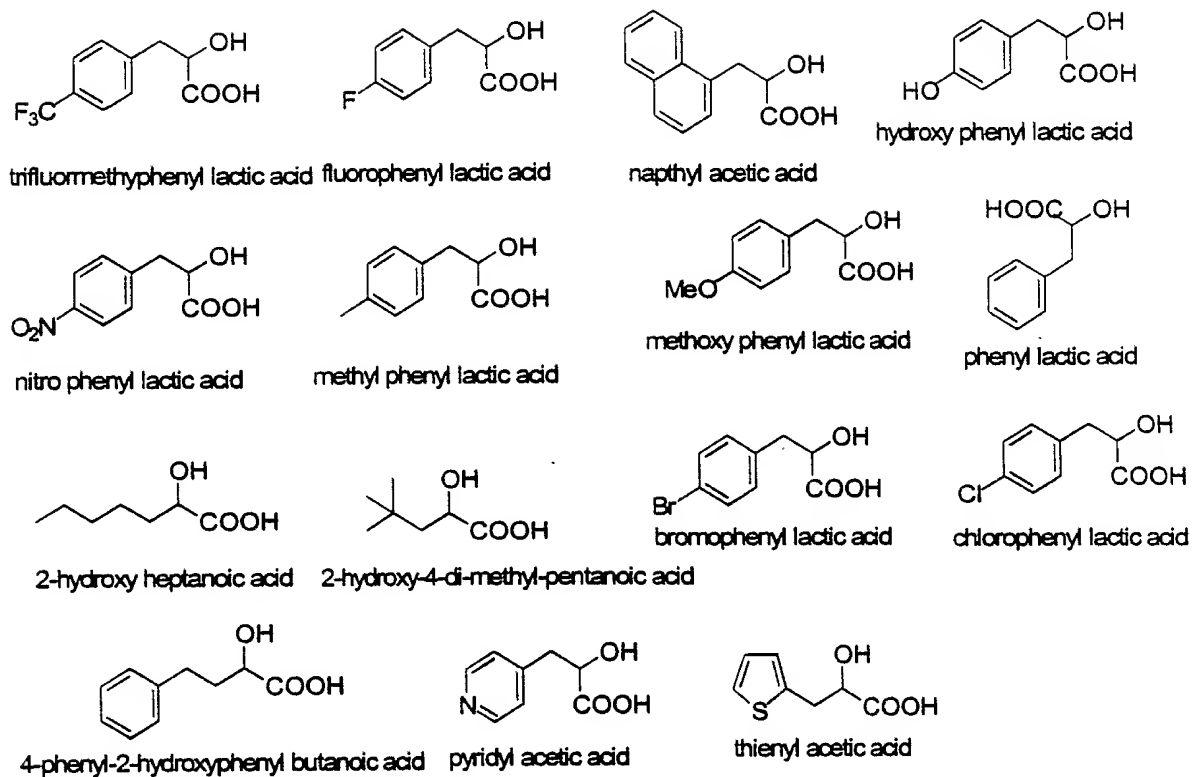


Figure 15

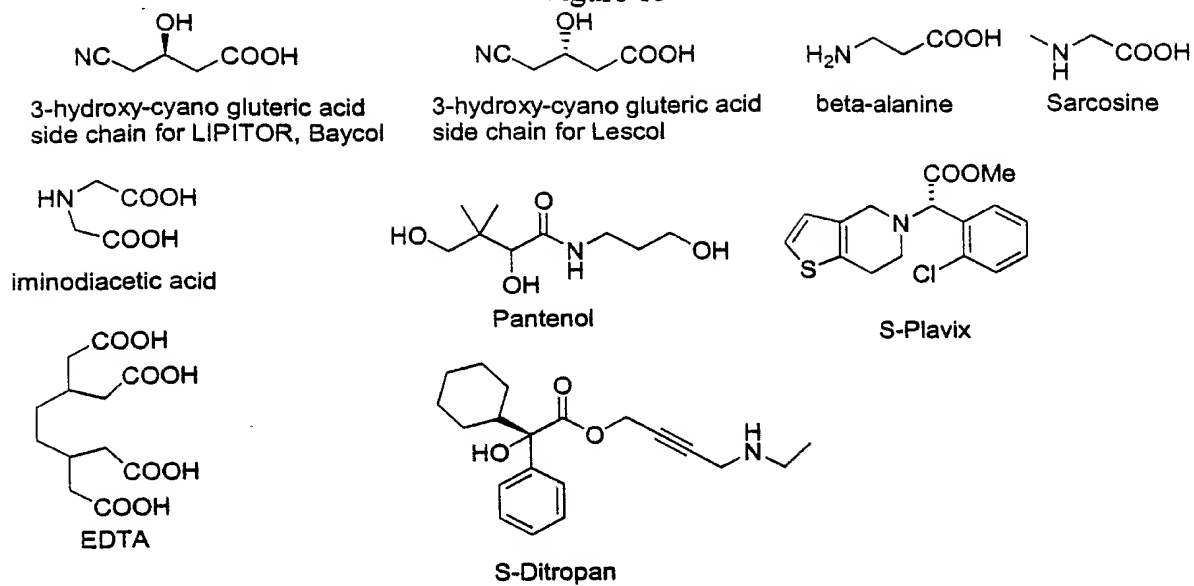
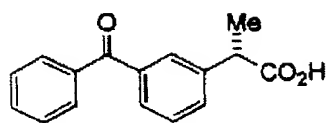
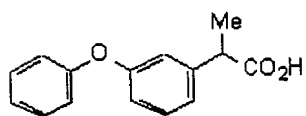
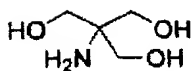


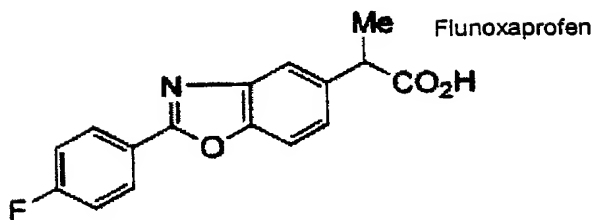
Figure 15



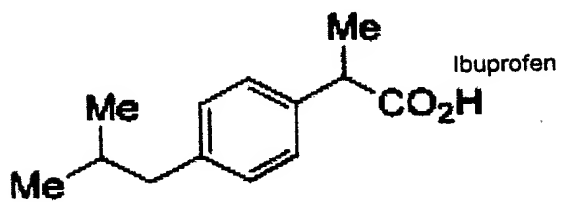
Dexketoprofen



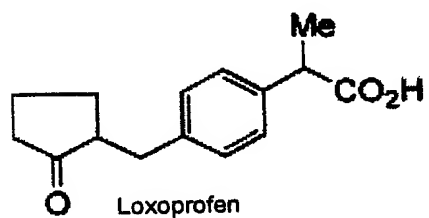
Fenoprofen



Flunoxaprofen

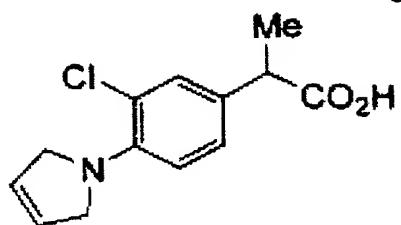


Ibuprofen

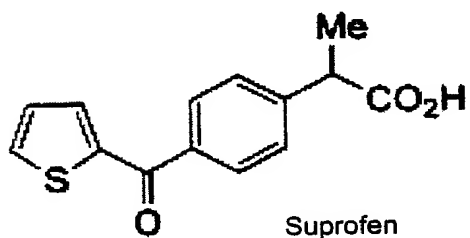


Loxoprofen

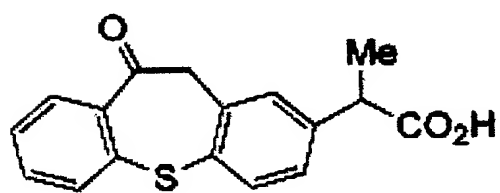
Figure 15



Pirprofen

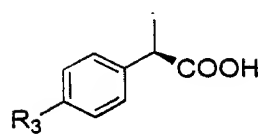


Suprofen

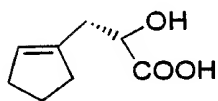


Zaltoprofen

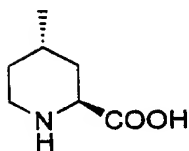
Figure 15



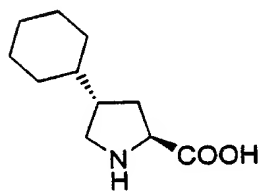
alpha-methyl benzyl cyanide derivatives



intermediate for Trocade

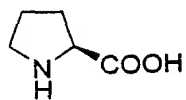


3-methyl-2-carboxy-piperidine

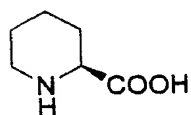


Fospril

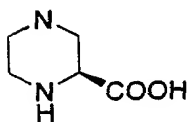
Figure 15



2-carboxy-cyclobutyl amine



2-carboxy-piperidine



2-carboxy-piperazine

Figure 16

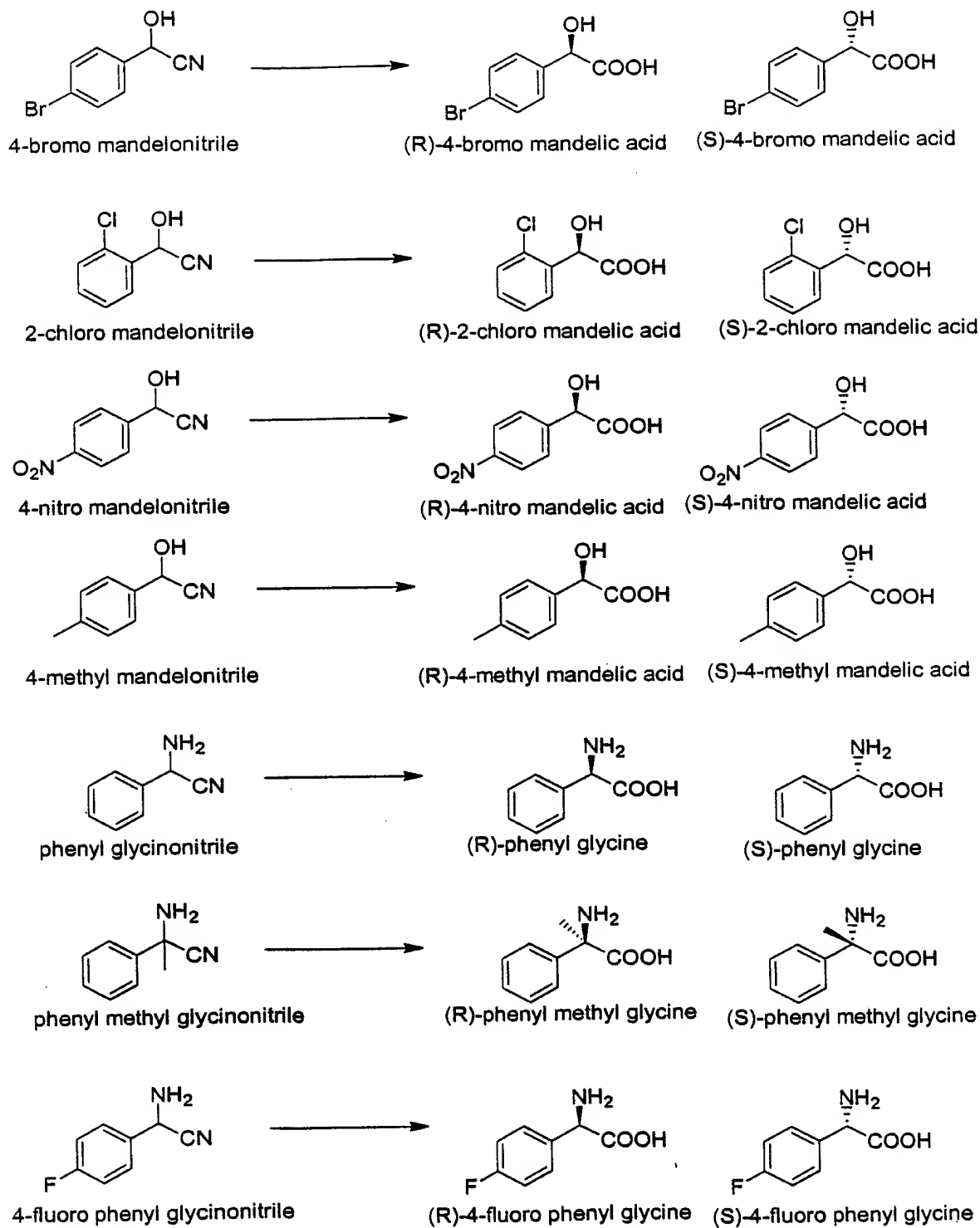


Figure 16

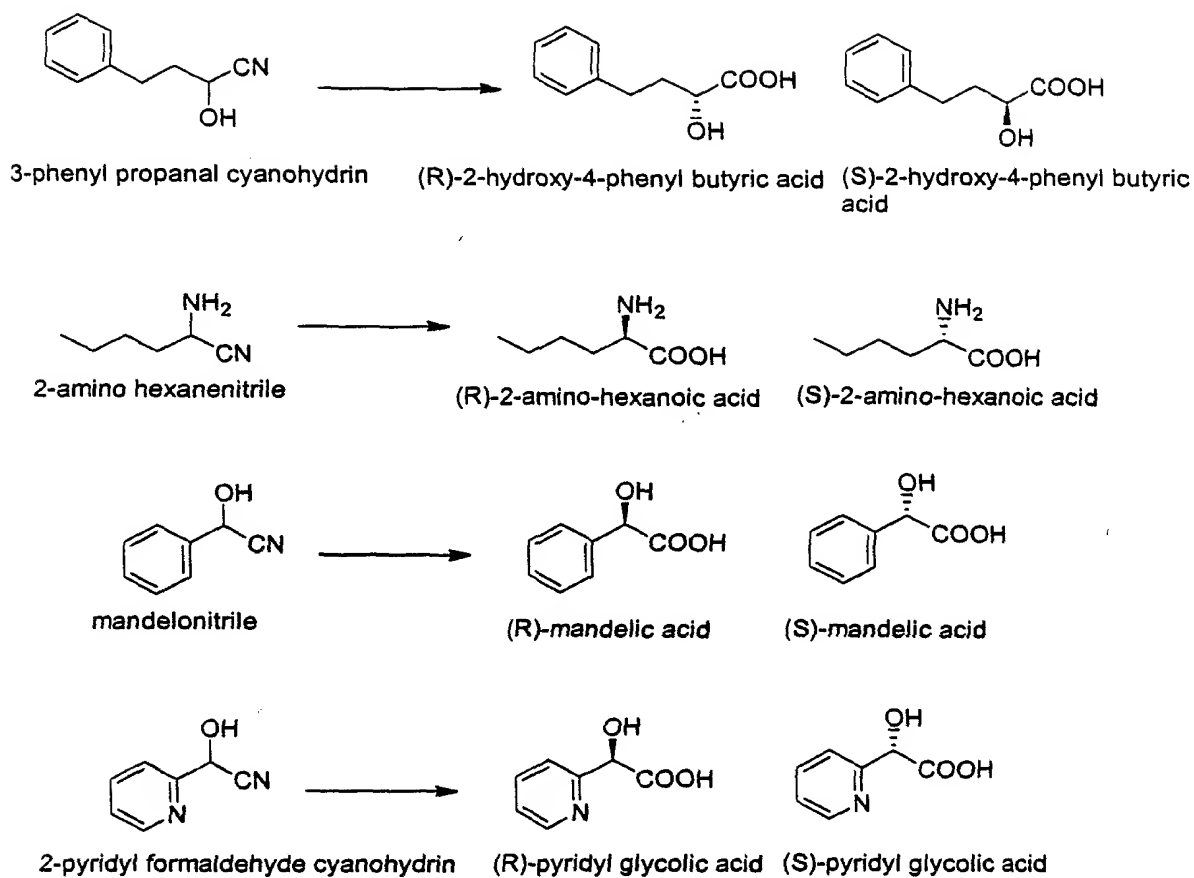


Figure 16

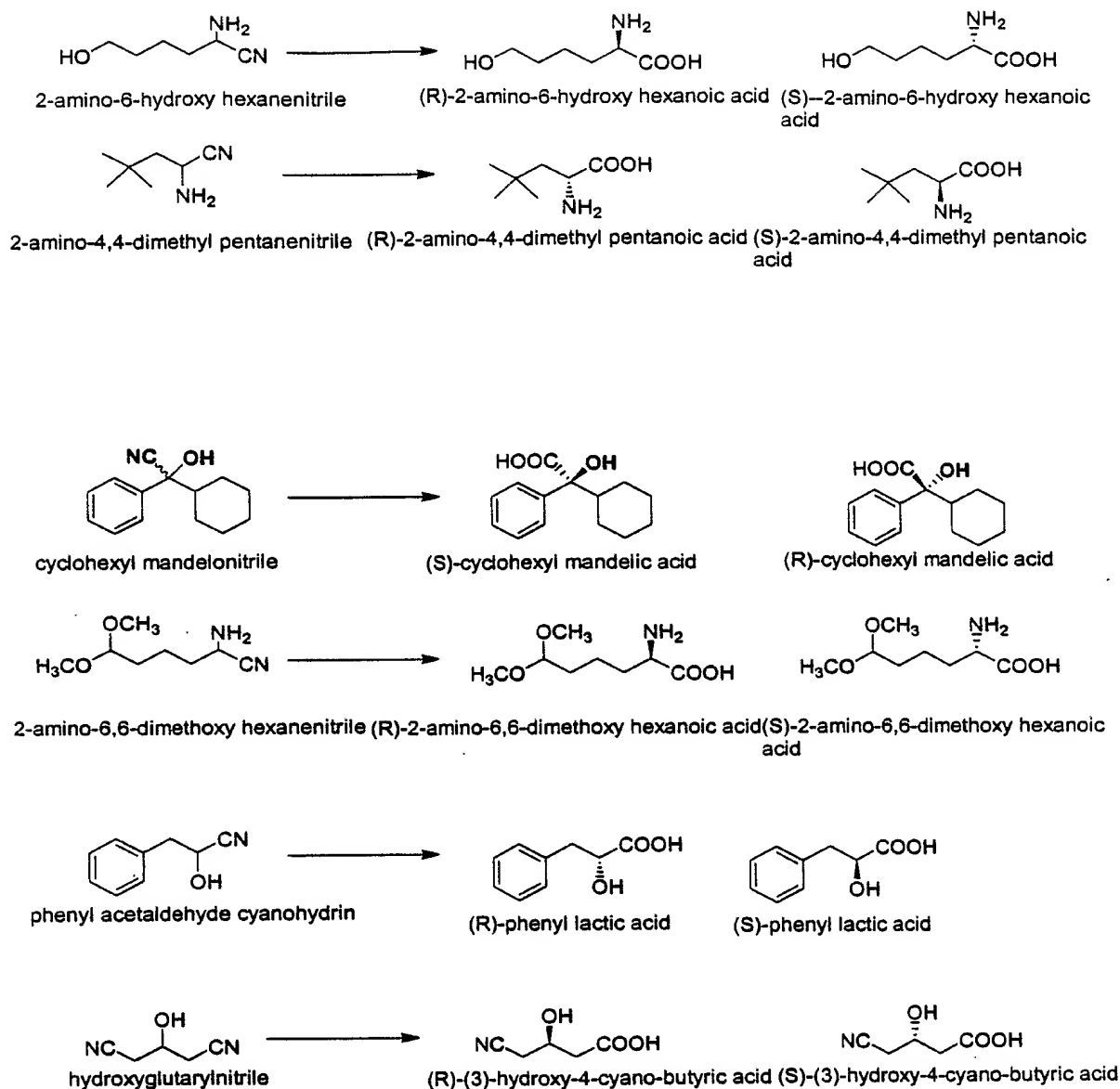


Figure 16

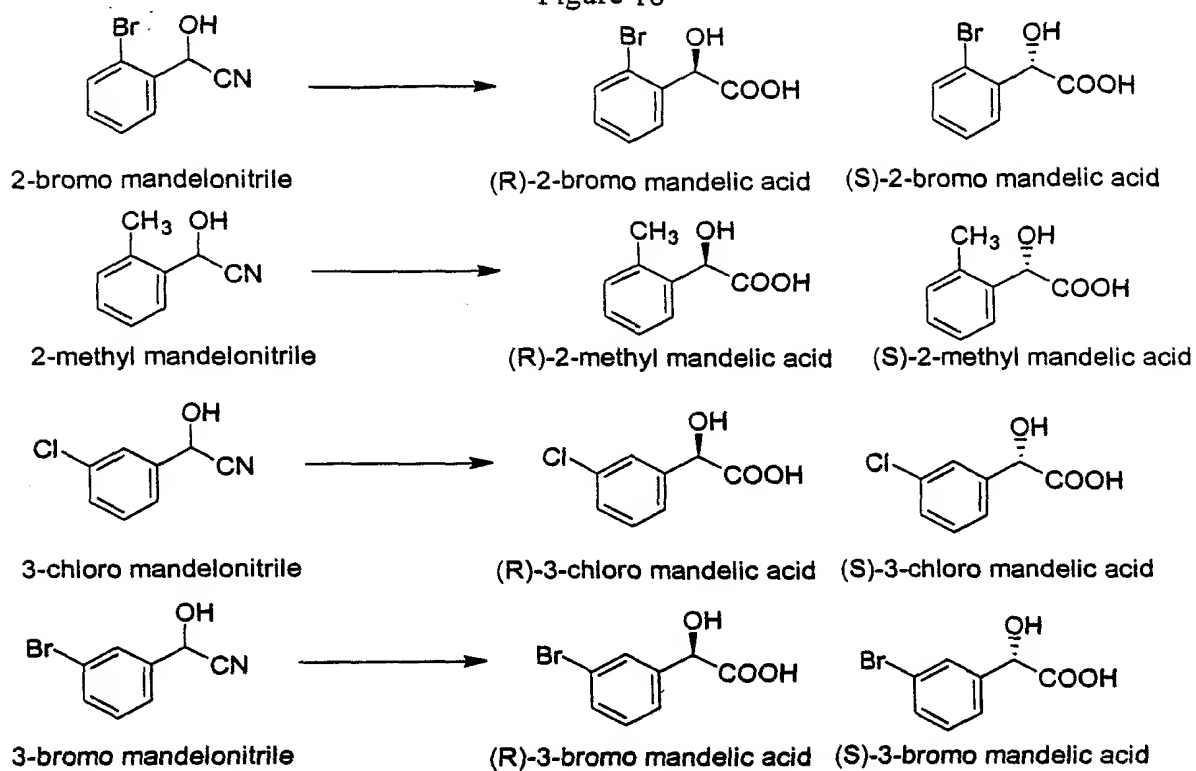


Figure 16

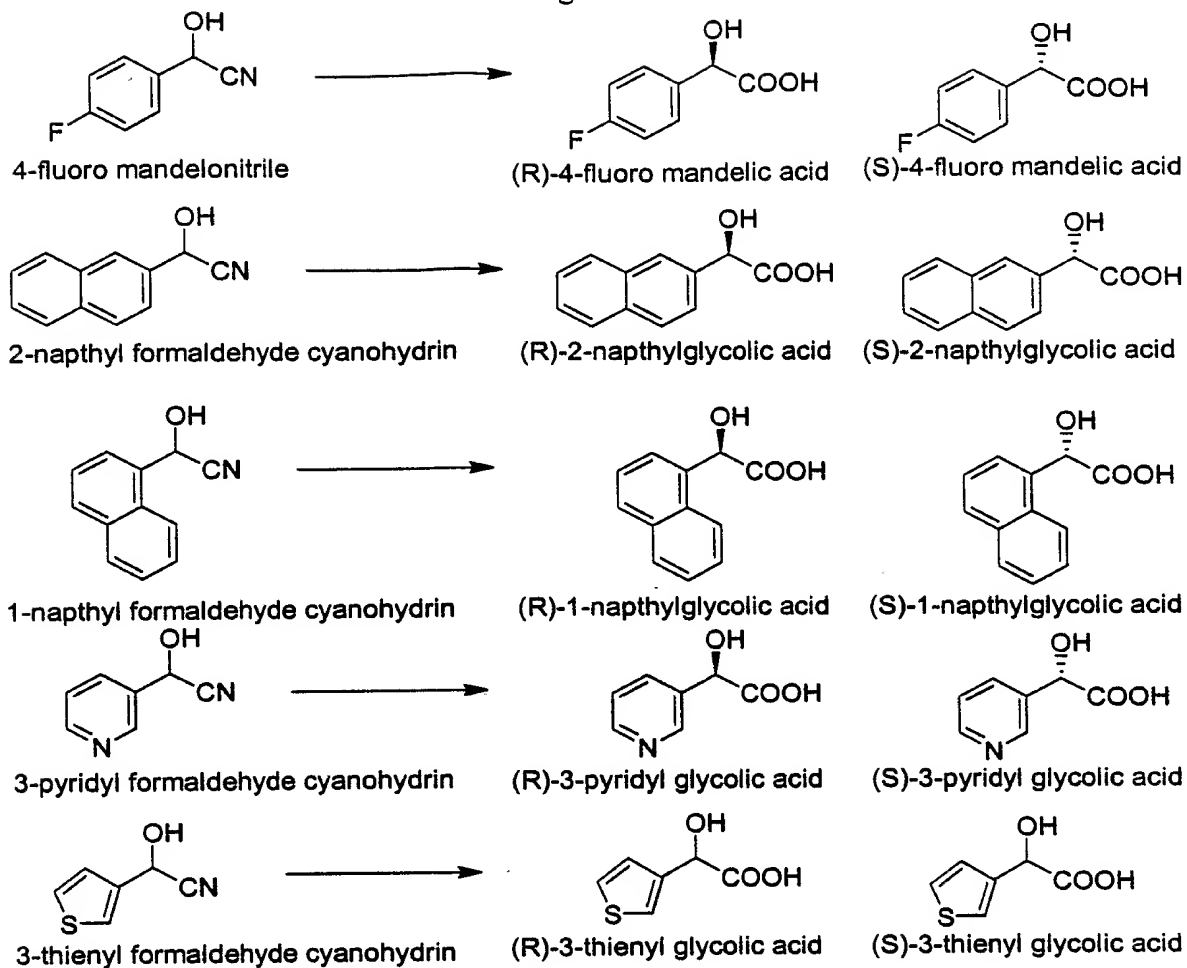


Figure 16

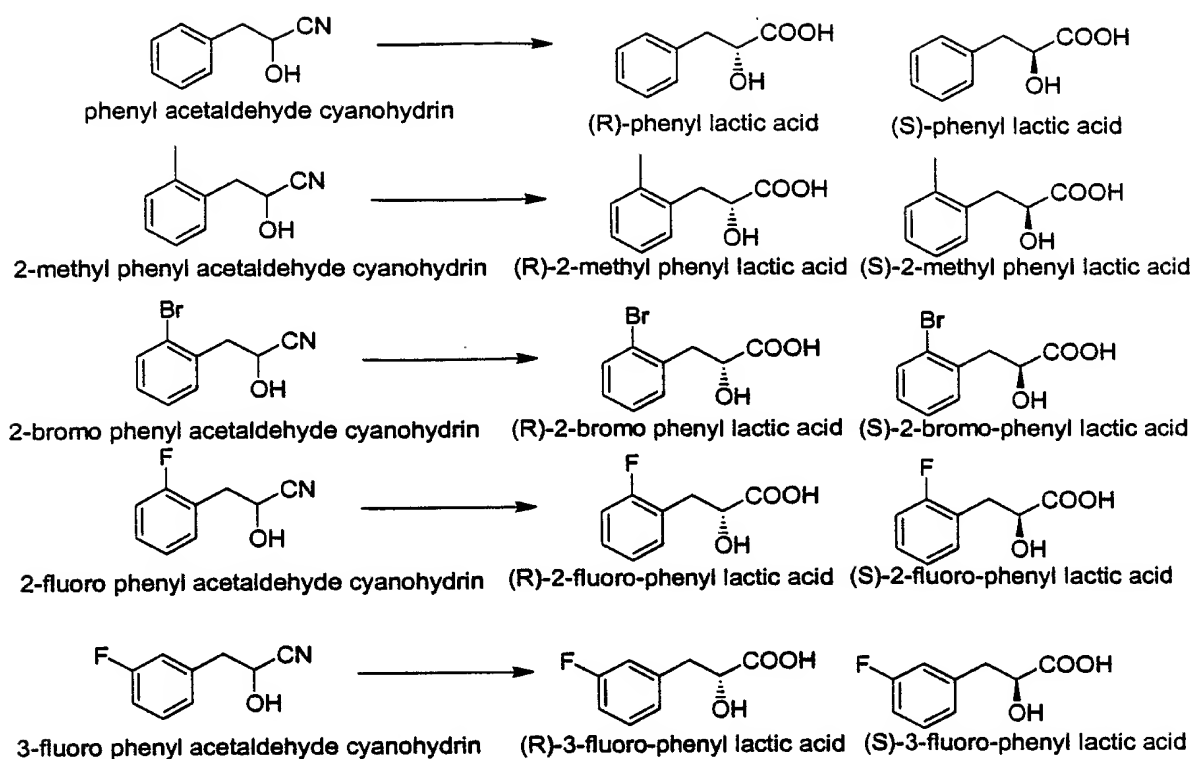


Figure 16

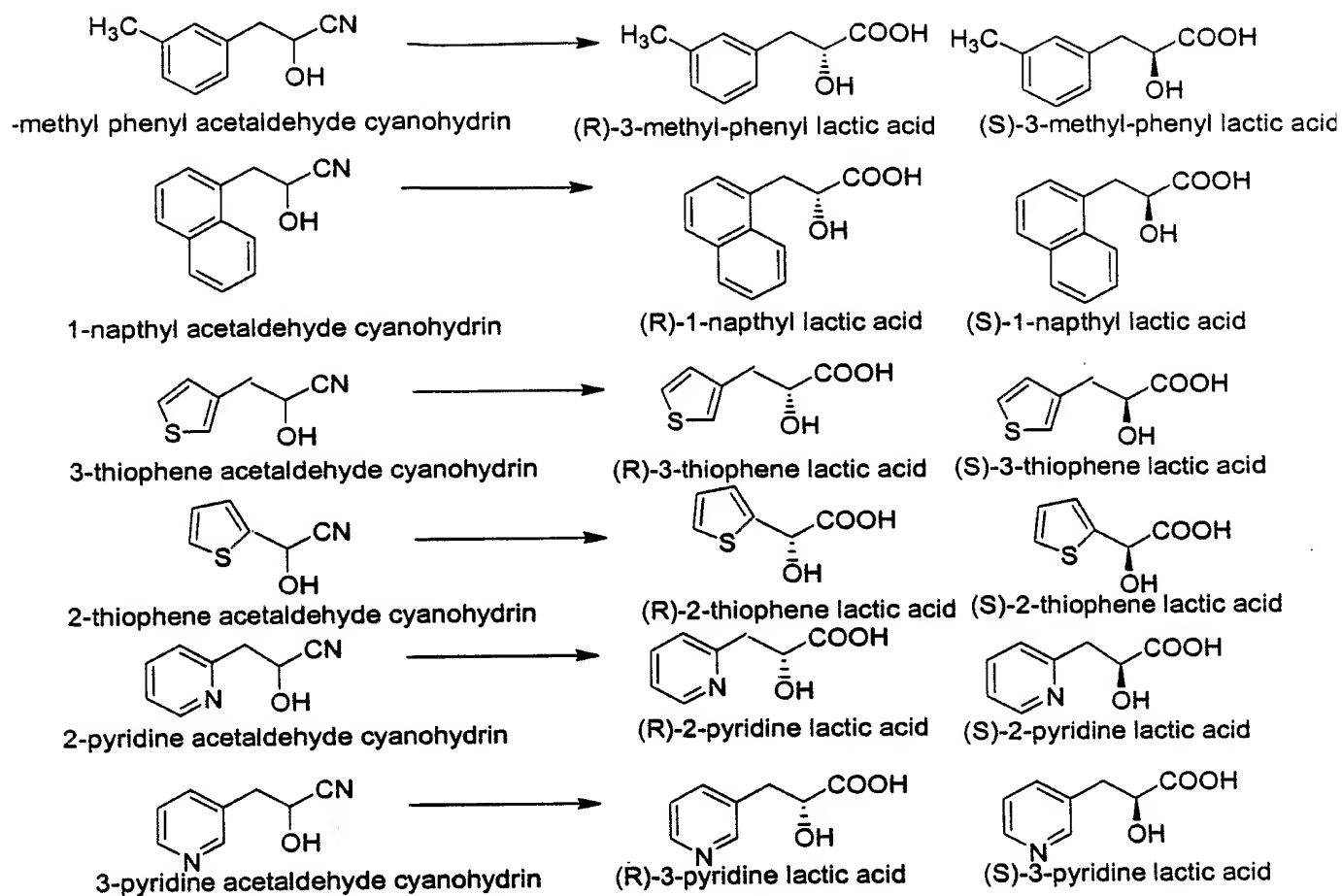
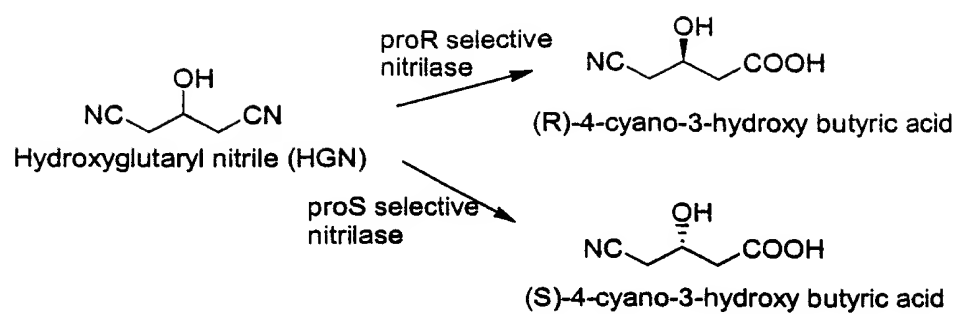


Figure 17



SEQUENCE LISTING

<110> DIVERSA CORPORATION

<120> Nitrilases, Nucleic Acids Encoding Them and Methods for Making and Using Them

<130> Docket No. 09010-120WO4

<140> Unknown

<141> 2003-05-15

<150> US 10/241,742

<151> 2002-09-09

<150> US 10/146,772

<151> 2002-05-15

<150> US 60/309,006

<151> 2001-07-30

<150> US 60/351,336

<151> 2002-01-22

<150> US 60/300,189

<151> 2001-06-21

<150> US 09/751,299

<151> 2000-12-28

<150> US 60/254,414

<151> 2000-12-07

<150> US 60/173,609

<151> 1999-12-29

<160> 386

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 939

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

atggaaaagt	atattaaagt	cgccgcaatt	cagatagcta	caaaaatagc	agattcaccc	60
gtgaatatag	aaaattgcga	acgtttggca	ttatcggcgg	tcaatgaggg	tgcgcgttgg	120
attgctttgc	cggagttctt	caatacgggc	gttagttgga	acaaaaaat	tgcttggct	180
attcagacgc	ctgacggcaa	ggctgcgatg	ttcttacgcg	acttttctgc	aagacatcat	240
gtattgatag	gaggctcatt	tctgtgcagg	ttgccgggatg	gcagtgtgcg	caaccgctat	300
atgtgttatg	ccaacggcgc	tctcgtgggc	aaacatgaca	aagacctacc	cacgatgtgg	360
gaaaatgctt	tttatgaagg	tggggattcc	agcgatattg	gggtgctggg	aacatttgaa	420
aatacgcgcg	ttggtgcagc	cgtctgttgg	gagttcatgc	ggacgatgac	tgcccggcgt	480
cttcgcaatc	aggtggatgt	catcatgggt	ggttcctgct	ggtggagcat	accgaccaat	540
ttccccgggtt	ttgtgcaaaa	gctgtgggaa	cctggaaata	gccgcaacgc	gcttgctgcc	600

```

atacaggata atgcgcgtct cattggcgtg cgggttggtc atgccgctca ttgcggtgaa      660
attgagtgtc cgatgccagg attgccgata ggttacaggg ggttctttga gggtaacgcg      720
gccattgtga atgcagaagg tcagggtgctt ggcgcacggg gtgctggcga gggcgaagga      780
attgtttgcg cggagatttt accggtagcc aaatcaaaca ggtcggaaat tcccaatcgt      840
tactggttgc gctgcagagg ctttctacct atttttgcct ggcatcagca acgttggttg      900
ggaaggcatt ggtatttgcg caatgtgcgc aggacttaa      939

```

<210> 2

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 2

```

Met Glu Lys Tyr Ile Lys Val Ala Ala Ile Gln Ile Ala Thr Lys Ile
 1          5          10          15
Ala Asp Ser Pro Val Asn Ile Glu Asn Cys Glu Arg Leu Ala Leu Ser
          20          25          30
Ala Val Asn Glu Gly Ala Arg Trp Ile Ala Leu Pro Glu Phe Phe Asn
          35          40          45
Thr Gly Val Ser Trp Asn Lys Lys Ile Ala Leu Ala Ile Gln Thr Pro
          50          55          60
Asp Gly Lys Ala Ala Met Phe Leu Arg Asp Phe Ser Ala Arg His His
          65          70          75          80
Val Leu Ile Gly Gly Ser Phe Leu Cys Arg Leu Pro Asp Gly Ser Val
          85          90          95
Arg Asn Arg Tyr Met Cys Tyr Ala Asn Gly Ala Leu Val Gly Lys His
          100          105          110
Asp Lys Asp Leu Pro Thr Met Trp Glu Asn Ala Phe Tyr Glu Gly Gly
          115          120          125
Asp Ser Ser Asp Ile Gly Val Leu Gly Thr Phe Glu Asn Thr Arg Val
          130          135          140
Gly Ala Ala Val Cys Trp Glu Phe Met Arg Thr Met Thr Ala Arg Arg
          145          150          155          160
Leu Arg Asn Gln Val Asp Val Ile Met Gly Gly Ser Cys Trp Trp Ser
          165          170          175
Ile Pro Thr Asn Phe Pro Gly Phe Val Gln Lys Leu Trp Glu Pro Gly
          180          185          190
Asn Ser Arg Asn Ala Leu Ala Ala Ile Gln Asp Asn Ala Arg Leu Ile
          195          200          205
Gly Val Pro Val Val His Ala Ala His Cys Gly Glu Ile Glu Cys Pro
          210          215          220
Met Pro Gly Leu Pro Ile Gly Tyr Arg Gly Phe Phe Glu Gly Asn Ala
          225          230          235          240
Ala Ile Val Asn Ala Glu Gly Gln Val Leu Ala His Arg Gly Ala Gly
          245          250          255
Glu Gly Glu Gly Ile Val Cys Ala Glu Ile Leu Pro Val Ala Lys Ser
          260          265          270
Asn Arg Ser Glu Ile Pro Asn Arg Tyr Trp Leu Arg Cys Arg Gly Phe
          275          280          285
Leu Pro Ile Phe Ala Trp His Gln Gln Arg Trp Leu Gly Arg His Trp
          290          295          300
Tyr Leu Arg Asn Val Arg Arg Thr
          305          310

```

<210> 3

<211> 981

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

```

atggggaatt cgttcaagat cgcgggtgga caagcctgtc cgttctttct ggatcgtggc      60
gcgacagtcg ccaaggcatg ccgcctgata gcggaggcag ccgcggcggg cgccagcctg      120
gtggtctttc cggaggcgtt tgtgcccgga taccactgtt ggtctctggtt cattccggca      180
gggcattcgc aaccactgcg ggagttatac gccgaactgg tggggaacgc cgtggcggta      240
ccgggcgatg ccaccgatcg gctttgcgcg gcagccagag aagccggcgt ggtagtggcg      300
atcggcataca atgaagtga cagcgaagcc agcggcacga cgatttaca tacgctgctg      360
tacatcggag cggacggcgc gattctgggc aaacaccgca aagtaatgcc gacgggcgga      420
gagcgcctgg tctgggcgct tggcgatggg agcgacctgg aggtctacga cctgcctttc      480
ggccgattgg gtggcctggt gtgctgggag aactacatgc ccctggcccg gtacgcgatg      540
tcggcatggg gaaccgagat ctacgtggct ccaacttggg atcgcggaga accgtggctg      600
tccacaatgc ggcatatcgc gaaagaaggg cgatgctacg tagtgggatg ctgcagttgc      660
atgaaaattg acgatgtacc cgaccggctg gcgttcaaag ggaagtatct gtcgacggcc      720
gagggctggc tcaaccccgg cgatagcgta atcgctcgatc cggacggcaa gctgatcgcg      780
ggcccggcaa gcgagcagga gacgattctg tatgccgatg ccgaccggtc taagatcacc      840
ggggccaggt ggcagttgga tgtggccggc cactacgcgc ggccggatat cttcgaactg      900
atcgtgcacc gcgaacctaa gcgatttttg acgatagctc cgcggacgaa ggaggagcgg      960
gagcctggggc cggaggcctg a                                     981

```

<210> 4

<211> 326

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 4

```

Met Gly Asn Ser Phe Lys Ile Ala Val Val Gln Ala Cys Pro Val Phe
 1          5          10          15
Leu Asp Arg Gly Ala Thr Val Ala Lys Ala Cys Arg Leu Ile Ala Glu
 20          25          30
Ala Ala Ala Gly Ala Ser Leu Val Val Phe Pro Glu Ala Phe Val
 35          40          45
Pro Gly Tyr Pro Leu Trp Val Trp Phe Ile Pro Ala Gly His Ser Gln
 50          55          60
Pro Leu Arg Glu Leu Tyr Ala Glu Leu Val Gly Asn Ala Val Ala Val
 65          70          75          80
Pro Gly Asp Ala Thr Asp Arg Leu Cys Ala Ala Arg Glu Ala Gly
 85          90          95
Val Val Val Ala Ile Gly Ile Asn Glu Val Asn Ser Glu Ala Ser Gly
100          105          110
Thr Thr Ile Tyr Asn Thr Leu Leu Tyr Ile Gly Ala Asp Gly Ala Ile
115          120          125
Leu Gly Lys His Arg Lys Val Met Pro Thr Gly Gly Glu Arg Leu Val
130          135          140
Trp Ala Leu Gly Asp Gly Ser Asp Leu Glu Val Tyr Asp Leu Pro Phe
145          150          155          160
Gly Arg Leu Gly Gly Leu Leu Cys Trp Glu Asn Tyr Met Pro Leu Ala
165          170          175
Arg Tyr Ala Met Ser Ala Trp Gly Thr Glu Ile Tyr Val Ala Pro Thr
180          185          190
Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Met Arg His Ile Ala Lys
195          200          205

```

Glu Gly Arg Cys Tyr Val Val Gly Cys Cys Ser Cys Met Lys Ile Asp
 210 215 220
 Asp Val Pro Asp Arg Leu Ala Phe Lys Gly Lys Tyr Leu Ser Thr Ala
 225 230 235 240
 Glu Gly Trp Leu Asn Pro Gly Asp Ser Val Ile Val Asp Pro Asp Gly
 245 250 255
 Lys Leu Ile Ala Gly Pro Ala Ser Glu Gln Glu Thr Ile Leu Tyr Ala
 260 265 270
 Asp Ala Asp Arg Ser Lys Ile Thr Gly Pro Arg Trp Gln Leu Asp Val
 275 280 285
 Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile Val His Arg
 290 295 300
 Glu Pro Lys Arg Phe Leu Thr Ile Ala Pro Arg Thr Lys Glu Glu Arg
 305 310 315 320
 Glu Pro Gly Pro Glu Ala
 325

<210> 5

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 5

```

atgggtacca agcaccgccc cttcaaggcc gcagtgggtcc aggccgcgcc ggaatgggtc 60
gatctcgacc gcaccgtcga caagaccatc gcgctgatcg aggaggccgc cggcgccggc 120
gcgaagctca ttgcgttccc ggaaacctgg attcccggct atccgtggca catctgggtc 180
ggcacgccgg cgtgggcgat cagccggcgc ttctgtcagc gctacttcga caattcactg 240
gcctacgaca gcccgcaggc ccagcgcatc gcggacgccg cgaagaagaa caagatcacc 300
gtggtgctcg gcctgtcggg gcgcgagggg ggcagccttt atatctcgca gtggctgatt 360
gggcccggacg gcgagaccat tgccaagcgc cgcaaactgc gccccacca cgtcgagcgc 420
accgtgttcg gcgatggcga cggcagccac atcgcggtgc acgagcgtgc tgacatcggc 480
cgccctcggcg cgctgtgctg ctggggagcac atccagccgc tgaccaaata cgccatgtat 540
gcccagaacg agcaggtgca cgtcgccgcc tggccgagct tctcgatgta cgagccgttc 600
gcccacgcgc tcggctggga agtcaacaat gcggcgagca agatctacgc cgtcgaaggc 660
tcgtgtttcg tgctcggcgc atgcgcggtg atctcgcagg cgatggtcga cgaaatgtgc 720
gacaccgagg acaagcgggc gctggtccat gccggcggcg gccacgcggt gatcttcggg 780
ccggacggca gatcgctggc ggacaagatt ccggagaccc aggaaggcct gctctatgcc 840
gacatcgacc tcggcgcaat tggcgtggcc aagaacgcgg ccgatccggc ggggcactac 900
tcgcgcccgg acgtgacgcg gctcctgttc aacaacaagc cggcgcgccg ggtcgagtat 960
ttctcgctgc cggtcgacgc ggtcgagacg ccgcgcgacg cctga 1005
  
```

<210> 6

<211> 334

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 6

Met Gly Thr Lys His Pro Ala Phe Lys Ala Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Glu Trp Leu Asp Leu Asp Arg Thr Val Asp Lys Thr Ile Ala Leu
 20 25 30
 Ile Glu Glu Ala Ala Gly Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45

Thr Trp Ile Pro Gly Tyr Pro Trp His Ile Trp Val Gly Thr Pro Ala
 50 55 60
 Trp Ala Ile Ser Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ala Tyr Asp Ser Pro Gln Ala Gln Arg Ile Ala Asp Ala Ala Lys Lys
 85 90 95
 Asn Lys Ile Thr Val Val Leu Gly Leu Ser Glu Arg Glu Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ser Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly
 130 135 140
 Asp Gly Asp Gly Ser His Ile Ala Val His Glu Arg Ala Asp Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Thr Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Met Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Gly Ala Cys Ala Val Ile Ser Gln Ala Met Val Asp Glu Met Cys
 225 230 235 240
 Asp Thr Glu Asp Lys Arg Ala Leu Val His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Phe Gly Pro Asp Gly Arg Ser Leu Ala Asp Lys Ile Pro Glu
 260 265 270
 Thr Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Phe Asn Asn Lys Pro Ala Arg Arg Val Glu Tyr
 305 310 315 320
 Phe Ser Leu Pro Val Asp Ala Val Glu Thr Pro Pro Gln Pro
 325 330

<210> 7
 <211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 7
 atgccgagtg attatcatgc tccattcaaa gtagcagttg tccaggcaac tcccgctcttt 60
 ctcgatcgca ggcgcacgat tgagaaggca tgtgagctaa ttgcctgtgc tggacgtgag 120
 ggcgcacgctc tgatcgtggt tcctgaagcg ttcattccca cctatcccga ttgggtctgg 180
 accattccac ctggggagat gcggctgctt ggcgaactct acacagagtt gcttgccaat 240
 gcggtcacga tccccagtaa tgcaacggat aggctctgcc aggctgcgaa acgagctgct 300
 gcgtatgtgg tcatgggaat gaacgaacgc aatatcgagg cgagtggag gagtctctat 360
 aacaccctgt tatacatcga tgctcagggc cagatcatgg gcaaacaccg caagttgata 420
 cccacagccg gtgagcgggt catatgggag caaggagatg ggagtacatt ccaggtctac 480
 gatactcctc tgggcaaact gggagggtc atctgctggg aaaactacat gcctctgggt 540
 cgctatcgca tgtatgcctg gggcacgcag atttatgtcg ccccgacatg ggatcgtggc 600
 aacctctggc tctctactct gcggcatatc gctaaggagg gaggcgtcta tgttcttggt 660
 tgtagtatgg tcatgcgcaa gaatgacatt cccgatcact ttgctttcaa agagcagttt 720
 tatgtactg tggacgaatg gatcaacgtt ggtgacagcg ccattgtcca tcccgagggg 780
 aactttcttg cgggaccggt gcgccacaaa gaagagattc tctatgcaga acttgatcca 840

```

cgccaatcgt gcgggtccggg atggatgctc gatgtggctg ggcaactatgc acgccctgat 900
gtgttttgaat tgattgtcca cacagagatg cgacccatga tgaagcaaga agaggttagga 960
ggagaaaaata catctgaggg aggtgtacga ttcttgtaa 999

```

<210> 8
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 8
Met Pro Ser Asp Tyr His Ala Pro Phe Lys Val Ala Val Val Gln Ala
1      5      10      15
Thr Pro Val Phe Leu Asp Arg Ser Ala Thr Ile Glu Lys Ala Cys Glu
20     25     30
Leu Ile Ala Cys Ala Gly Arg Glu Gly Ala Arg Leu Ile Val Phe Pro
35     40     45
Glu Ala Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Thr Ile Pro Pro
50     55     60
Gly Glu Met Arg Leu Leu Gly Glu Leu Tyr Thr Glu Leu Leu Ala Asn
65     70     75     80
Ala Val Thr Ile Pro Ser Asn Ala Thr Asp Arg Leu Cys Gln Ala Ala
85     90     95
Lys Arg Ala Ala Tyr Val Val Met Gly Met Asn Glu Arg Asn Ile
100    105    110
Glu Ala Ser Gly Arg Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala
115    120    125
Gln Gly Gln Ile Met Gly Lys His Arg Lys Leu Ile Pro Thr Ala Gly
130    135    140
Glu Arg Leu Ile Trp Ala Gln Gly Asp Gly Ser Thr Phe Gln Val Tyr
145    150    155    160
Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr
165    170    175    180
Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile Tyr
180    185    190
Val Ala Pro Thr Trp Asp Arg Gly Asn Leu Trp Leu Ser Thr Leu Arg
195    200    205
His Ile Ala Lys Glu Gly Gly Val Tyr Val Leu Gly Cys Ser Met Val
210    215    220
Met Arg Lys Asn Asp Ile Pro Asp His Phe Ala Phe Lys Glu Gln Phe
225    230    235    240
Tyr Ala Thr Val Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val
245    250    255
His Pro Glu Gly Asn Phe Leu Ala Gly Pro Val Arg His Lys Glu Glu
260    265    270
Ile Leu Tyr Ala Glu Leu Asp Pro Arg Gln Ser Cys Gly Pro Gly Trp
275    280    285
Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu
290    295    300
Ile Val His Thr Glu Met Arg Pro Met Met Lys Gln Glu Glu Val Gly
305    310    315    320
Gly Glu Asn Thr Ser Glu Gly Gly Val Arg Phe Leu
325    330

```

<210> 9
 <211> 945
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

```

atggcggtc acaagatcgc ggtgggttcag ggcgccagcg ttctcctcga tcgcgagggc 60
tcggtcgcgc gcgcggtcac gctgctcgac gaggcggcgg cggccggcgc ccgcctggtc 120
gtgtttccgg aggcctacat ccccggttac cgggactgga tctggcgcct gcgccctac 180
ccggacgtca agctggccgc cgagctgcac gaacgggtgc tcgccaacgc ggtggatctc 240
tccaccgacg tgctggcgcc ggtgctggcg gcggcggcgc gtcacgggct caccgtggtc 300
atgtgcgtgc aggagcgcga cgcggttc agcgcgcga cactttacaa caccgcgtg 360
gtcatcgacg ccgcgggcaa gatcgcgaa cggcacgcga agctcatgcc caccaacccc 420
gagcgaatgg tgtggggatt cggtagcgcc tcggggctgc ggggtggtgag cagccccgtc 480
gggcgggtgg gcacgctcct gtgctgggag agctacatgc ccctggcgcg ctgcgcgctc 540
tacgccgagg gggtcgagat ctacgtgacc ccgacctggg actacggcga aggctggcgc 600
gccagcatgc agcacatcgc ccgcgagggg cgctgctggg tggtagaccg ttgcatgtgc 660
gtgcaggcgc gcgacgtgcc ggccgacttc cccgggcgcg ccagctcta cccgacgag 720
gaggagtggg tgaaccccg cgttcgctg gtggtcgacc ccggcgcaa gatcgtggcc 780
ggtccgatgt cgcgcgagaa ggggatcttg tacgcggaga tcgatccgga tcgcgtggcg 840
ggggcgcacc gctcgttcga cgtcgtgggc cactactcgc gtcccgacgt gttccggctg 900
gaggtcgatc ggacaccggc ggcgccgtg agcttcaaaa aatga 945

```

<210> 10

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 10

```

Met Ala Ala His Lys Ile Ala Val Val Gln Ala Pro Ser Val Leu Leu
1          5          10          15
Asp Arg Glu Gly Ser Val Ala Arg Ala Val Thr Leu Leu Asp Glu Ala
20        25        30
Ala Ala Ala Gly Ala Arg Leu Val Val Phe Pro Glu Ala Tyr Ile Pro
35        40        45
Gly Tyr Pro Asp Trp Ile Trp Arg Leu Arg Pro Tyr Pro Asp Val Lys
50        55        60
Leu Ala Ala Glu Leu His Glu Arg Leu Leu Ala Asn Ala Val Asp Leu
65        70        75        80
Ser Thr Asp Val Leu Ala Pro Val Leu Ala Ala Ala Ala Arg His Gly
85        90        95
Leu Thr Val Val Met Cys Val Gln Glu Arg Asp Ala Gly Phe Ser Arg
100       105       110
Ala Thr Leu Tyr Asn Thr Ala Leu Val Ile Asp Ala Ala Gly Lys Ile
115       120       125
Ala Asn Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val
130       135       140
Trp Gly Phe Gly Asp Ala Ser Gly Leu Arg Val Val Ser Thr Pro Val
145       150       155       160
Gly Arg Val Gly Thr Leu Leu Cys Trp Glu Ser Tyr Met Pro Leu Ala
165       170       175
Arg Cys Ala Leu Tyr Ala Glu Gly Val Glu Ile Tyr Val Thr Pro Thr
180       185       190
Trp Asp Tyr Gly Glu Gly Trp Arg Ala Ser Met Gln His Ile Ala Arg
195       200       205
Glu Gly Arg Cys Trp Val Val Thr Ala Cys Met Cys Val Gln Ala Arg
210       215       220

```

```

Asp Val Pro Ala Asp Phe Pro Gly Arg Ala Gln Leu Tyr Pro Asp Glu
225                230                235                240
Glu Glu Trp Leu Asn Pro Gly Asp Ser Leu Val Val Asp Pro Gly Gly
                245                250                255
Lys Ile Val Ala Gly Pro Met Ser Arg Glu Lys Gly Ile Leu Tyr Ala
                260                265                270
Glu Ile Asp Pro Asp Arg Val Ala Gly Ala His Arg Ser Phe Asp Val
                275                280                285
Val Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Glu Val Asp Arg
                290                295                300
Thr Pro Ala Ala Pro Val Ser Phe Lys Lys
305                310

```

<210> 11
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 11
atgactggat cttatcctaa agacacactg atcggtgggc tagctcaaat cgctcctgtc      60
tggctggatc gggcggggac actgtcaaaag atactggctc aagtccatgc ggcaaatcaa      120
gcggtgtgtc atctcgtagc atttggcgaa gggctgcttc ctggatatcc gttttggatt      180
gagcgaacaa atggcgcgct gttcaactcg actgtacaaa aggaaatcca cgcgcattat      240
atggatcagg cggtgcagat cgaagccggt catctcgatc cgctttgtgc aacagccaag      300
aaatttggaa tcaccgttgt actcggatgc atcgaacgcc cactcgatcg gggcggtcac      360
agcttgtatg caagtctggt atatattgat tccgagggca gcattcaatc cgtgcatcgc      420
aaactaatgc caacctacga agaacgactt acctgggtcgt caggcgatgg gcacggttta      480
cgagtgcata ccttaggtgc gtttacggtg ggtggtctca actggtggga aaattggatg      540
cccttggcgc gcgcagcgat gtatggtcag ggtgaagatt tacatggtgc gatctggcca      600
ggcggttctc atctcacgca ggatattacc cgctttattg cgctcgaatc acgttcgtac      660
gtattatctg tctccggtct gatgcgcgca accgattttc caaaagatac tccccatctt      720
gcctccatcc tagctaaagg tgaagagatt cttgcgaatg gtggttcttg tattgcaggt      780
cctgacggca agtgggtcgt tgggcctctt gtaggagaag agaagttaat tgtcgaacc      840
attgatcaact gccgcgtgcg cgaagaacgt cagaatttcg atccttcogc gcattacagc      900
cggcccgatg tactgcaatt aaaaatcaac agggaacgcc agagcacaat ttcatttagc      960
gagtag

```

<210> 12
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 12
Met Thr Gly Ser Tyr Pro Lys Asp Thr Leu Ile Val Gly Leu Ala Gln
1          5          10          15
Ile Ala Pro Val Trp Leu Asp Arg Ala Gly Thr Leu Ser Lys Ile Leu
                20                25                30
Ala Gln Val His Ala Ala Asn Gln Ala Gly Cys His Leu Val Ala Phe
                35                40                45
Gly Glu Gly Leu Leu Pro Gly Tyr Pro Phe Trp Ile Glu Arg Thr Asn
                50                55                60
Gly Ala Leu Phe Asn Ser Thr Val Gln Lys Glu Ile His Ala His Tyr
                65                70                75                80

```

<210> 14

<211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 14
 Met Gly Ile Gln His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Ala Lys Ser Ile Ala Leu
 20 25 30
 Ile Glu Glu Ala Ala Ala Asn Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Ala Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Leu Asp Ser Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Leu Ala Val Lys Lys
 85 90 95
 Ala Gly Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Glu Gly Gly Ser
 100 105 110
 Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Gly Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Lys Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Asp Asp Lys His Gly Leu Leu His Val Gly Gly Gly His Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Ser Ile Ala Glu Lys Leu Pro Pro
 260 265 270
 Glu Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Ile Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Ser Lys Arg Val Glu His
 305 310 315 320
 Phe Ser Leu Pro Val Asp Asn Val Glu Pro Glu Ile Asp Ala Ala Ala
 325 330 335
 Ser

<210> 15
 <211> 1047
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 15
atgccaatat caaaacaatt tagagtgcgt gcagttcaag ccgccccggt atttcttgac      60
ctggaggggcg caataagcaa aggcattctcc ctcattgagg aggcgcgttc caatggagcc      120
aagctcattg ccttcccggg aacgtggatt cccggtacc cctgggtggat ctggctggac      180
tcacccgctt ggggcatgcg ctttgtccag cgctattttg acaactogct catgctgggt      240
agttagcaag ccaagcgcat gaaccaggct gccgccaata acaagattta cgtggtgatg      300
ggttatagcg aacgcagtgg cggcagcctc tacatgggcc aatccattat caacgacaag      360
ggtgaaaacga tttttaccgg ccgcaaactc aagccaactc atgtcgagcg taccgtgttt      420
ggggaggggag acggcagcca tctttgcgta atggataccg agattggccg cgtcggcgcg      480
atgtgctggt gggaacattt gcagccgctc agcaaatatg caatgtattc tcaggatgaa      540
caaattcaca ttgcctcctg gccgagcttt tcggttatatc ggggggagc ctatgcactc      600
ggccccgaac tgaacaacgc cgccagccaa atgtatgcag ccgaaggcca gtgctttgtc      660
cttgcccctt gcgccaccgt ctcaaaggag atgatcgaaa tgctgataga tgatcccagg      720
aaagagccgc ttctgctgga aggtggcggg ttcacatga ttacggccc cgatgggcga      780
cctctgggta aaccgttgcc tgaaaacgag gaagggctgc tatatgccga tattgacctg      840
ggcatgattt caatggccaa ggctgccgcc gaccggcag gtcactacgc acgcccggat      900
gtcactcgcc tactattcaa ttccgcgcc gccaatcgcg tcgagtatat caacccagcg      960
tcaggcccaa ccgaatcctt aaaagatatg ggaaagatgc aaatggaggc cgaacagcaa      1020
aaggcggccc tgcgagagat gatctaa                                     1047

```

```

<210> 16
<211> 348
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<400> 16
Met Pro Thr Ser Lys Gln Phe Arg Val Ala Ala Val Gln Ala Ala Pro
1      5      10      15
Val Phe Leu Asp Leu Glu Gly Ala Ile Ser Lys Gly Ile Ser Leu Ile
20      25      30
Glu Glu Ala Ala Ser Asn Gly Ala Lys Leu Ile Ala Phe Pro Glu Thr
35      40      45
Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ser Pro Ala Trp
50      55      60
Gly Met Arg Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu Met Leu Gly
65      70      75      80
Ser Glu Gln Ala Lys Arg Met Asn Gln Ala Ala Asn Asn Lys Ile
85      90      95
Tyr Val Val Met Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Met
100     105     110
Gly Gln Ser Ile Ile Asn Asp Lys Gly Glu Thr Ile Phe Thr Arg Arg
115     120     125
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Asp
130     135     140
Gly Ser His Leu Cys Val Met Asp Thr Glu Ile Gly Arg Val Gly Ala
145     150     155     160
Met Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Met Tyr
165     170     175
Ser Gln Asp Glu Gln Ile His Ile Ala Ser Trp Pro Ser Phe Ser Leu
180     185     190
Tyr Arg Gly Ala Ala Tyr Ala Leu Gly Pro Glu Leu Asn Asn Ala Ala
195     200     205
Ser Gln Met Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Pro Cys
210     215     220
Ala Thr Val Ser Lys Glu Met Ile Glu Met Leu Ile Asp Asp Pro Arg
225     230     235     240
Lys Glu Pro Leu Leu Leu Glu Gly Gly Gly Phe Thr Met Ile Tyr Gly
245     250     255

```

```

Pro Asp Gly Arg Pro Leu Ala Lys Pro Leu Pro Glu Asn Glu Glu Gly
      260      265      270
Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Met Ala Lys Ala
      275      280      285
Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Thr Arg Leu
      290      295      300
Leu Phe Asn Ser Ala Pro Ala Asn Arg Val Glu Tyr Ile Asn Pro Ala
      305      310      315      320
Ser Gly Pro Thr Glu Ser Leu Lys Asp Met Gly Lys Met Gln Met Glu
      325      330      335
Ala Glu Gln Gln Lys Ala Ala Leu Arg Glu Met Ile
      340      345

```

<210> 17
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 17
atgagaggttg ttaaagccgc agctgtccaa ctgagtcocg tcctctatag ccgcgaggga      60
acggtcgaga aggtcgtgcg gaagatccat gaacttgccg aagagggagt cgagttcgtc      120
acctttcctg agaccgtggt gccttattac cgtactttt cgttcgttca gacgcccttg      180
cagcaaattct tcggaacaga gtatctgagg ctgctcgacc aggcagtcac cgtgccatcc      240
gccgccaccg acgcgatcgg cgaggctgcc aggttcgctg gaggttgtgt ctcgatcggc      300
gtcaacgagc gagacggggg aactctgtac aacactcagc ttctcttcga tgccgacgga      360
agcttaattc agcggcgccg caagatcacg cccacccatt acgagcgcat gatctggggc      420
caggggtgacg gctcaggtct gcgggccggt gatagcaagg ccggccgcat tggtcagctg      480
gcatgctggg agcacaacaa tccactggcg cgtaacgcgc tgatagccga cggcgagcag      540
atccattcgg ccatgtatcc gggctccatg ttccggcgact cgtttgccaa aaagaccgaa      600
atcaatatcc ggcagcatgc gctggagtct gctgtcttcg tcgtgaacgc aacggcctgg      660
ctggacggcg atcaacaggc gcaaatacat aaggacaccg gctgcagcat cggcccgatc      720
tccggcggtt gcttcaccac tatcgtggcg ccggacgggt ccctgatcgg cgagcccctc      780
cgctcgggtg agggcggtgt catcgccgac ctgcacttca cgttaatcga caggcgtaag      840
caggtgatgg actcgcgagg ccactacagc cggccggagt tgctcagcct cttaatagac      900
cgcaccccta ccgcgcactt tcacgaacgc gcttcgcacc ccacgacagg agctgagcaa      960
ggctccgagg atgtgttcga ggctaacatt taa                                     993

```

<210> 18
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 18
Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
  1      5      10      15
Ser Arg Glu Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
      20      25      30
Ala Glu Glu Gly Val Glu Phe Val Thr Phe Pro Glu Thr Val Val Pro
      35      40      45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Gln Ile Phe
      50      55      60
Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
      65      70      75      80
Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Phe Ala Gly Val Val
      85      90      95

```

```

Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
      100      105
Gln Leu Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Arg Arg Arg Lys
      115      120      125
Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
      130      135      140
Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
      145      150      155
Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Ile Ala
      165      170      175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
      180      185      190
Asp Ser Phe Ala Lys Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
      195      200      205
Glu Ser Ala Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Gly Asp
      210      215      220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
      225      230      235
Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Ser Leu Ile
      245      250      255
Gly Glu Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp
      260      265      270
Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
      275      280      285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
      290      295      300
Ala His Phe His Glu Arg Ala Ser His Pro Thr Thr Gly Ala Glu Gln
      305      310      315      320
Gly Ser Glu Asp Val Phe Glu Ala Asn Ile
      325      330

```

<210> 19

<211> 1050

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 19

```

atggaaagca acttccttgc cgcagcagtg caagcagaac cggtttactt caatgctttt      60
cagacggccg aaaaggccgc gtcattgatt gacgatgccg gtcggcaggg ggctcgctta      120
gtgacatttc ccgaaacgtg gctgcccggg taccctgact ggatctggct tgggtgcccc      180
gcctggggaa tgcattcatt catcctaaag taccatcaaa actcgccggg tgcaggagga      240
ccagaggaac agatcctttg tcaggcggcc cgccgcaacg ggatttttgt cgtcatggga      300
ctcagcgaga aaatcggggc aagcctctac atggcgagtg ggttcacag tccagacggc      360
aaagtggctg ctgcgggacg caaattgaag cctactcacg tcgaacgttc ggtcttcggg      420
gaaggggatg gttccgacat tgtogttctt gatacacccc ttggaaaggc cgggggcctt      480
tgctgctggg agcacatgca gccactttcg aagtacgccg tgtactcgca aggcgagcag      540
atccatgctg cttcttggcc gagtggttagc gtctatcgcg ataaaaattt cgttctgggg      600
ccggagctga acggtgccgc caatcacatg tatgcggcag aaggtcagtg tttcgtcttg      660
gcatcctggg caacgggttc acaagcggtc atcgatcttt tttgcgacac gcccagacaag      720
gccgcgctca tgaaaattgg tgggtggtttt tcccagatct atgggccaga cgggtgcccc      780
ctggcgaagc cgttgccgga ggacgtcgaa ggattggtga ccgctgagat tgacttcaat      840
gccatcacgc gcgtgaaagc agcggcggac cccgtagggc actatagccg gcccgatgta      900
ttccgcctgt tgttcaatcg tacgcgccaa gaacgcgtgg tttctgtcaa cacgtttgtg      960
ccaggtgtca cccagcgaac cgccaagaat gggtcggcgg acgaattggc cggtcacccg      1020
gagaacgctg tcgcccgggc tgcagagtaa

```

<210> 20

<211> 349

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 20

```

Met Glu Ser Asn Phe Leu Ala Ala Ala Val Gln Ala Glu Pro Val Tyr
1      5      10      15
Phe Asn Ala Phe Gln Thr Ala Glu Lys Ala Ala Ser Leu Ile Asp Asp
20      25      30
Ala Gly Arg Gln Gly Ala Arg Leu Val Thr Phe Pro Glu Thr Trp Leu
35      40      45
Pro Gly Tyr Pro Tyr Trp Ile Trp Leu Gly Ala Pro Ala Trp Gly Met
50      55      60
His His Phe Ile Leu Lys Tyr His Gln Asn Ser Pro Val Ala Gly Gly
65      70      75      80
Pro Glu Glu Gln Ile Leu Cys Gln Ala Ala Arg Arg Asn Gly Ile Phe
85      90      95
Val Val Met Gly Leu Ser Glu Lys Ile Gly Ala Ser Leu Tyr Met Ala
100     105     110
Gln Trp Phe Ile Ser Pro Asp Gly Lys Val Val Ala Arg Arg Arg Lys
115     120     125
Leu Lys Pro Thr His Val Glu Arg Ser Val Phe Gly Glu Gly Asp Gly
130     135     140
Ser Asp Ile Val Val Leu Asp Thr Pro Leu Gly Lys Val Gly Gly Leu
145     150     155     160
Cys Cys Trp Glu His Met Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ser
165     170     175
Gln Gly Glu Gln Ile His Ala Ala Ser Trp Pro Ser Val Ser Val Tyr
180     185     190
Arg Asp Lys Ile Tyr Val Leu Gly Pro Glu Leu Asn Gly Ala Ala Asn
195     200     205
Gln Met Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Ser Trp Ala
210     215     220
Thr Val Ser Gln Ala Ala Ile Asp Leu Phe Cys Asp Thr Pro Asp Lys
225     230     235     240
Ala Ala Leu Met Lys Ile Gly Gly Gly Phe Ser Gln Ile Tyr Gly Pro
245     250     255
Asp Gly Cys Pro Leu Ala Lys Pro Leu Pro Glu Asp Val Glu Gly Leu
260     265     270
Val Thr Ala Glu Ile Asp Phe Asn Ala Ile Thr Arg Val Lys Ala Ala
275     280     285
Ala Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Leu
290     295     300
Phe Asn Arg Thr Arg Gln Glu Arg Val Val Ser Val Asn Thr Phe Val
305     310     315     320
Pro Gly Val Thr Gln Arg Thr Ala Lys Asn Gly Ser Ala Asp Glu Leu
325     330     335
Val Gly His Pro Glu Asn Ala Val Ala Arg Ala Ala Glu
340     345

```

<210> 21
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 21

```

atggcactag aacatccgaa gtacgtggcg gccgtggttc aggcgcgcgc cgaattcctg      60
aatctagaca gagggatcga aaagacgacg gcattgatcg acgaagcggg acagaaaggg      120
goggccctga ttgcatttcc ggaaacctgg ctgccggggt atccgtttca tgtctgggtc      180
ggctcctccg catgggcgct tggctcagga ttctgccagc gctatttcga caactcgatg      240
acgtacgata gtcctcaggc cgctgcaact agggacgctg ccgcgcgcga cgggatcacg      300
gtggtatttg gcttgctcga gcgatgcggc ggcagcctct atatcgcgca atggatcatc      360
ggcccggtat gcgcgacggg cgccacgcgc cgcaaattgc ggccgactca tatcgagcgc      420
accgttttct gcgatggcga cggcagcgat ctggcagtac acgatctcaa catcgccgcg      480
cttggcgcac tgtgctgctg ggagcacatt cagccgctga ccaagtacgc gatgtatgcg      540
cagcacgaac aggtgcacgt cgcgccctgg ccgagcttct ccatgtatga attcgcgccc      600
gcgctcggtc acgaggtgaa caacgcagtc agccgcgtct atgccgttga gggatcgtgc      660
ttcgtgctcg ccgcgtgcgc ggtcatcagc gagcaaatgg tcgacatggt gtgcgacacg      720
gcagacaagc gcgcgatgat acgtgccggc ggccgggcacg cagtggcggt cgggcccggac      780
ggcgaagctc tggctcgagaa actgccggaa aatgaggaag gcttgctgct ggtcgatatc      840
gatctcggtc gcatctcgct tgcgaaggct gcggccgacc ccgtcggtca ctacgcgcgc      900
cccgatgtct tgccggtctg gttcgacaag caaccgcggc ggtgcgtcga acatgccggc      960
gagaacgacg cgtcgcgcag gtcgcacggg tcgtccgggt cacaatcgcc ggcgccaggat     1020
gggccggcga acgacatggt agaccgtcag gaaaacgtcg attga                               1065

```

<210> 22

<211> 354

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 22

```

Met Ala Leu Glu His Pro Lys Tyr Val Ala Ala Val Val Gln Ala Ala
 1          5          10          15
Pro Glu Phe Leu Asn Leu Asp Arg Gly Ile Glu Lys Thr Ile Ala Leu
 20          25          30
Ile Asp Glu Ala Gly Gln Lys Gly Ala Ala Leu Ile Ala Phe Pro Glu
 35          40          45
Thr Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Pro Pro Ala
 50          55          60
Trp Ala Leu Gly Ser Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Met
 65          70          75          80
Thr Tyr Asp Ser Pro Gln Ala Ala Ala Leu Arg Asp Ala Ala Ala Arg
 85          90          95
Asn Gly Ile Thr Val Val Leu Gly Leu Ser Glu Arg Cys Gly Gly Ser
 100          105          110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Ala Thr Val Ala
 115          120          125
Thr Arg Arg Lys Leu Arg Pro Thr His Ile Glu Arg Thr Val Phe Gly
 130          135          140
Asp Gly Asp Gly Ser Asp Leu Ala Val His Asp Leu Asn Ile Gly Arg
 145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Thr Lys Tyr
 165          170          175
Ala Met Tyr Ala Gln His Glu Gln Val His Val Ala Ala Trp Pro Ser
 180          185          190
Phe Ser Met Tyr Glu Phe Ala Pro Ala Leu Gly His Glu Val Asn Asn
 195          200          205
Ala Val Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val Leu Ala
 210          215          220
Pro Cys Ala Val Ile Ser Glu Gln Met Val Asp Met Leu Cys Asp Thr
 225          230          235          240
Ala Asp Lys Arg Ala Met Ile Arg Ala Gly Gly Gly His Ala Val Ala
 245          250          255
Phe Gly Pro Asp Gly Glu Ala Leu Val Glu Lys Leu Pro Glu Asn Glu

```

```

                260                265                270
Glu Gly Leu Leu Leu Val Asp Ile Asp Leu Gly Arg Ile Ser Leu Ala
                275                280                285
Lys Ala Ala Ala Asp Pro Val Gly His Tyr Ala Arg Pro Asp Val Leu
                290                295                300
Arg Leu Trp Phe Asp Lys Gln Pro Arg Arg Cys Val Glu His Ala Gly
305                310                315                320
Glu Asn Asp Ala Ser Arg Arg Ser His Gly Ser Ser Gly Ser Gln Ser
                325                330                335
Pro Ala Gln Asp Gly Pro Ala Asn Asp Met Val Asp Arg Gln Glu Asn
                340                345                350
Val Asp

```

<210> 23
 <211> 1005
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 23
atgaccgtta tcaaagcagc cgccattcaa atcagccccc tgctctacag ccgggccccg 60
acagtcgaga aagttgttag gaaggtaga gagctcggg ccaaagggtg ccgattcgct 120
acctttcccg aaaccatcat accgtactac ccgtacttct cggttcgttca gtcggcggtc 180
gacatgaagc ttgggagtga acatcagcgg ctgctcgacg aatcagtcac aattccttcg 240
tccgagacgg acgcgatcgc ccaggccgcc aaggaagcgg gcatgggtgg gtccgctcggg 300
gtcaatgagc gcgatgggcg atccatctac aacactcaac ttctgttcga cgctgatggc 360
acgctcattc agcgtaggcg aaagatcacc ccgacctatc acgagcgcat gatttggggt 420
caaggcgatg gatccggcct acgcgcggtc gatagcgccg tgggcccggat cggccagctt 480
gcctgctggg agcactacct tcccctggcg cggtacgccc tcatcgcgga cggagagcaa 540
atccactcgg caatgtatcc aggtcgttcc gctgggtccg tatttgccga gcagatagag 600
gtagtatccc gccagcacgc gcttgagtca gctgcttcg tcgtcaacgc gaccggatgg 660
cttagcgccg agcagcaagc tcaaatagtg aaggataccg gatgcgtcgt tggaccaatc 720
tccggtggct gctttacggc gattgttgat ccggagggtc ggatcatggg ggcgccactc 780
aaggcagggt agggggagggt catcgagat ctcgattttg cgcagattga tttccgcaag 840
cgtgtgatgg atacgcgagg gcactacagc cgccccgaac ttctaagcct cagcatcgac 900
cgcagtcagc accatcacat gactgagcga ggcgccgac accgtgtaga ccacgcaaag 960
ccaacgggtca ccgcagagca gtcggccgctc gagccggcgg aatga 1005

```

<210> 24
 <211> 334
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 24
Met Thr Val Ile Lys Ala Ala Ala Ile Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Ala Gly Thr Val Glu Lys Val Val Arg Lys Val Arg Glu Leu
20     25     30
Gly Ala Lys Gly Val Arg Phe Ala Thr Phe Pro Glu Thr Ile Ile Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Ser Ala Phe Asp Met Lys Leu
50     55     60
Gly Ser Glu His Gln Arg Leu Leu Asp Glu Ser Val Thr Ile Pro Ser
65     70     75     80
Ser Glu Thr Asp Ala Ile Ala Gln Ala Ala Lys Glu Ala Gly Met Val

```

<210>	25
<211>	939
<212>	DNA
<213>	Unknown

[illegible]

Page 17

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 26

Val Ser Ser Thr Ile Lys Val Ala Ile Ile Gln Ala Ala Pro Ala Tyr
 1 5 10 15
 Tyr Asp Leu Gln Ala Ser Leu Ala Lys Ala Ala Ser Leu Ile Arg Glu
 20 25 30
 Ala Ala Arg Gly Gly Ala Gln Phe Val Ala Phe Gly Glu Thr Trp Leu
 35 40 45
 Pro Gly Tyr Pro Met Trp Leu Asp Trp Cys Pro Gly Ala Ile Ile Trp
 50 55 60
 Asp Asn Pro Ala Thr Lys Thr Val Phe Ala Arg Leu His Glu Asn Ser
 65 70 75 80
 Val Ala Val Pro Gly Arg Glu Thr Ala Phe Leu Ala Asp Leu Ala Met
 85 90 95
 Ser Leu Ser Ile Val Leu Cys Ile Gly Val Asn Glu Lys Val Met Asn
 100 105 110
 Gly Pro Gly His Gly Thr Leu Tyr Asn Thr Leu Leu Thr Phe Asp Ala
 115 120 125
 Thr Gly Glu Ile Ile Asn His His Arg Lys Leu Met Pro Thr Tyr Gly
 130 135 140
 Glu Arg Leu Val Trp Gly Pro Gly Asp Ala Val Gly Val Gln Ala Val
 145 150 155 160
 Asp Ser Thr Val Gly Arg Ile Gly Gly Leu Ile Cys Trp Glu His Trp
 165 170 175
 Met Pro Leu Pro Arg Gln Leu Met His Asn Ser Gly Glu Gln Ile His
 180 185 190
 Val Cys Ala Trp Pro Gly Val His Glu Met His Gln Ile Ala Ser Arg
 195 200 205
 His Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Leu Ile
 210 215 220
 Met Pro Ala Phe Asp Leu Pro Ser Glu Leu Glu Phe Pro Pro Glu Leu
 225 230 235 240
 Ala Asp Lys Arg Asp Tyr Leu Leu Met Asn Gly Gly Ser Ala Ile Ile
 245 250 255
 Lys Pro Asn Gly Lys Tyr Leu Ala Gly Pro Val Tyr Asp Glu Glu Thr
 260 265 270
 Ile Leu Cys Ala Asp Leu Asp Leu Thr Glu Asn Ile Lys Glu Gln Met
 275 280 285
 Thr Leu Asp Val Thr Gly His Tyr Ala Arg Ala Glu Leu Phe Asp Leu
 290 295 300
 Asn Val Val Arg Arg Arg Asn Ala
 305 310

<210> 27

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 27

atgccaaacc	ccagcgatca	tttcaaaatc	gccgctgttc	aggcctcgcc	cgtgtttctg	60
gaccgggagg	ccactgtgga	aaaggcctgc	cggttgatcg	ccgaagccgc	aaagcagggc	120
gccgcctca	tcgtctttcc	ggaatctttc	atcccgcact	acccggattg	ggtgtgggccc	180
gttcccccg	gaagggaag	aatcctgaac	cagctgtatt	ctgaattcct	ggccaatgcc	240
gtcgatgttc	ccggcgcggc	gaccgaacaa	cttgcccagg	ctgcacgaat	ggccggcgcc	300

```

tatgtgatta tgggcgtcac cgaaagagac acctcggcca gcggggccag cctctacaac 360
accctgctct acttcagccc cgaaggcatc ctaatgggca aacaccggaa gctggttccc 420
acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac 480
actccgctgg gaaagatcgg cgggctgata tgctgggaga actacatgcc cctggcccgg 540
tacacgatgt acgcctgggg caccagatt tacatcgccg ccacctggga ccgcggggaa 600
ccgtggctct ccaccctgcg gcatatcgcc aaggaaggaa gggctctacgt catcgggtgc 660
tgcacgccc tgcgccaggg ggatatcccg gaccggttcg agtacaaggg aaaattttat 720
tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaaccc ggacggggaa 780
ttcatcgccg ggccggtgcg gatgaaggag gagatcctgt atgccgagat agacccccgg 840
cagatgcggg gccccaagtg gatgctcgat gtggccggtc attacgcccg gccggatatc 900
ttcgagctca tcgtccaccg gaatccccac ccgatgatca aaatcgccga agacaggggc 960
acggggatcg cctcaagttt gattcgcccc cgccctaacc ttcccccatc aagggggagg 1020
aaatcggcaa gaagcaaacg caagcccaaa aaatga 1056

```

<210> 28

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 28

```

Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
 1          5          10          15
Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
 20          25          30
Ile Ala Glu Ala Ala Lys Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
 35          40          45
Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50          55          60
Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
 65          70          75          80
Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
 85          90          95
Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
100          105          110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
115          120          125
Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130          135          140
Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
145          150          155          160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
165          170          175
Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
180          185          190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
195          200          205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
210          215          220
Arg Gln Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gly Lys Phe Tyr
225          230          235          240
Ser Gly Ser Arg Glu Trp Ile Asn Glu Gly Asp Ser Ala Ile Val Asn
245          250          255
Pro Asp Gly Glu Phe Ile Ala Gly Pro Val Arg Met Lys Glu Glu Ile
260          265          270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Arg Gly Pro Lys Trp Met
275          280          285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile
290          295          300

```

Val	His	Arg	Asn	Pro	His	Pro	Met	Ile	Lys	Ile	Ala	Glu	Asp	Arg	Gly
305					310				315						320
Thr	Gly	Ile	Ala	Ser	Ser	Leu	Ile	Arg	Pro	Arg	Pro	Asn	Leu	Pro	Pro
				325					330					335	
Ser	Arg	Gly	Arg	Lys	Ser	Ala	Arg	Ser	Lys	Arg	Lys	Pro	Lys	Lys	
			340					345					350		

<210> 29
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 29

atgggcatcg	aacatacgaa	atacaaggtg	gcggtggtgc	aggcggcgcc	ggcctggctc	60
gacctcgagg	cctcgatcgg	caagtccatc	ggcctaata	aggaggccgc	ggacaagggc	120
gccaaagtga	tcgcctttcc	ggaggccttc	atccccggtt	acccctggta	tatctggatg	180
gactcgccgg	cctgggcgat	cggccgcggc	ttcgtccagc	gctatttcga	caattcgctc	240
tcctacgaca	gtccccaggc	cgagcggctg	cgtgatgccg	tgcgccaggc	caagctcacc	300
gccgtgatcg	gcctgtccga	acgcgacggc	ggcagccttt	acctggcgca	atggttgatc	360
gggcccagcg	gcgaaaccat	tgccaagcgc	cgcaagctgc	ggccgaccca	tgccgagcgc	420
accgtctatg	gcgaaggcga	cggcagcgat	ctggccgtac	atgcccggcc	cgacatcggt	480
cgcttggggc	cgctgtgctg	ctgggagcat	cttcagccgt	tgctgaagta	cgcaatgtac	540
gccagaacg	agcaggtcca	cgtcgctgcc	tggccgagct	tctcgctcta	cgatcccttc	600
gccccggcgc	tcggcgccga	ggtcaacaac	gctgcctcgc	gcgtctatgc	ggtggagggc	660
tcctgcttgc	tgctcgcgcc	ttgcgcgacg	gtgtcgcagg	ccatgatcga	cgaactctgc	720
gatcgcccg	ataagcatgc	gctgctgcat	gccggcggag	gctttgccgc	gatctacggc	780
cccagcgcca	gccagatcgg	cgagaagctg	gcgccggatc	aggagggctc	gctgatcgcc	840
gagattgata	tgggcgccat	cgggtgttgc	aagaacgcgg	cagatccgcg	cggtcattat	900
tcacggccgg	atgtgacgcg	gttgctgctc	aacaagaagc	ggtaccagcg	cgtcgagcaa	960
tttgccttgc	cgcgcgacat	ggtcgagccc	gcggacatag	gcgcggcgcc	gagctga	1017

<210> 30
 <211> 338
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 30

Met	Gly	Ile	Glu	His	Thr	Lys	Tyr	Lys	Val	Ala	Val	Val	Gln	Ala	Ala
1				5				10						15	
Pro	Ala	Trp	Leu	Asp	Leu	Glu	Ala	Ser	Ile	Gly	Lys	Ser	Ile	Gly	Leu
			20					25					30		
Ile	Lys	Glu	Ala	Ala	Asp	Lys	Gly	Ala	Lys	Leu	Ile	Ala	Phe	Pro	Glu
		35					40					45			
Ala	Phe	Ile	Pro	Gly	Tyr	Pro	Trp	Tyr	Ile	Trp	Met	Asp	Ser	Pro	Ala
	50				55				60						
Trp	Ala	Ile	Gly	Arg	Gly	Phe	Val	Gln	Arg	Tyr	Phe	Asp	Asn	Ser	Leu
65				70				75						80	
Ser	Tyr	Asp	Ser	Pro	Gln	Ala	Glu	Arg	Leu	Arg	Asp	Ala	Val	Arg	Gln
			85					90					95		
Ala	Lys	Leu	Thr	Ala	Val	Ile	Gly	Leu	Ser	Glu	Arg	Asp	Gly	Gly	Ser
		100					105					110			
Leu	Tyr	Leu	Ala	Gln	Trp	Leu	Ile	Gly	Pro	Asp	Gly	Glu	Thr	Ile	Ala
		115				120					125				
Lys	Arg	Arg	Lys	Leu	Arg	Pro	Thr	His	Ala	Glu	Arg	Thr	Val	Tyr	Gly
	130					135					140				

Glu Gly Asp Gly Ser Asp Leu Ala Val His Ala Arg Pro Asp Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Glu Lys Leu Ala Pro
 260 265 270
 Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Arg Tyr Gln Arg Val Glu Gln
 305 310 315 320
 Phe Ala Leu Pro Ala Asp Met Val Glu Pro Ala Asp Ile Gly Ala Ala
 325 330 335
 Ala Ser

<210> 31
 <211> 933
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 31
 atgaccagaa tagccattat tcagcgaccg cccgtgctgc tcgatcgaag cgccaccatt 60
 gcccgggccc tgcaatcggt cgcogaagcg gcagcgcaag gcgcgaccct gattgtcttg 120
 cccgaatcgt acatccctgg ctatccctca tggatctggc ggctcgcgcc tggcaaagac 180
 ggcgcgatcg tgggccagtt gcatgcgcgc ttgctggcca atgcggtcga cctgagcagc 240
 actgacctcg atgcgcttct tgaagcgccc cgtcagcacg gcgtgaccat tgtttgcggc 300
 atgaacgagt gcgaacggcg tcgcggcgcc ggcaccttgt acaacacggg ggtcgtgatc 360
 ggaccggacg gcgtcatgct caaccggcat cgcaaattga tgccgaccaa tcccagagcg 420
 atggtgcatg gctttggcga tgcattcgga ctgaaagcag ttgatacgcc tgccggccgg 480
 ctgggcacgc tgatctgctg ggagagctac atgccgctgg cagcctatgc cctgtacgag 540
 caaggcatcg agatctacat cgcaccaact tatgacagtg gtgacggctg gatcagcacc 600
 atgcgccaca ttgactcga agggcgctgc tgggtgattg gcagcggcac ggtcctgaaa 660
 ggcagtata ttccggacga tttcccgaa cgggcacgcc tgttccctga tccggatgag 720
 tggatcaacg atggtgattc ggtagttatc gatccgcagg gaaagatcgt tgccggtccg 780
 atgcgtaggg aagcaggcat tctatacgcc gatatcgacg tcgcgcgcgt agcaccatca 840
 cgccgcacgc tggatgtcgc ggggcattac gcgcgtccgg acgtcttcga gcttcgggta 900
 caccaggcac cgggggcacg agtaagtaat tga 933

<210> 32
 <211> 310
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 32

```

Met Thr Arg Ile Ala Ile Ile Gln Arg Pro Pro Val Leu Leu Asp Arg
1      5      10      15
Ser Ala Thr Ile Ala Arg Ala Val Gln Ser Val Ala Glu Ala Ala Ala
20      25      30
Gln Gly Ala Thr Leu Ile Val Leu Pro Glu Ser Tyr Ile Pro Gly Tyr
35      40      45
Pro Ser Trp Ile Trp Arg Leu Ala Pro Gly Lys Asp Gly Ala Ile Val
50      55      60
Gly Gln Leu His Ala Arg Leu Leu Ala Asn Ala Val Asp Leu Ser Ser
65      70      75      80
Thr Asp Leu Asp Ala Leu Leu Glu Ala Ala Arg Gln His Gly Val Thr
85      90      95
Ile Val Cys Gly Met Asn Glu Cys Glu Arg Arg Arg Gly Gly Gly Thr
100     105     110
Leu Tyr Asn Thr Val Val Val Ile Gly Pro Asp Gly Val Met Leu Asn
115     120     125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val His Gly
130     135     140
Phe Gly Asp Ala Ser Gly Leu Lys Ala Val Asp Thr Pro Ala Gly Arg
145     150     155     160
Leu Gly Thr Leu Ile Cys Trp Glu Ser Tyr Met Pro Leu Ala Arg Tyr
165     170     175
Ala Leu Tyr Glu Gln Gly Ile Glu Ile Tyr Ile Ala Pro Thr Tyr Asp
180     185     190
Ser Gly Asp Gly Trp Ile Ser Thr Met Arg His Ile Ala Leu Glu Gly
195     200     205
Arg Cys Trp Val Ile Gly Ser Gly Thr Val Leu Lys Gly Ser Asp Ile
210     215     220
Pro Asp Asp Phe Pro Glu Arg Ala Arg Leu Phe Pro Asp Pro Asp Glu
225     230     235     240
Trp Ile Asn Asp Gly Asp Ser Val Val Ile Asp Pro Gln Gly Lys Ile
245     250     255
Val Ala Gly Pro Met Arg Arg Glu Ala Gly Ile Leu Tyr Ala Asp Ile
260     265     270
Asp Val Ala Arg Val Ala Pro Ser Arg Arg Thr Leu Asp Val Ala Gly
275     280     285
His Tyr Ala Arg Pro Asp Val Phe Glu Leu Arg Val His Gln Ala Pro
290     295     300
Gly Ala Arg Val Ser Asn
305     310

```

<210> 33

<211> 1026

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 33

```

atgttaagtc ccgtgacgca gtatcgcgcc gccgcggtgc aggcggcgcc atcttttctc      60
gatctcgacc gcaccgtcga gaagacgata gcgatcatcg agcaggcggc cgagcaggat      120
gtgcgcctga tcgcgtttcc ggaaacctgg attcccggct atccgctctg gatctggctc      180
ggctcgccgg cctggggcat gcgcttcgtg cagcgctatt tcgagaactc gctgggtcgc      240
ggcagcaaac agtggaaacgc gatcgccgat gcggcgcggc gccaccgcat gaccgtcgtc      300
gtcggcttca gcgagcgcgc gggaggcagc ctctacatgg gccaggcgat cttcggcccc      360
gaaggcgagc tcatcgcggc gcgcgggaag ctcaagccga cacacgccga gcgaacggtg      420
ttcggcgagg gcgacggcag ccacttgccc gtttacgaga cgggcgttgg tcgcatcggc      480
gccctctgct gctgggagca catccagccg ctctcgaaat acgcgatgta tgcggccaac      540
gaacaggtgc atgtggcctc gtggccgtgc ttcagccttt atcgcggcac gccctatgcg      600

```

```

ctcggggccgg aggtgaacac cgccgcgagc caggtctacg cggtcgaggg cggctgctac 660
gtgctggcct cctgtctcgt cgtgacaccc gagatcctga aggtgctgat cgacacgccc 720
gacaaggagc cgttgctgct cgccggcggg gggttctoga tgatcttcgg ccccgacggc 780
cgcgcgctcg ccagcgcgct gccggagacc gaagaggggc tcgtcacggc cgagatcgat 840
ctcggcgcgga tcgcgctcgc caaggccgcg gccgatcccg ccggccatta cgcgcggccc 900
gacgtgacgc ggttggtgct gaacccgcgc cccgcggcgc gcgtcgaagc gctgggtccg 960
cgcttcgagg tcgtgcagag cgagcaggcc gagccgcca cgcaaccggc cgaagcggcg 1020
gattga 1026

```

<210> 34
 <211> 341
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 34

Met	Leu	Ser	Pro	Val	Thr	Gln	Tyr	Arg	Ala	Ala	Ala	Val	Gln	Ala	Ala	1	5	10	15
Pro	Ser	Phe	Leu	Asp	Leu	Asp	Arg	Thr	Val	Glu	Lys	Thr	Ile	Ala	Ile	20	25	30	
Ile	Glu	Gln	Ala	Ala	Glu	Gln	Asp	Val	Arg	Leu	Ile	Ala	Phe	Pro	Glu	35	40	45	
Thr	Trp	Ile	Pro	Gly	Tyr	Pro	Leu	Trp	Ile	Trp	Leu	Gly	Ser	Pro	Ala	50	55	60	
Trp	Gly	Met	Arg	Phe	Val	Gln	Arg	Tyr	Phe	Glu	Asn	Ser	Leu	Val	Arg	65	70	75	80
Gly	Ser	Lys	Gln	Trp	Asn	Ala	Ile	Ala	Asp	Ala	Ala	Arg	Arg	His	Arg	85	90	95	
Met	Thr	Val	Val	Val	Gly	Phe	Ser	Glu	Arg	Ala	Gly	Gly	Ser	Leu	Tyr	100	105	110	
Met	Gly	Gln	Ala	Ile	Phe	Gly	Pro	Glu	Gly	Glu	Leu	Ile	Ala	Ala	Arg	115	120	125	
Arg	Lys	Leu	Lys	Pro	Thr	His	Ala	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	130	135	140	
Asp	Gly	Ser	His	Leu	Ala	Val	Tyr	Glu	Thr	Gly	Val	Gly	Arg	Ile	Gly	145	150	155	160
Ala	Leu	Cys	Cys	Trp	Glu	His	Ile	Gln	Pro	Leu	Ser	Lys	Tyr	Ala	Met	165	170	175	
Tyr	Ala	Ala	Asn	Glu	Gln	Val	His	Val	Ala	Ser	Trp	Pro	Cys	Phe	Ser	180	185	190	
Leu	Tyr	Arg	Gly	Met	Ala	Tyr	Ala	Leu	Gly	Pro	Glu	Val	Asn	Thr	Ala	195	200	205	
Ala	Ser	Gln	Val	Tyr	Ala	Val	Glu	Gly	Gly	Cys	Tyr	Val	Leu	Ala	Ser	210	215	220	
Cys	Leu	Val	Val	Thr	Pro	Glu	Ile	Leu	Lys	Val	Leu	Ile	Asp	Thr	Pro	225	230	235	240
Asp	Lys	Glu	Pro	Leu	Leu	Leu	Ala	Gly	Gly	Gly	Phe	Ser	Met	Ile	Phe	245	250	255	
Gly	Pro	Asp	Gly	Arg	Ala	Leu	Ala	Gln	Pro	Leu	Pro	Glu	Thr	Glu	Glu	260	265	270	
Gly	Leu	Val	Thr	Ala	Glu	Ile	Asp	Leu	Gly	Ala	Ile	Ala	Leu	Ala	Lys	275	280	285	
Ala	Ala	Ala	Asp	Pro	Ala	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Thr	Arg	290	295	300	
Leu	Leu	Leu	Asn	Pro	Arg	Pro	Ala	Ala	Arg	Val	Glu	Ala	Leu	Gly	Pro	305	310	315	320
Arg	Phe	Glu	Val	Val	Gln	Ser	Glu	Gln	Ala	Glu	Pro	Pro	Thr	Gln	Pro	325	330	335	
Ala	Glu	Ala	Ala	Asp															

340

<210> 35
 <211> 942
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 35
 atgacagctc taaaaaattgc tgctgttcaa atgtgcgcgc aattggggcgc tacagatcga 60
 aacctgagtg cagctggatc attcgtgcgc gacgcatttc gcgaagggtgc ccagtgggta 120
 atcctcccag agtttttttac ctccgcaatg gcattcgcac cttcgatggc gcaagcttgg 180
 ttgccacttg aaggaaaggc gctagcgaatg atgcgcagcc ttgcgcgtca attcgatggg 240
 gttgtttggag gctcatatgt tgccagagag gggaacgact gcgtaaatgc ctttcttctc 300
 gtctttccgg atggaagcta ctaccggcat gacaaagata ttccaacaat gtgggagAAC 360
 tgttactaca tcggcggcgt cgacgatggg gtgctggaaa caccaattgg tgcggtggga 420
 gttgcactgt gttgggagtt catccgaaca caaaccgccc gaagactgaa ggatcgcgtt 480
 caattagtgg ttggcgggtac ttgctggtgg gattttccga tgctgttacc tgaacgatat 540
 ctgaggctga ccaggcatat ctccaggaac tttgagcgcg atgctccggc gcggttggcc 600
 agtatgttgg gtgtgcctgt tgtacacgct tcccatgctg gggattttac tgctgtcacc 660
 ccaggcaatg aaacgaagaa ttaccgatcc aactatctgg gagagaccca gatcgtcgat 720
 gccaatggaa atgtgttgaa gcgaatgaca gtggctgatg gtgaggggta cgtcattgct 780
 gacgttcaat tggggggccat atcaaccggt cgaacttcga tccccgacac cttctggacc 840
 tgcaagctaa cgccaggggc acaacaggct tgggatgaac aaaatgcttt tgggtgtggc 900
 tactatgaga acgtcacacg caaacaccta atcggtcgat ga 942

<210> 36
 <211> 313
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 36
 Met Thr Ala Leu Lys Ile Ala Ala Val Gln Met Cys Ala Glu Leu Gly
 1 5 10 15
 Ala Thr Asp Arg Asn Leu Ser Ala Ala Gly Ser Phe Val Arg Asp Ala
 20 25 30
 Phe Arg Glu Gly Ala Gln Trp Val Ile Leu Pro Glu Phe Phe Thr Ser
 35 40 45
 Ala Met Ala Phe Ala Pro Ser Met Ala Gln Ala Trp Leu Pro Leu Glu
 50 55 60
 Gly Lys Ala Leu Ala Met Met Arg Ser Leu Ala Arg Gln Phe Asp Gly
 65 70 75 80
 Val Val Gly Gly Ser Tyr Val Ala Arg Glu Gly Asn Asp Cys Val Asn
 85 90 95
 Ala Phe Leu Leu Val Phe Pro Asp Gly Ser Tyr Tyr Arg His Asp Lys
 100 105 110
 Asp Ile Pro Thr Met Trp Glu Asn Cys Tyr Tyr Ile Gly Gly Val Asp
 115 120 125
 Asp Gly Val Leu Glu Thr Pro Ile Gly Ala Val Gly Val Ala Leu Cys
 130 135 140
 Trp Glu Phe Ile Arg Thr Gln Thr Ala Arg Arg Leu Lys Asp Arg Val
 145 150 155 160
 Gln Leu Val Val Gly Gly Thr Cys Trp Trp Asp Phe Pro Met Pro Val
 165 170 175
 Pro Glu Arg Tyr Leu Arg Leu Thr Arg His Ile Ser Arg Asn Phe Glu
 180 185 190

```

Arg Asp Ala Pro Ala Arg Leu Ala Ser Met Leu Gly Val Pro Val Val
   195           200           205
His Ala Ser His Ala Gly Asp Phe Thr Ala Val Thr Pro Gly Asn Glu
   210           215           220
Thr Lys Asn Tyr Arg Ser Asn Tyr Leu Gly Glu Thr Gln Ile Val Asp
  225           230           235           240
Ala Asn Gly Asn Val Leu Lys Arg Met Thr Val Ala Asp Gly Glu Gly
           245           250           255
Tyr Val Ile Ala Asp Val Gln Leu Gly Ala Ile Ser Thr Gly Arg Thr
           260           265           270
Ser Ile Pro Asp Thr Phe Trp Thr Cys Lys Leu Thr Pro Gly Ala Gln
           275           280           285
Gln Ala Trp Asp Glu Gln Asn Ala Phe Gly Cys Gly Tyr Tyr Glu Asn
  290           295           300
Val Thr Arg Lys His Leu Ile Gly Arg
  305           310

```

<210> 37
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 37
atggattcag atatgacgga tactttttaag gcagccatta ttcagcacgc gcctgttttt      60
ttaaattctcg aagagagtct ggacaaagcc ggcagcctta tagaaaaggc tgccgatcaa      120
ggcgcgaaaag tgatcgctt tcctgaaaca tggctgcccg gttatcccgt atggctcgac      180
tactctccaa aagcgggtct gtgggactat cagcctgcaa aatctctcta tcgtctgcta      240
gtcgataatt cagtcacctt acccggaaca cacctcgatc aactcctctc catagcgcaa      300
aagaccggcg catatgttgt aatgggggca cacgaacgag tgggtggaac actctataac      360
acgacgatct atgttgggat tgatgggaag gagtacaaac ttcatagaaa gctgggtgccg      420
acctataccg aaagattgat ctggggggcg ggagacggca gcacattgag tgtgttgatg      480
acggattatg gcgttcttgg aggattgatc tgctgggagc actggatgcc tctggcaaga      540
gccgcaatgc atgccagata tgaaaccctt catgtggcgc aatggccggc tgtaaaagat      600
atccatcaga tagcaagcag acattatgct tttgaaggcc gaaggattca actcactggc tcgcgccgat      720
ggctctgttc tgactogaag agatataata gaaggattca actcactggc tcgcgccgat      780
agtgatgcat tggaacttct gaaagctatt tcggggagaag atagtgatct tattttgaat      840
gggggaagcg cgataattgc gccgaatgga gagtatcttg cgggcccggt ctttaatgaa      900
ccctccatta tttatgctga aattgatcct gcaactgataa gtgagggcca tcttacactg      960
gatacaagcg gacactactc gcgccctgac atttttcgtc tggagataaa cgatcaacct      993
caacatgatg taactttcag atcggggcat tag

```

<210> 38
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 38
Met Asp Ser Asp Met Thr Asp Thr Phe Lys Ala Ala Ile Ile Gln His
  1           5           10           15
Ala Pro Val Phe Leu Asn Leu Glu Glu Ser Leu Asp Lys Ala Gly Ser
           20           25           30
Leu Ile Glu Lys Ala Ala Asp Gln Gly Ala Lys Val Ile Ala Phe Pro
           35           40           45
Glu Thr Trp Leu Pro Gly Tyr Pro Val Trp Leu Asp Tyr Ser Pro Lys
           50           55           60

```

Ala	Gly	Leu	Trp	Asp	Tyr	Gln	Pro	Ala	Lys	Ser	Leu	Tyr	Arg	Leu	Leu
65					70					75					80
Val	Asp	Asn	Ser	Val	Thr	Leu	Pro	Gly	Lys	His	Leu	Asp	Gln	Leu	Leu
				85					90					95	
Ser	Ile	Ala	Gln	Lys	Thr	Gly	Ala	Tyr	Val	Val	Met	Gly	Ala	His	Glu
			100					105					110		
Arg	Val	Gly	Gly	Thr	Leu	Tyr	Asn	Thr	Thr	Ile	Tyr	Val	Gly	Ile	Asp
		115					120					125			
Gly	Lys	Glu	Tyr	Lys	Leu	His	Arg	Lys	Leu	Val	Pro	Thr	Tyr	Thr	Glu
	130						135				140				
Arg	Leu	Ile	Trp	Gly	Arg	Gly	Asp	Gly	Ser	Thr	Leu	Ser	Val	Leu	Met
145					150					155					160
Thr	Asp	Tyr	Gly	Val	Leu	Gly	Gly	Leu	Ile	Cys	Trp	Glu	His	Trp	Met
				165					170					175	
Pro	Leu	Ala	Arg	Ala	Ala	Met	His	Ala	Arg	Tyr	Glu	Thr	Leu	His	Val
			180					185					190		
Ala	Gln	Trp	Pro	Ala	Val	Lys	Asp	Ile	His	Gln	Ile	Ala	Ser	Arg	His
		195					200					205			
Tyr	Ala	Phe	Glu	Gly	Arg	Cys	Phe	Val	Leu	Ala	Ala	Gly	Ser	Val	Leu
	210					215					220				
Thr	Arg	Arg	Asp	Ile	Ile	Glu	Gly	Phe	Asn	Ser	Leu	Ala	Arg	Ala	Asp
225					230					235					240
Ser	Asp	Ala	Leu	Glu	Leu	Leu	Lys	Ala	Ile	Ser	Gly	Glu	Asp	Ser	Asp
			245						250					255	
Leu	Ile	Leu	Asn	Gly	Gly	Ser	Ala	Ile	Ile	Ala	Pro	Asn	Gly	Glu	Tyr
			260					265					270		
Leu	Ala	Gly	Pro	Val	Phe	Asn	Glu	Pro	Ser	Ile	Ile	Tyr	Ala	Glu	Ile
		275					280					285			
Asp	Pro	Ala	Leu	Ile	Ser	Glu	Gly	His	Leu	Thr	Leu	Asp	Thr	Ser	Gly
	290					295					300				
His	Tyr	Ser	Arg	Pro	Asp	Ile	Phe	Arg	Leu	Glu	Ile	Asn	Asp	Gln	Pro
305					310					315					320
Gln	His	Asp	Val	Thr	Phe	Arg	Ser	Gly	His						
				325					330						

<210> 39

<211> 1008

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 39

atgaaaaata	tcaaaaaactc	agaaaaaaagc	agcacagtaa	gagtcgctgc	ggtacaaatc	60
agtcgggtgt	tgtacaaccg	cgaagctacc	gttcaaaaag	tagtcaacaa	aatccttgaa	120
ctaggaaaac	aaggggtaca	attcgccact	tttccggaaa	cgatagtgcc	ttattatcct	180
tattttctctt	ttattcaggc	gccttatgcc	atggggcaaag	aacacctgcg	cttgcttgaa	240
caatcagtta	ctgttccgtc	agccgcgacc	gatgccataa	gtgaggcggc	aaaggaagcc	300
aatatggtag	tgtctattgg	tgtcaatgaa	cgagacgggtg	gtaccattta	caatacgcaa	360
ctcctttttg	atgctgacgg	aacattaatt	cagcgcagac	gtaaaacttac	accaacgtat	420
catgaaagaa	tgatttgggg	acaaggtgac	gcttcagggtc	ttcgtgccac	agacagcgct	480
gttggggcgta	tcgggcagtt	ggcttggttg	gaacattaca	atccattggt	ccgttatgct	540
ttgattgctg	atggagaaca	aatccattct	gccatgtatc	ccggatcatt	tttaggtgcg	600
ttgcacgggtg	aacaaaccga	aatcaatgta	cgccaacacg	ctttagaatc	ggccagcttc	660
gtcgtagttg	ctaccggttg	gttggaatgc	gatcaacaag	cacaaattgc	gaaagacacc	720
ggtggacca	tcgggacga	ttcgggaggt	tggttttacg	ccgttatagg	ccctgacgga	780
caactaatcg	gggaagccct	tacatcaggt	gaaggggag	tgattgccga	tattgatttg	840
gcacaaattg	atgcccgcaa	aagattaatg	gatgccagtg	gtcactacaa	ccgtcctgaa	900
ttgttgagct	tgcatatcga	tcacactccg	actgctccta	tgcatgaaag	agtagttttac	960
actgagccgg	gattagcaaa	aagacaaaat	gaaaattcat	caaattaa		1008

<210> 40
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 40
 Met Lys Asn Ile Lys Asn Ser Glu Lys Ser Ser Thr Val Arg Val Ala
 1 5 10 15
 Ala Val Gln Ile Ser Pro Val Leu Tyr Asn Arg Glu Ala Thr Val Gln
 20 25 30
 Lys Val Val Asn Lys Ile Leu Glu Lys Gln Gly Val Gln Phe
 35 40 45
 Ala Thr Phe Pro Glu Thr Ile Val Pro Tyr Tyr Pro Tyr Phe Ser Phe
 50 55 60
 Ile Gln Ala Pro Tyr Ala Met Gly Lys Glu His Leu Arg Leu Leu Glu
 65 70 75 80
 Gln Ser Val Thr Val Pro Ser Ala Ala Thr Asp Ala Ile Ser Glu Ala
 85 90 95
 Ala Lys Glu Ala Asn Met Val Val Ser Ile Gly Val Asn Glu Arg Asp
 100 105 110
 Gly Gly Thr Ile Tyr Asn Thr Gln Leu Leu Phe Asp Ala Asp Gly Thr
 115 120 125
 Leu Ile Gln Arg Arg Arg Lys Leu Thr Pro Thr Tyr His Glu Arg Met
 130 135 140
 Ile Trp Gly Gln Gly Asp Ala Ser Gly Leu Arg Ala Thr Asp Ser Ala
 145 150 155 160
 Val Gly Arg Ile Gly Gln Leu Ala Cys Trp Glu His Tyr Asn Pro Leu
 165 170 175
 Phe Arg Tyr Ala Leu Ile Ala Asp Gly Glu Gln Ile His Ser Ala Met
 180 185 190
 Tyr Pro Gly Ser Phe Leu Gly Ala Leu His Gly Glu Gln Thr Glu Ile
 195 200 205
 Asn Val Arg Gln His Ala Leu Glu Ser Ala Ser Phe Val Val Val Ala
 210 215 220
 Thr Gly Trp Leu Asp Ala Asp Gln Gln Ala Gln Ile Ala Lys Asp Thr
 225 230 235 240
 Gly Gly Pro Ile Gly Pro Ile Ser Gly Gly Cys Phe Thr Ala Val Ile
 245 250 255
 Gly Pro Asp Gly Gln Leu Ile Gly Glu Ala Leu Thr Ser Gly Glu Gly
 260 265 270
 Glu Val Ile Ala Asp Ile Asp Leu Ala Gln Ile Asp Ala Arg Lys Arg
 275 280 285
 Leu Met Asp Ala Ser Gly His Tyr Asn Arg Pro Glu Leu Leu Ser Leu
 290 295 300
 His Ile Asp His Thr Pro Thr Ala Pro Met His Glu Arg Val Val Tyr
 305 310 315 320
 Thr Glu Pro Gly Leu Ala Lys Arg Gln Asn Glu Asn Ser Ser Asn
 325 330 335

<210> 41
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 41
atgcccaatg agaataacat cgctacattc aaagttgccg cagtccaggc cacaccggtg      60
tttcttgatc gtgaagcaac catcgacaaa gcttgogggt tgattgccac tgccggcaat      120
gaaggagcgc gcctgattgt gtttccagaa gcgttcatcc caacctatcc tgaatggggt      180
tggggatttc cttccggtga gcaagggtta ctcaatgaac tctatgcaga gctgctcacc      240
aatgcggtca ctattcccag tgacgcgact gacaggctgt gcgaggccgc gcagcttgcg      300
aatgcctacg tagtgatggg aatgagcgaa cggaatgtcg aggcgagtg gcaagccta      360
tataatacgc tgttgtagat caatgcgcag ggggagattt tagggaaaca tcgaaagctg      420
gtgccaacgg ggggcgaacg cctggtagtg gcgcagggtg atggcagcac gctgcaggtc      480
tacgatacgc cattgggaaa actcgggtgt ctcatttgct gggaaaatta tatgccgctg      540
gcacgctatg ctatgtatgc ctgggggaca caaatctatg tcgcggcaac gtgggatcga      600
ggccaaccct ggctttctac attacggcat atcgccaaag aaggcagggt atacgtgatt      660
ggttgctgta tcgcgatgcg aaaagacgat attccggata gttactccat gaagcagaaa      720
taccatgctg aaatggatga atggattaat gttggcgaca gtgtgattgt caatcccga      780
ggacacttta tcgcagggcc tgtgcgcaag caagaagaaa ttctctacgc ggagatcgat      840
ccacgtagtg tgcaaggccc gaagtggatg ctcgatgtgg cggggcatta tgcgagacca      900
gatgtgtcc agttgacggg gcatacgaat gtgagagaga tgatgcgggt ggaagatgat      960
tcataa

```

```

<210> 42
<211> 321
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<400> 42
Met Pro Asn Glu Asn Asn Ile Ala Thr Phe Lys Val Ala Ala Val Gln
1      5      10      15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
20      25      30
Gly Leu Ile Ala Thr Ala Gly Asn Glu Gly Ala Arg Leu Ile Val Phe
35      40      45
Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
50      55      60
Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ala Glu Leu Leu Thr
65      70      75      80
Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
85      90      95
Ala Gln Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
100      105      110
Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asn
115      120      125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
130      135      140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145      150      155      160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
165      170      175
Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
180      185      190
Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
195      200      205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
210      215      220
Ala Met Arg Lys Asp Asp Ile Pro Asp Ser Tyr Ser Met Lys Gln Lys
225      230      235      240
Tyr His Ala Glu Met Asp Glu Trp Ile Asn Val Gly Asp Ser Val Ile
245      250      255
Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu

```

```

                260                265                270
Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
                275                280                285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
                290                295                300
Leu Thr Val His Thr Asn Val Arg Glu Met Met Arg Val Glu Asp Asp
305                310                315                320
Ser

```

<210> 43
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 43
atgagagtcg ttaaagccgc ggcggtccaa ctgaaacctg tcctctatag ccgagagggg      60
actgtcgaaa acgtcgtccg taaaatccac gagcttggac agcaaggggt acagttcgcg      120
acgtttccag agactgtggt gccttactac ccgtactttt cgatcgtgca gtccggctat      180
caaattcttg gcggtggtga gttcctgaag ctgcttgatc agtcagtaac cgtgccatct      240
ctcgctacgg aagcgatcgg cgaggcttgc aggcaggcgg gcgtcgttgt ctccatcggc      300
gtcaacgagc gtgatggagg aactctatac aacacgcaac ttctctttga tgcgacgga      360
acattgattc aaagacgacg caagatcaca cccacccatt acgagcgcat ggtctggggc      420
cagggcgatg gctcagggtt acggggccatt gacagcaagg tcgcgcgcat tgggtcaactg      480
gcgtgttttg agcactacaa ccctctcgca cgttacgcga tgatggccga tggcgagcag      540
atccattctg cgatgttccc cggtccatg ttcggcgata atttttcaga gaaggtggaa      600
atcaacataa ggcagcatgc aatggagtct ggggtgcttg tcgtttgcgc tactgcctgg      660
ttggatgctg accagcaggc tcaaatcatg aaagacacgg gatgtgagat cggaccgatc      720
tcaggagggt gcttcacagc gatcgcgcca ccagatggaa gccttatagg tgaacccatc      780
cgctcagggt aaggcggttg tattgcccgc ctcgatttca aacttatcga caagcgggaag      840
cacgtagtag acacacgcgg ccattatagc cggccagaat tgctcagcct cctgattgat      900
cggacgccga cggcccacat acacgaaagg accgagcaac cgagggcggc catcgagaaa      960
gagtcgcagg atgtttttcac cgctgttgct taa      993

```

<210> 44
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 44
Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Lys Pro Val Leu Tyr
 1                5                10                15
Ser Arg Glu Gly Thr Val Glu Asn Val Val Arg Lys Ile His Glu Leu
                20                25                30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35                40                45
Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Gly
 50                55                60
Gly Gly Glu Phe Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
 65                70                75                80
Leu Ala Thr Glu Ala Ile Gly Glu Ala Cys Arg Gln Ala Gly Val Val
                85                90                95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
100                105                110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys

```

Ile	Thr	Pro	Thr	His	Tyr	Glu	Arg	Met	Val	Trp	Gly	Gln	Gly	Asp	Gly	
	130					135					140					
Ser	Gly	Leu	Arg	Ala	Ile	Asp	Ser	Lys	Val	Ala	Arg	Ile	Gly	Gln	Leu	
145					150					155					160	
Ala	Cys	Phe	Glu	His	Tyr	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Met	Met	Ala	
				165					170						175	
Asp	Gly	Glu	Gln	Ile	His	Ser	Ala	Met	Phe	Pro	Gly	Ser	Met	Phe	Gly	
			180					185					190			
Asp	Asn	Phe	Ser	Glu	Lys	Val	Glu	Ile	Asn	Ile	Arg	Gln	His	Ala	Met	
	195						200					205				
Glu	Ser	Gly	Cys	Phe	Val	Val	Cys	Ala	Thr	Ala	Trp	Leu	Asp	Ala	Asp	
	210						215				220					
Gln	Gln	Ala	Gln	Ile	Met	Lys	Asp	Thr	Gly	Cys	Glu	Ile	Gly	Pro	Ile	
225					230					235					240	
Ser	Gly	Gly	Cys	Phe	Thr	Ala	Ile	Ala	Ala	Pro	Asp	Gly	Ser	Leu	Ile	
				245					250					255		
Gly	Glu	Pro	Ile	Arg	Ser	Gly	Glu	Gly	Val	Cys	Ile	Ala	Asp	Leu	Asp	
			260					265					270			
Phe	Lys	Leu	Ile	Asp	Lys	Arg	Lys	His	Val	Val	Asp	Thr	Arg	Gly	His	
		275					280					285				
Tyr	Ser	Arg	Pro	Glu	Leu	Leu	Ser	Leu	Leu	Ile	Asp	Arg	Thr	Pro	Thr	
	290					295					300					
Ala	His	Ile	His	Glu	Arg	Thr	Glu	Gln	Pro	Arg	Ala	Ala	Ile	Glu	Lys	
305					310					315					320	
Glu	Ser	Gln	Asp	Val	Phe	Thr	Ala	Val	Ala							
				325					330							

<210>	45
<211>	996
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	45						
gtgaaaccgc	cgacgtcatt	cgcgctggcc	gccgttcagg	cctgtcccgt	ctacctgat		60
cgcgacctga	cgatcggcaa	ggcagaaggg	ttgatcgccg	aggcggttgg	aaacggcgcg		120
aacctcatcg	tgttccccga	agcgttcgtg	cctggctatc	cgggtgtggg	gtgggttcac		180
ccgccccgtc	gcacggcgga	tcttcgcgaa	gcgtacagcg	tcctccacgc	caactcgatc		240
cgggtcccca	gccagtgcgc	cggagctctg	tgcgcggcgg	cgcggcgcgc	tggcgctcgc		300
gtggcgattg	gtgtcaacga	aagaaacagc	gaggccagcg	gcggcagcct	cttcaacacg		360
ctgctgtaca	tcggaaccga	cggcacgctg	ctcggtaaac	accgaaaagc	ggtgccaac		420
ggcggagagc	gtcttgtctg	ggccagcttg	gacggcagcg	accttgccgt	gttccacctg		480
cctttcgcgc	gagtcggcgg	actgatactg	tgggagaact	acatgccgct	cgcocgctac		540
cgcctggcgg	cctggggtgc	gcaaattccac	gtggcgccga	cctgggaccg	cgccgagccg		600
tggctctcaa	cactgcgtca	tgtcgcgaag	gaaggtagag	ccgtgacgat	cggctgctgt		660
caggccgtcc	gcaaggaaga	cattccggac	gggctggcat	tcaagtcccg	atacctggcc		720
gacgtggggc	cctgggtcaa	cccaggcggg	agcgtcatcg	tcgatcccga	cggaaaaatt		780
cttgccggac	ctgcgaacga	aaccgaaggg	atcttgtacg	ctgacatcag	ggccgcatcg		840
ctcgtcgggc	cgagatggca	actcgacatt	gccggacact	cgcgcgggcc	ggacgtcttc		900
gagctgatcg	tgcatcgcg	ttcgacgcgc	atgattcgcg	aggtctcggc	gcctcgtcgt		960
cgcgcaagaa	cgggaaagcg	accgcgacgc	cgctga				996

<210>	46
<211>	331
<212>	PRT
<213>	Unknown

$\langle 220 \rangle$

<223> Obtained from an environmental sample

<400> 46

Val	Lys	Pro	Pro	Thr	Ser	Phe	Arg	Val	Ala	Ala	Val	Gln	Ala	Cys	Pro
1				5					10					15	
Val	Tyr	Leu	Asp	Arg	Asp	Leu	Thr	Ile	Gly	Lys	Ala	Glu	Gly	Leu	Ile
		20						25				30			
Ala	Glu	Ala	Ala	Gly	Asn	Gly	Ala	Asn	Leu	Ile	Val	Phe	Pro	Glu	Ala
	35					40					45				
Phe	Val	Pro	Gly	Tyr	Pro	Val	Trp	Val	Trp	Phe	Ile	Pro	Pro	Gly	Arg
	50				55					60					
Thr	Ala	Asp	Leu	Arg	Glu	Ala	Tyr	Ser	Val	Leu	His	Ala	Asn	Ser	Ile
65				70					75					80	
Ala	Val	Pro	Ser	Gln	Ser	Thr	Glu	Arg	Leu	Cys	Ala	Ala	Ala	Arg	Arg
			85					90						95	
Ala	Gly	Val	Ala	Val	Ala	Ile	Gly	Val	Asn	Glu	Arg	Asn	Ser	Glu	Ala
		100					105						110		
Ser	Gly	Gly	Ser	Leu	Phe	Asn	Thr	Leu	Leu	Tyr	Ile	Gly	Pro	Asp	Gly
	115					120					125				
Thr	Leu	Leu	Gly	Lys	His	Arg	Lys	Leu	Val	Pro	Thr	Gly	Gly	Glu	Arg
	130				135					140					
Leu	Val	Trp	Ala	Ser	Gly	Asp	Gly	Ser	Asp	Leu	Ala	Val	Phe	Thr	Leu
145				150					155						160
Pro	Phe	Ala	Arg	Val	Gly	Gly	Leu	Ile	Cys	Trp	Glu	Asn	Tyr	Met	Pro
			165				170							175	
Leu	Ala	Arg	Tyr	Ala	Leu	Ala	Ala	Trp	Gly	Ala	Gln	Ile	His	Val	Ala
		180					185					190			
Pro	Thr	Trp	Asp	Arg	Gly	Glu	Pro	Trp	Leu	Ser	Thr	Leu	Arg	His	Val
	195					200						205			
Ala	Lys	Glu	Gly	Arg	Ala	Val	Thr	Ile	Gly	Cys	Cys	Gln	Ala	Val	Arg
	210				215					220					
Lys	Glu	Asp	Ile	Pro	Asp	Gly	Leu	Ala	Phe	Lys	Ser	Arg	Tyr	Leu	Ala
225				230					235					240	
Asp	Val	Gly	Ala	Trp	Val	Asn	Pro	Gly	Gly	Ser	Val	Ile	Val	Asp	Pro
		245					250							255	
Asp	Gly	Lys	Ile	Leu	Ala	Gly	Pro	Ala	Asn	Glu	Thr	Glu	Gly	Ile	Leu
		260				265						270			
Tyr	Ala	Asp	Ile	Arg	Ala	Asp	Gln	Leu	Val	Gly	Pro	Arg	Trp	Gln	Leu
	275					280					285				
Asp	Ile	Ala	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Phe	Glu	Leu	Ile	Val
	290				295					300					
His	Arg	Arg	Ser	Thr	Pro	Met	Ile	Arg	Glu	Val	Ser	Ala	Pro	Arg	Arg
305				310					315					320	
Arg	Ala	Arg	Thr	Gly	Lys	Arg	Pro	Arg	Arg	Arg					
			325				330								

<210> 47

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 47

gtgaaagaag	caatcaaagt	agcctgtgtg	caagcagctc	cagtctttct	cgacctggac	60
gccacagtgg	acaagaccgt	cgccctgatt	gaggaggcag	cccgtaacgg	cgcacgccta	120
atgcctttc	cagagacctg	gattccaggc	tacccatggg	tcctttggct	ggactcacca	180
gcctggggga	tgcaattcgt	gcgccgatac	cacgagaact	cactggtcct	cgacagccct	240
caggccaagc	gcacagtgga	ggccgcccag	cgccgggta	tatacgtcgc	gctagggtac	300
agcgaacgcg	tgagcggaac	cctctacatg	gggcagtggc	tcattgacga	taagggcgaa	360

```

acagctgggc tgcgccgaaa gctgaaacca acccatgtag agcgaaccct cttcgggtgaa 420
ggcgacggat catccctttc cactttcgac acaccgttgg ggggtgctggg cggactctgc 480
tgttgggaac acttacaacc tctttogaaa tatgcgctct acgcacagaa cgaggaaata 540
cacttcgccg cctggcctag cttcagcatc taccgtcaag cgacagaagt ccttggaacca 600
gaagtaaagt tcgcagcttc tcggatctac gccgtggaag ggcagtgttt tgttctcgct 660
tcctgcgcgc tcgtctcgcc agagatgata gaaatgctct gcactgacga aagcaagcac 720
agccttcttc aggccggcgg cgggtactcc cgcattatcg gtcccgatgg cagcgacctc 780
gcgcgcccct tgggcgaaaa cgaggaaggt attctctatg ccactctgga ccctgccgct 840
cgaatctatg caaagaccgc agctgatcca gccgggcact actccagacc agacgtcact 900
cggctgctga tcaatcgag tgccaatcag ccagtcgtag aggttggaag ggaaatacct 960
gcatcggccc aaggctttga agttgaggcg gccccgggt acgaaggcga ttga 1014

```

<210> 48

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 48

```

Val Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Val Phe
  1           5           10           15
Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Val Ala Leu Ile Glu Glu
      20           25           30
Ala Ala Arg Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
      35           40           45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Gly Met
      50           55           60
Gln Phe Val Arg Arg Tyr His Glu Asn Ser Leu Val Leu Asp Ser Pro
      65           70           75           80
Gln Ala Lys Arg Ile Ser Glu Ala Ala Gln Arg Ala Gly Ile Tyr Val
      85           90           95
Ala Leu Gly Tyr Ser Glu Arg Val Ser Gly Thr Leu Tyr Met Gly Gln
      100          105          110
Trp Leu Ile Asp Asp Lys Gly Glu Thr Ala Gly Leu Arg Lys Leu
      115          120          125
Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
      130          135          140
Ser Leu Ser Thr Phe Asp Thr Pro Leu Gly Val Leu Gly Gly Leu Cys
      145          150          155          160
Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Leu Tyr Ala Gln
      165          170          175
Asn Glu Glu Ile His Phe Ala Ala Trp Pro Ser Phe Ser Ile Tyr Arg
      180          185          190
Gln Ala Thr Glu Val Leu Gly Pro Glu Val Asn Val Ala Ala Ser Arg
      195          200          205
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
      210          215          220
Val Ser Pro Glu Met Ile Glu Met Leu Cys Thr Asp Glu Ser Lys His
      225          230          235          240
Ser Leu Leu Gln Ala Gly Gly Gly Tyr Ser Arg Ile Ile Gly Pro Asp
      245          250          255
Gly Ser Asp Leu Ala Arg Pro Leu Gly Glu Asn Glu Glu Gly Ile Leu
      260          265          270
Tyr Ala Thr Leu Asp Pro Ala Ala Arg Ile Tyr Ala Lys Thr Ala Ala
      275          280          285
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu Ile
      290          295          300
Asn Arg Ser Ala Asn Gln Pro Val Val Glu Val Gly Arg Glu Ile Pro
      305          310          315          320

```

Ala Ser Ala Gln Gly Phe Glu Val Glu Ala Ala Pro Gly Tyr Glu Gly
 325 330 335

Asp

<210> 49
 <211> 1038
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 49
 atgaacaaag tctgtggctgc tgccgttcag tgcagcccgg tgctttactc ttgcgccgga 60
 actgtaaata aaatttgcca gtggattgca gattttgggca aacaaggggt tgagctggcg 120
 gtgttcgcgg aaaccctggg gccttactac ccgtattttt cttttatcca ggctccttgt 180
 gcgatggggc cgcaacattt gttgttgatg caagaatcag tagaggttcc ttccatctac 240
 acgcaacaaa ttgccgctgc agcaaaagca gcgaagatgg tgggtgtcagt tgggtattaac 300
 gaacgcgacg gcgggttctat ttataacgcg caattattat ttgatgcggg cggtcagctt 360
 gttcagcacc gccgaaaaat tacgccgaca ttcatgagc gcatgggtgtg ggggcagggc 420
 gatggctccg gtttgtgcgc agtggatacg gcagttgggtc gtgttgggtc gctcgcttgc 480
 tgggaacatt acaaccact cgcgcggttac gcattgatgg cagatcgcca acaaatcac 540
 gtgagtatgt ttcccggttc tttggtcggc gaaatttttg ccgagcaaat tgaagcaact 600
 attcgtcacc acgcattgga gtccggttgc tttgtggtaa atgcgacggg ctggttaacg 660
 ccggaacagc aagctcaaat cgtaaaagat actggtgggtc ctatcgctgc cattagcggg 720
 gggtgtttca ccgccattgt ttcaccggaa ggaaaattgc tcggcacgcc attgcgcagt 780
 gattccgggg aggggtgcctg tatcgccgaa ctggatttta atctcatcaa taagcgtaag 840
 cgcgatgatg attctgtcgg ccattacagt cgtcctgaat tgctcagttt gctgattgat 900
 aaaacaccca caagtcatac acatccgctt aaaaaacctt tgggtcccag tgaaaaaaat 960
 acgccagagg atatcgccac tggtttaaca ctggtcactc ccgtttcaaa tgcaaacctt 1020
 ttcagcgcaa gcaactag 1038

<210> 50
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 50
 Met Asn Lys Val Val Ala Ala Ala Val Gln Cys Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Cys Ala Gly Thr Val Asn Lys Ile Cys Glu Trp Ile Ala Asp Leu
 20 25 30
 Gly Lys Gln Gly Val Glu Leu Ala Val Phe Ala Glu Thr Leu Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Ile Gln Ala Pro Cys Ala Met Gly Ala
 50 55 60
 Gln His Leu Leu Leu Met Gln Glu Ser Val Glu Val Pro Ser Ile Tyr
 65 70 75 80
 Thr Gln Gln Ile Ala Ala Ala Ala Lys Ala Ala Lys Met Val Val Ser
 85 90 95
 Val Gly Ile Asn Glu Arg Asp Gly Gly Ser Ile Tyr Asn Ala Gln Leu
 100 105 110
 Leu Phe Asp Ala Gly Gly Gln Leu Val Gln His Arg Arg Lys Ile Thr
 115 120 125
 Pro Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
 130 135 140
 Leu Cys Ala Val Asp Thr Ala Val Gly Arg Val Gly Ser Leu Ala Cys

```

145          150          155          160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Arg
          165          170          175
Glu Gln Ile His Val Ser Met Phe Pro Gly Ser Leu Val Gly Glu Ile
          180          185          190
Phe Ala Glu Gln Ile Glu Ala Thr Ile Arg His His Ala Leu Glu Ser
          195          200          205
Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Pro Glu Gln Gln
          210          215          220
Ala Gln Ile Val Lys Asp Thr Gly Gly Pro Ile Ala Ala Ile Ser Gly
225          230          235          240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Thr
          245          250          255
Pro Leu Arg Ser Asp Ser Gly Glu Gly Ala Cys Ile Ala Glu Leu Asp
          260          265          270
Phe Asn Leu Ile Asn Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275          280          285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Lys Thr Pro Thr
          290          295          300
Ser His Thr His Pro Leu Lys Lys Pro Leu Ala Pro Ser Glu Lys Asn
305          310          315          320
Thr Pro Glu Asp Ile Ala Thr Gly Leu Thr Leu Val Thr Pro Val Ser
          325          330          335
Asn Ala Asn Leu Phe Ser Ala Ser Asn
          340          345

```

<210> 51
 <211> 897
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 51
gtgaacgtcc gcgctcgcggt ggtgcaggcc acgccggccg tgctcgacgg gccggcgctcg      60
gtgcggaagg cctgccgcct gatcggcgag gccgcggccg gcggcgcccg cctgatcgcc      120
ctgcccagagg gcttcgtgcc catcatgccg cgctcctgct gggggcacca cttcgcgctg      180
atcgccctcgc cgaagtcggc ggccctgcac cgccgcacat gggagaacgc cgtcgacgtc      240
ggcgggcccgc tggcccgcga gctcggcgac gccgcgcgcc gcgcggacgc ctgggtggcc      300
atcggggtgta acgagcgcca cgcccgcggc ccggggcacgc tctggaacac gctgctctgg      360
ttcgcgcccg acgggagcct ggcccggcgc caccgcaagc tcgtgccac catgcacgag      420
cgcacgttct gggggcagg cgcgggcgac gacctcgagg cgctggccgc ggacttcggc      480
cgcttgggcg gcctgatctg ctgggagaaac ttcattgccg ccgcgcgcgg gcgcctgcac      540
cgggacgggg tcgacttcta cctggccccc acggcgagac accgggacat ctgggtcgcc      600
gcgatgcgca cgttcgccct cgaggccggc gccttcgtcc tctcgccggg gcagtacctg      660
cggaccgccc acttcccgga ggacttcccg ctgcgcgagg agctcgccga ctgccccgag      720
gtccagttca ccggggggag cgtgatctgc gaccgtggg gcaacctcct ggcggggccc      780
gtccacgggg gcgaggagat cctctacgcc gactgcgac tcgacctcgt cctcgaggcc      840
cgacgggtgc tcgacacggc cggccactac gaccgcccgg acctcgctc ggcctga      897

```

<210> 52
 <211> 298
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 52
Val Asn Val Arg Val Ala Val Val Gln Ala Thr Pro Ala Val Leu Asp

```

1 5 10 15
 Gly Pro Ala Ser Val Arg Lys Ala Cys Arg Leu Ile Gly Glu Ala Ala
 20 25 30
 Ala Gly Gly Ala Arg Leu Ile Ala Leu Pro Glu Gly Phe Val Pro Ile
 35 40 45
 Met Pro Arg Ser Cys Trp Gly His His Phe Ala Leu Ile Ala Ser Pro
 50 55 60
 Lys Ser Ala Ala Leu His Arg Arg Ile Trp Glu Asn Ala Val Asp Val
 65 70 75 80
 Gly Gly Pro Leu Ala Arg Glu Leu Gly Asp Ala Ala Arg Arg Ala Asp
 85 90 95
 Ala Trp Val Ala Ile Gly Val Asn Glu Arg Asp Ala Arg Arg Pro Gly
 100 105 110
 Thr Leu Trp Asn Thr Leu Leu Trp Phe Ala Pro Asp Gly Ser Leu Ala
 115 120 125
 Arg Arg His Arg Lys Leu Val Pro Thr Met His Glu Arg Thr Phe Trp
 130 135 140
 Gly Gln Gly Ala Gly Asp Asp Leu Glu Ala Leu Ala Ala Asp Phe Gly
 145 150 155 160
 Arg Leu Gly Gly Leu Ile Cys Trp Glu Asn Phe Met Pro Ala Ala Arg
 165 170 175
 Arg Arg Leu His Arg Asp Gly Val Asp Phe Tyr Leu Ala Pro Thr Ala
 180 185 190
 Asp Asp Arg Asp Ile Trp Val Ala Ala Met Arg Thr Phe Ala Phe Glu
 195 200 205
 Ala Gly Ala Phe Val Leu Ser Pro Val Gln Tyr Leu Arg Thr Ala Asp
 210 215 220
 Phe Pro Glu Asp Phe Pro Leu Arg Glu Glu Leu Ala Asp Cys Pro Glu
 225 230 235 240
 Val Gln Phe Thr Gly Gly Ser Val Ile Cys Asp Pro Trp Gly Asn Leu
 245 250 255
 Leu Ala Gly Pro Val His Gly Gly Glu Glu Ile Leu Tyr Ala Asp Cys
 260 265 270
 Asp Leu Asp Leu Val Leu Glu Ala Arg Arg Val Leu Asp Thr Ala Gly
 275 280 285
 His Tyr Asp Arg Pro Asp Leu Ala Ser Ala
 290 295

<210> 53
 <211> 954
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 53
 atgggtcaatt caaagagtca gattaaaaatc gcggcgggtgc aggctgcccc ggtctttctg 60
 gaacgggagg cgacgattga caaagcttgc cggttgattg cggaggcagg cgagcagggc 120
 gcgaatctgg tggctctccc tgagtcattc gtcccggctt atcccgattg ggtctggggc 180
 gttccggcag gtgaaacaac gtcctgaac acgctctatg ccgaactgct ggccaatgcc 240
 gttgaaattc cgggtccggc gacagagcgg ctgagccagg cagccaacct ggccgggggtt 300
 tatgtcgcga ttggcttgac cgagcggaaac atcgaggcca gtggggcgag cctgtacaat 360
 actttgctct ttctcgactc agccggcggc atgttaggca agcatcgcaa actgatcccc 420
 accggcgggc agcgcctggt ctgggctcag ggtgatggca gcaactctggc ggtgtacgag 480
 actaggtttg gaaaaatggg agggttgatt tgctgggaga attacatgcc cctggcccgt 540
 tatgccttgt atgcctggg gacgcagatt tacatcgcg ccacctggga tcgaggcgag 600
 ccgtggctgt caacgctgcg gcatatcgcc gcggaaggcc gggttgttgt cgtcggctgt 660
 ggcattggccc tgcgcaaagc cgacctgccc gaccgctttg aactcaagca gcgattttac 720
 cagaacgccg atgagtggat caatgtcggc gacagcgcg ttgttaacct tgatggtgaa 780
 ttcatcgccg ggccgctgcg cgagcaggaa ggcacacct atgctgagat tgatctggcc 840

cagatgcgcg gccccaaatg gatgctcgac gtggccggcc attacgctcg cccggatgtg 900
 tttgaactca tcgttcacgcg ggaggcgcg cccatgattg cgctaatttc atga 954

<210> 54
 <211> 317
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 54
 Met Val Asn Ser Lys Ser Gln Ile Lys Ile Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Glu Arg Glu Ala Thr Ile Asp Lys Ala Cys Arg Leu
 20 25 30
 Ile Ala Glu Ala Gly Glu Gln Gly Ala Asn Leu Val Val Phe Pro Glu
 35 40 45
 Ser Phe Val Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala Gly
 50 55 60
 Glu Thr Thr Leu Leu Asn Thr Leu Tyr Ala Glu Leu Leu Ala Asn Ala
 65 70 75 80
 Val Glu Ile Pro Gly Pro Ala Thr Glu Arg Leu Ser Gln Ala Ala Asn
 85 90 95
 Leu Ala Gly Val Tyr Val Ala Ile Gly Leu Thr Glu Arg Asn Ile Glu
 100 105 110
 Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Phe Leu Asp Ser Ala
 115 120 125
 Gly Gly Met Leu Gly Lys His Arg Lys Leu Ile Pro Thr Gly Gly Glu
 130 135 140
 Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Ala Val Tyr Glu
 145 150 155 160
 Thr Arg Phe Gly Lys Met Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
 180 185 190
 Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
 195 200 205
 Ile Ala Ala Glu Gly Arg Val Val Val Val Gly Cys Gly Met Ala Leu
 210 215 220
 Arg Lys Ala Asp Leu Pro Asp Arg Phe Glu Leu Lys Gln Arg Phe Tyr
 225 230 235 240
 Gln Asn Ala Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val Asn
 245 250 255
 Pro Asp Gly Glu Phe Ile Ala Gly Pro Leu Arg Glu Gln Glu Gly Ile
 260 265 270
 Leu Tyr Ala Glu Ile Asp Leu Ala Gln Met Arg Gly Pro Lys Trp Met
 275 280 285
 Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
 290 295 300
 Val His Arg Glu Ala Arg Pro Met Ile Ala Leu Ile Ser
 305 310 315

<210> 55
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 55

```

atgggtatcg aacatccgaa gtacaaggtc gccgtggtgc aggcagctcc cgcttggtc 60
gatctcgacg cgctgatcga caagtcgacg gcgctgatcg aggaggcggc ccaaaaaggc 120
gccaaagctga tcgcattccc cgaggccttc attcccggct atccctggca catctggatg 180
gactcgccgg cctggggcgat cggccgcggc tttgtgcagc gctattttga caattcgctc 240
gcctatgaca gcccgagggc cgagaagctg cgcgcggcgg tgcgcaaggc aaagctcacc 300
gccgtgctcg ggctgtccga gcgcgaacgc gccagtcctc atctggcgca atggttgatc 360
gggcccgatg gcgagaccat cgcaaaaacg cgcaagctgc ggccgacaca tgccgagcgc 420
acggtgtacg gcgagggcga cggcagcgat ctgcagctcc acaaccgtcc cgatatcggc 480
cgcctcggcg cgctctgctg ctgggagcat ttgcagccac tgtcgaaata cgcgatgtac 540
gcgcagaacg agcaggtgca tgctcgggcc tggccgagct tttcgctcta cgatcccttt 600
gcggtggcgc tcggcgccga ggtgaacaac gcggcctcgc gcgtctatgc agtcgaaggc 660
tcctgcttcg tgctggcgcc atgcgccacc gtctcgagg ccatgatcga cgagctctgc 720
gaccgaccgg acaagcatab gctgctgcat gtcggcggcg gttttgccgc gatctatggt 780
cctgacggca gccagatcgg cgacaagctc gcgcccgacc aggaagggct gttgatcgcg 840
gagatcgacc ttggggccat tggcgctcgcc aagaacgcgg ccgatcccg cgggcattat 900
tcgcggcccg acgtgacgcg gctcctgctc aacaagaaac cgtacaagcg cgctcgagcag 960
ttctcgccac cggccgaggc ggtcgagccc acagatatcg cagcggcggc aagctga 1017

```

<210> 56

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 56

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1      5      10      15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Ser Ile Ala Leu
20     25     30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35     40     45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
50     55     60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65     70     75     80
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
85     90     95
Ala Lys Leu Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100    105    110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115    120    125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130    135    140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
145    150    155    160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165    170    175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180    185    190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
195    200    205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210    215    220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225    230    235    240
Asp Arg Pro Asp Lys His Thr Leu Leu His Val Gly Gly Gly Phe Ala
245    250    255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro

```

```

                260                265                270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
                275                280                285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
                290                295                300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
305                310                315                320
Phe Ser Pro Pro Ala Glu Ala Val Glu Pro Thr Asp Ile Ala Ala Ala
                325                330                335
Ala Ser

```

<210> 57
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 57
gtgaaagaag caatcaaagt agcctgtgtg caagcagctc cagtctttct cgacctggac      60
gccacagtgg acaagaccgt cgccctgatt gaggaggcag cccgtaacgg cgcacgccta      120
atcgcccttc cagagacctg gattccaggc taccocatgt tcctttggct ggactcacca      180
gctgggggga tgcaattcgt gcgccgatac cacgagaact cactggtcct cgacagccct      240
caggccaagc gcatcagtga ggccgcccag cgcgcgggta tatacgtcgc gctaggggtac      300
agcgaacgcg tgagcggaac cctctacatg gggcagtggc tcattgacga taagggcgaa      360
acagctgggc tgcgccgaaa gctgaaacca acccatgtag agogaaccct cttcggtgaa      420
ggcgacggat catccctttc cactttcgac acaccgttgg ggggtgctggg cggactctgc      480
tggtgggaac acttacaacc tctttcgaaa tatgcgctct acgcacagaa cgaggaaata      540
cacttcgccg cctggcctag cttcagcatc taccgtcaag cgacagaagt ccttggacca      600
gaagtaaatg tcgcagcttc tcggatctac gccgtggaag ggcagtggtt tgttctcgct      660
tcctgcgcgc tcgtctcgcc agagatgata gaaatgctct gcaactgacga aagcaagcac      720
agccttcttc aggcgcggcg cgggtactcc cgcattatcg gtcccgatgg cagcgaccta      780
gcgcgcccct tgggcgaaaa cgaggaaggt attctctatg ccactctgga ccctgccgct      840
cgaatctatg caaagacgc agctgatcca gccgggcaact actccagacc agacgtcact      900
cggctgctga tcaatcgag tgccaatcag ccagtcgtag aggttggaac ggaaatacct      960
gcatcgcccc aaggctttga agttgaggcg gccccgggt acggaggcga ttga      1014

```

<210> 58
 <211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 58
Val Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Val Phe
1          5          10          15
Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Val Ala Leu Ile Glu Glu
20          25          30
Ala Ala Arg Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
35          40          45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Gly Met
50          55          60
Gln Phe Val Arg Arg Tyr His Glu Asn Ser Leu Val Leu Asp Ser Pro
65          70          75          80
Gln Ala Lys Arg Ile Ser Glu Ala Ala Gln Arg Ala Gly Ile Tyr Val
85          90          95
Ala Leu Gly Tyr Ser Glu Arg Val Ser Gly Thr Leu Tyr Met Gly Gln

```

<210>	59
<211>	987
<212>	DNA
<213>	Unknown

<400>	59								
atgcgagata	ggaatttcaa	actggcggcc	attcaggcgg	agccggtttt	ctttaatcgc				60
cgggcctcga	cggaaaaggc	ctgcagattg	atcaaaagaa	cgggcgcgat	gggcgcgat				120
atcgcgggcat	tcagcgcgac	ctggcttccc	gggtatccct	tttttatctg	gggcgcgaagc				180
gccgatccat	cctctgctctg	gaaggcttct	gcggaatacc	tggccaatgc	cggtcaaata				240
cccggtcccg	agacggatca	attatgcgag	gcggcgaaaa	aggccggcat	cgatgtggcg				300
atcggagtg	ttgaactcga	cgagtttacg	aagggaacgg	cttactgcac	gctgctcttc				360
atcggcaaa	aagggaagat	cctgggaaag	caccgcaaac	tcaagccgac	gcaccgggag				420
cgcacggtat	ggggagaggg	cgatgcgcac	ggactcagtg	tccatgagcg	tccttactcgg				480
cggatcagcg	gcctgaactg	ctgggagcat	aatatggtcc	tgcccggcta	tgtcttgatg				540
tctcagggca	cgcacattca	tatcgcgccc	tggccgggtt	cggaagggaa	agcacctccc				600
gcgccgtctc	cgatgtggga	gcgccagctt	ctgctctccc	gcgctttcgc	ttcgcaatcc				660
gccgcatacg	tgattctggt	cggaggactc	ctgaaccgcg	agaatattcc	ggcgccctac				720
gatgaacttg	ccgtcaagta	ccggggagac	agtttcatca	tcgatccgcg	cggggagatc				780
atcgccgggc	cggccaaggg	ggaaaccatt	ctcatcgccg	aaggctcgat	ggaacaggtc				840
ctcgcgcaa	agtcgcgctt	cgatgtcgcg	ggacattatt	ccgcgccga	cgcttttcaa				900
ctctgcgtca	accgcaaac	gtaccggcgt	gtaaggga	cttcggagca	ggaccaacc				960
gcttctgaaa	gagaatcgg	atcgtaa							987

Page 39

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 60
Met Arg Asp Arg Asn Phe Lys Leu Ala Ala Ile Gln Ala Glu Pro Val
1 5 10 15
Phe Phe Asn Arg Arg Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile Lys
20 25 30
Glu Ala Gly Ala Met Gly Ala Asp Ile Ala Gly Phe Ser Glu Thr Trp
35 40 45
Leu Pro Gly Tyr Pro Phe Phe Ile Trp Gly Ala Ser Ala Asp Pro Ser
50 55 60
Leu Leu Trp Lys Ala Ser Ala Glu Tyr Leu Ala Asn Ala Val Gln Ile
65 70 75 80
Pro Gly Pro Glu Thr Asp Gln Leu Cys Glu Ala Ala Lys Lys Ala Gly
85 90 95
Ile Asp Val Ala Ile Gly Val Val Glu Leu Asp Glu Phe Thr Lys Gly
100 105 110
Thr Ala Tyr Cys Thr Leu Leu Phe Ile Gly Lys Glu Gly Lys Ile Leu
115 120 125
Gly Lys His Arg Lys Leu Lys Pro Thr His Arg Glu Arg Thr Val Trp
130 135 140
Gly Glu Gly Asp Ala Thr Gly Leu Ser Val His Glu Arg Pro Tyr Gly
145 150 155 160
Arg Ile Ser Gly Leu Asn Cys Trp Glu His Asn Met Val Leu Pro Gly
165 170 175
Tyr Val Leu Met Ser Gln Gly Thr His Ile His Ile Ala Ala Trp Pro
180 185 190
Gly Ser Glu Gly Lys Ala Pro Pro Ala Pro Ser Pro Met Trp Glu Arg
195 200 205
Gln Leu Leu Leu Ser Arg Ala Phe Ala Ser Gln Ser Ala Ala Tyr Val
210 215 220
Ile Leu Val Gly Gly Leu Leu Asn Pro Gln Asn Ile Pro Ala Pro Tyr
225 230 235 240
Asp Glu Leu Ala Val Lys Tyr Arg Gly Asp Ser Phe Ile Ile Asp Pro
245 250 255
Arg Gly Glu Ile Ala Gly Pro Ala Lys Gly Glu Thr Ile Leu Ile
260 265 270
Ala Glu Gly Ser Met Glu Gln Val Leu Ala Ala Lys Ser Ala Phe Asp
275 280 285
Val Ala Gly His Tyr Ser Arg Pro Asp Val Phe Gln Leu Cys Val Asn
290 295 300
Arg Lys Pro Tyr Arg Arg Val Arg Glu Thr Ser Glu Gln Asp Gln Pro
305 310 315 320
Ala Ser Glu Arg Glu Ser Glu Ser
325

<210> 61
<211> 966
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 61
atgactcgat cttaccgcgaa tgacacactc acgggttgggc ttgcgcaaatt tgctccagtc 60
tggttggatc gtacagggac aatttcaaag atattagctc aagtccatgc ggcaaattgaa 120

```

gcgggctgtc atcttgtcgc gtttggcgaa ggtctcctcc cgggatatcc gttttggatt 180
gagcgaacaa atggtgcagt cttcaactcg cccaogcaga aagaaattca cgcg cattat 240
ctggatcagg ctgtccagat cgaagcaggt catcttgagg cgctttgcga agcagccaag 300
gaatatgaga tcgcaattgt cctgggatgc attgaacgtc cgcaagatcg tggagggcac 360
agtctgtatg caagccttgt atatatgtat tcagacggca tcatccaatc tgtgcatcga 420
aagttaatgc caacatatga agaacggctc acctgggtcg cagggtgacgg acatggatta 480
cgggtgcaca aattaggtgc ctttacggtt ggcggcctca actgttggga aaactggatg 540
cctttggcac gcgcgcccat gtatgggtcaa ggcgaggatt tgcattattgc catttggccc 600
ggcggtctcc acaatacgca agacattaca cgctttattg cactagaatc gcgttcctat 660
gttttatctg tgtcagggtt aatgcgctca ggcgattttc caaaagagac cccacatctt 720
gcatccatcc tggctaaagg tgaggatatt cttgccaacg gtggttcatt tatcgccggt 780
cctgacggca aatggatcgt tgagccgctt gtaggagaag agaagttaat tgttgcaacg 840
attgatcatt gtcgtgtgcg cgaagagcgt caaaattttg atccttcagg acattacagc 900
aggccagatg tattgcaact gaaaataaac aggcaacgcc agagtacaat ctcgtttgga 960
gagtaa

```

<210> 62

<211> 321

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 62

```

Met Thr Arg Ser Tyr Pro Asn Asp Thr Leu Thr Val Gly Leu Ala Gln
1      5      10
Ile Ala Pro Val Trp Leu Asp Arg Thr Gly Thr Ile Ser Lys Ile Leu
20     25     30
Ala Gln Val His Ala Ala Asn Glu Ala Gly Cys His Leu Val Ala Phe
35     40     45
Gly Glu Gly Leu Leu Pro Gly Tyr Pro Phe Trp Ile Glu Arg Thr Asn
50     55     60
Gly Ala Val Phe Asn Ser Pro Thr Gln Lys Glu Ile His Ala His Tyr
65     70     75     80
Leu Asp Gln Ala Val Gln Ile Glu Ala Gly His Leu Glu Ala Leu Cys
85     90     95
Glu Ala Ala Lys Glu Tyr Glu Ile Ala Ile Val Leu Gly Cys Ile Glu
100    105    110
Arg Pro Gln Asp Arg Gly Gly His Ser Leu Tyr Ala Ser Leu Val Tyr
115    120    125
Ile Asp Ser Asp Gly Ile Ile Gln Ser Val His Arg Lys Leu Met Pro
130    135    140
Thr Tyr Glu Glu Arg Leu Thr Trp Ser Pro Gly Asp Gly His Gly Leu
145    150    155    160
Arg Val His Lys Leu Gly Ala Phe Thr Val Gly Gly Leu Asn Cys Trp
165    170    175
Glu Asn Trp Met Pro Leu Ala Arg Ala Ala Met Tyr Gly Gln Gly Glu
180    185    190
Asp Leu His Ile Ala Ile Trp Pro Gly Gly Ser His Asn Thr Gln Asp
195    200    205
Ile Thr Arg Phe Ile Ala Leu Glu Ser Arg Ser Tyr Val Leu Ser Val
210    215    220
Ser Gly Leu Met Arg Ser Gly Asp Phe Pro Lys Glu Thr Pro His Leu
225    230    235    240
Ala Ser Ile Leu Ala Lys Gly Glu Asp Ile Leu Ala Asn Gly Gly Ser
245    250    255
Cys Ile Ala Gly Pro Asp Gly Lys Trp Ile Val Glu Pro Leu Val Gly
260    265    270
Glu Glu Lys Leu Ile Val Ala Thr Ile Asp His Cys Arg Val Arg Glu
275    280    285

```

Glu Arg Gln Asn Phe Asp Pro Ser Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 Leu Gln Leu Lys Ile Asn Arg Gln Arg Gln Ser Thr Ile Ser Phe Gly
 305 310 315 320
 Glu

<210> 63
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 63
 atgcaagata gagtaccgat tgtacgagct gcggtatcc aggctgaacc catagtccctt 60
 gattgtgacg cgaccgtgga aaaagcctgc cgattgatcg gtgaagcagc agaaaatggg 120
 gcaaacctga tcgtgtttcc cgaagccttc attcccgttt atcccaatgc ggcgatctgg 180
 ggtcgaggtc tggccacttt tggcggacag cgccagaaat acgtatggac gcgactatgg 240
 aacaattcgg tggaaatccc tggtcgggcc accgacaggc tggcaaaggc agcacacgag 300
 gctcgagcca ccgttgtcat gggattgaat gagcgcgcg tcgataacaa cacgctttac 360
 aacaccctgc tatttattgg gccagacggg cgcttgctgg gcaagcaccg taagctcatg 420
 cccaccaatc acgaacggat gatctggggg atgggagatg ggagcaccct gcgggttttt 480
 gatacaccct gtggaaaagt aggcggtctc atctgctggg aaaactacat gcctctggcg 540
 cgttatgcac tctatggaca gggcgaacaa atccatgtcg cgccgactgc gcacgatggg 600
 gagatcactc tggatcaatgc acgcaatacc gcctatgagg gacgcttatt cgtcatctcc 660
 gtgtgcatga tccttcgcaa gtccagcttt ccccatgatt ttgagctggg cgaggaattg 720
 gcgaggcagc atgacttcat aaaatcaggc ggcagcgcg tctgtgggcc agatggcgag 780
 gtgctggcgg gtccattgtg gaatgaagag aatatactgt atgcgatct tgacttgaat 840
 cgaattgtgg atgagagacg agtatttgat gtgacggggc attattcacg tccagatgtt 900
 ctacgactgc actttaatgc ttcccctcag aaaactattg aaagatatga gcaacctctc 960
 gatccgtctg aggggttaa 978

<210> 64
 <211> 325
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 64
 Met Gln Asp Arg Val Pro Ile Val Arg Ala Ala Ala Ile Gln Ala Glu
 1 5 10 15
 Pro Ile Val Leu Asp Cys Asp Ala Thr Val Glu Lys Ala Cys Arg Leu
 20 25 30
 Ile Gly Glu Ala Ala Glu Asn Gly Ala Asn Leu Ile Val Phe Pro Glu
 35 40 45
 Ala Phe Ile Pro Val Tyr Pro Asn Ala Ala Ile Trp Gly Arg Gly Leu
 50 55 60
 Ala Thr Phe Gly Gly Gln Arg Gln Lys Tyr Val Trp Thr Arg Leu Trp
 65 70 75 80
 Asn Asn Ser Val Glu Ile Pro Gly Pro Ala Thr Asp Arg Leu Ala Lys
 85 90 95
 Ala Ala His Glu Ala Arg Ala Thr Val Val Met Gly Leu Asn Glu Arg
 100 105 110
 Ala Val Asp Asn Asn Thr Leu Tyr Asn Thr Leu Leu Phe Ile Gly Pro
 115 120 125
 Asp Gly Arg Leu Leu Gly Lys His Arg Lys Leu Met Pro Thr Asn His
 130 135 140

Glu Arg Met Ile Trp Gly Met Gly Asp Gly Ser Thr Leu Arg Val Phe
 145 150 155 160
 Asp Thr Pro Cys Gly Lys Val Gly Gly Leu Ile Cys Trp Glu Asn Tyr
 165 170 175
 Met Pro Leu Ala Arg Tyr Ala Leu Tyr Gly Gln Gly Glu Gln Ile His
 180 185 190
 Val Ala Pro Thr Ala His Asp Gly Glu Ile Thr Leu Val Asn Ala Arg
 195 200 205
 Asn Thr Ala Tyr Glu Gly Arg Leu Phe Val Ile Ser Val Cys Met Ile
 210 215 220
 Leu Arg Lys Ser Ser Phe Pro His Asp Phe Glu Leu Gly Glu Glu Leu
 225 230 235 240
 Ala Glu Ala Asp Asp Phe Ile Lys Ser Gly Gly Ser Ala Ile Val Gly
 245 250 255
 Pro Asp Gly Glu Val Leu Ala Gly Pro Leu Trp Asn Glu Glu Asn Ile
 260 265 270
 Leu Tyr Ala Asp Leu Asp Leu Asn Arg Ile Val Asp Glu Arg Arg Val
 275 280 285
 Phe Asp Val Thr Gly His Tyr Ser Arg Pro Asp Val Leu Arg Leu His
 290 295 300
 Phe Asn Ala Ser Pro Gln Lys Thr Ile Glu Arg Tyr Glu Gln Pro Leu
 305 310 315 320
 Asp Pro Ser Glu Gly
 325

<210> 65
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 65
 atgccgaccc ccacttcaaa attcaaaatc ggcgccgtgc aggcacgcgc ggtttttctg 60
 gaccgggaag ccactgcgca aaaagcctgc aaattgattg ccgaagcggg agggcagggc 120
 gcgcggctga tcgttttccc ggagtccttc attccacact atcctgattg ggtctgggag 180
 gtcccgcggg gaagaggaaa agtggttaag gaactttacg ccgagctgct ggccaatgcc 240
 gtggaagtcc ccgggcccgt caccgatcag ctgggtgaag cagcccaaaa aacgggcgcc 300
 tatgtcgtca tgggcgtcac ggaaaaggac accgacgcaa gcggcgcgag cctttacaac 360
 acgtcctctt atttcaaccc cgcgggggac ctccctggaa aacaccggaa gcttggtcct 420
 accggcgggg agcggctggt ctgggcgcag ggcgacggca gcaccctgga agtgtagcac 480
 actcccctgg gaaaaatcgg aggcctcatc tgctgggaaa actacatgcc cctcgcccgg 540
 tacacgatgt atgcctgggg gacccagatt tatatcgcgg ccacatggga ccagggggag 600
 acgtggcttg ccaccctgcg gcatatcgct aagggaaggac ggggtgtacgt catcggtgc 660
 tgcacgcgcg tcgggcggga cgacatcccc gaccggctgg aatacaagaa gaagttctac 720
 tcggggctgc gggaatggat caatatgggg gacagcgcca tcgtgaacct ggaaggcgaa 780
 ttcattgcgg gccccgtgcg gatgaaggag gagatcctgt atgccgaggt ggaccccctc 840
 ctgatggcgg gatcgaaatg gatgctcgac gtcgcggggc attacgcgcg ccccgacgtc 900
 tttgaactca tcgtccaccg ccagccccac ccgatgatcc gggtaatcga gaaagaggga 960
 ggggccggaa gaaccgggga cgagaagaag gaaaatgagt ga 1002

<210> 66
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 66

```

Met Pro Thr Pro Thr Ser Lys Phe Lys Ile Gly Ala Val Gln Ala Ser
 1          5          10          15
Pro Val Phe Leu Asp Arg Glu Ala Thr Ala Gln Lys Ala Cys Lys Leu
 20          25          30
Ile Ala Glu Ala Gly Gly Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
 35          40          45
Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50          55          60
Arg Gly Lys Val Leu Ser Glu Leu Tyr Ala Glu Leu Leu Ala Asn Ala
 65          70          75          80
Val Glu Val Pro Gly Pro Val Thr Asp Gln Leu Gly Glu Ala Ala Gln
 85          90          95
Lys Thr Gly Ala Tyr Val Val Met Gly Val Thr Glu Lys Asp Thr Asp
 100         105         110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Asn Pro Ala
 115         120         125
Gly Asp Leu Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130         135         140
Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145         150         155         160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165         170         175
Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
 180         185         190
Ala Ala Thr Trp Asp Gln Gly Glu Thr Trp Leu Ala Thr Leu Arg His
 195         200         205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
 210         215         220
Arg Arg Asp Asp Ile Pro Asp Arg Leu Glu Tyr Lys Lys Lys Phe Tyr
 225         230         235         240
Ser Gly Ser Arg Glu Trp Ile Asn Met Gly Asp Ser Ala Ile Val Asn
 245         250         255
Pro Glu Gly Glu Phe Ile Ala Gly Pro Val Arg Met Lys Glu Glu Ile
 260         265         270
Leu Tyr Ala Glu Val Asp Pro Leu Leu Met Ala Gly Ser Lys Trp Met
 275         280         285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
 290         295         300
Val His Arg Gln Pro His Pro Met Ile Arg Val Ile Glu Lys Glu Gly
 305         310         315         320
Gly Ala Gly Arg Thr Gly Asp Glu Lys Lys Glu Asn Glu
 325         330

```

<210> 67

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 67

```

atgccccgtg tggcgggtggt ccagcgcccg ccggtgtttc tcgaccgcgc cgcgaccctc      60
gagaacgccg tggcttcgct cgccgaggcc gcgtcgaacg gggctcgctt cgcggtcttt      120
ccggaagccc tggttcccgg ctatccggcg tggatgtggc ggctgcggcc cgggcccgcac      180
atggcgctca ccgagcggat tcacgcgcgc ttgcgggcga actcggtagg cctcgccgcc      240
gacgagctcg cgccgtgctg cgagggcgcc cgccgccacg agctcaccgt agtgtgcggc      300
ctgcacgagc gcgacgaggc gctcggcgcc ggcacgctct ataacaccgt cgtcacgata      360
ggcgccgacg gcgcggtgct caaccgccac cggaagctga tgcccaccaa ccccgagcgc      420
atggtctggg gctcggcgca tgccagcggg ctcaggacgg tccccacca gtgcggggcg      480
gtcggcgccc tgatctgctg ggaaagctac atgccgcttg cacgctacgc gctgtacgcc      540

```

```

caggggaatcg acctctacgt cacgccgacc tacgacagcg gcgagcgggc ggttgcgacc 600
atgcagcaca ttgccgcga aggcggctgc tgggtggtga gctgcggctc ggcgtttcag 660
gcgcgcgaag tcccggacgc gtttcgggg aagagcgagc ttttcgcga caacgacgag 720
tggatcaacc cgggcgactc ggtcgtggtc gcgccgggcg gcaaggctcg cgcggggccg 780
ctgcacaaag aacgcgcgat cctgtacgcc gagatcgacc tcgagcgggg cggcgtggcg 840
cgccgcagcc tggacgtggt cggccattat gcgcggccc acctcttcga cctgcacgtg 900
aacgcccgcc cgcaaagcgt ggttgaattg cgctga 936

```

<210> 68
 <211> 311
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 68
Met Pro Arg Val Ala Val Val Gln Arg Pro Pro Val Phe Leu Asp Arg
 1          5          10          15
Ala Ala Thr Leu Glu Asn Ala Val Ala Ser Leu Ala Glu Ala Ala Ser
 20          25          30
Asn Gly Ala Arg Leu Ala Val Phe Pro Glu Ala Leu Val Pro Gly Tyr
 35          40          45
Pro Ala Trp Met Trp Arg Leu Arg Pro Gly Pro Asp Met Ala Leu Thr
 50          55          60
Glu Arg Ile His Ala Arg Leu Arg Ala Asn Ser Val Ser Leu Ala Ala
 65          70          75          80
Asp Glu Leu Ala Pro Leu Arg Glu Ala Ala Arg Arg His Glu Leu Thr
 85          90          95
Val Val Cys Gly Leu His Glu Arg Asp Glu Ala Leu Gly Gly Gly Thr
100          105          110
Leu Tyr Asn Thr Val Val Thr Ile Gly Ala Asp Gly Ala Val Leu Asn
115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
130          135          140
Cys Gly Asp Ala Ser Gly Leu Arg Thr Val Pro Thr Gln Cys Gly Arg
145          150          155          160
Val Gly Ala Leu Ile Cys Trp Glu Ser Tyr Met Pro Leu Ala Arg Tyr
165          170          175
Ala Leu Tyr Ala Gln Gly Ile Asp Leu Tyr Val Thr Pro Thr Tyr Asp
180          185          190
Ser Gly Glu Arg Ala Val Ala Thr Met Gln His Ile Ala Arg Glu Gly
195          200          205
Gly Cys Trp Val Val Ser Cys Gly Ser Ala Phe Gln Ala Arg Asp Val
210          215          220
Pro Asp Ala Phe Pro Gly Lys Ser Glu Leu Phe Arg Asp Asn Asp Glu
225          230          235          240
Trp Ile Asn Pro Gly Asp Ser Val Val Val Ala Pro Gly Gly Lys Val
245          250          255
Val Ala Gly Pro Leu His Lys Glu Arg Ala Ile Leu Tyr Ala Glu Ile
260          265          270
Asp Leu Glu Arg Val Gly Val Ala Arg Arg Ser Leu Asp Val Val Gly
275          280          285
His Tyr Ala Arg Pro Asp Leu Phe Asp Leu His Val Asn Ala Arg Pro
290          295          300
Gln Ser Val Val Glu Leu Arg
305          310

```

<210> 69
 <211> 939
 <212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 69

```

gtgaccgagt ttccggacggt gcggggtcgca gcggtgcagg cgacgcgggt gaccctcgac      60
gccgatgcct cggtcgagaa ggcgatcggg ctgatcggcg aggcgggtggc cgggtggagcg      120
cagctcgctc tgctgcccga ggccttcgtg tcgctctacc cgtcgaacgc gtggggcgca      180
gcggccgccc gattcggcgg cttcgacgag ctctgggagc ggatgtgggc cagctcgctc      240
gacgtcccgg gcccgctggt cgaccggctg gtcgatgcgt gccgcaggca tgacgtggta      300
tgctgtatcg gcgtgaacga gcgcgaaagc gaaaggccgg ggtcgcttta caacacgatg      360
ctgaccctcg gcccgtcggg cctcctgcac cggcaccgca agctcatgcc gacgcaccac      420
gagcggctgt tccatgggat cggcgacggt caagacctcg gcgttggtga gaccgacgcg      480
ggacggatcg ggggactgat ctgctgggag aaccgaatgc cgctcgcgcg ctacgcggtc      540
taccagggtg gaccgcagat ctgggtcgcg ccgacggccg atgactccga cggctggctc      600
gcgagcatgc gccacatcgc gatcgagtgc ggcgcgttcg tcgtgtcggg gccgcagttc      660
atcccgcgct ccgcgttccc cgacgatttc cccgtcgagc taccgccggg caaggaggtg      720
ttcggccgcg gcggtgcggc gatcgtcgag ccgacctggg gcgagtaat cgccggggccg      780
ctctacgatc gggaggggat cgtgttcgcc gaactgtgacc tcgcacgcgg cttgcatgcc      840
aagcgctggt tcgactccgt cggccattac agccgcgcgg aggtgctcga tggcggcgctc      900
gagcgcgtcc cggcgccggt ggacggcgaa tcgccgtga      939

```

<210> 70

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 70

```

Val Thr Glu Phe Arg Thr Val Arg Val Ala Ala Val Gln Ala Thr Pro
1      5      10      15
Val Thr Leu Asp Ala Asp Ala Ser Val Glu Lys Ala Ile Gly Leu Ile
20     25     30
Gly Glu Ala Val Ala Gly Gly Ala Gln Leu Val Val Leu Pro Glu Ala
35     40     45
Phe Val Ser Leu Tyr Pro Ser Asn Ala Trp Ala Arg Ala Ala Ala Gly
50     55     60
Phe Gly Gly Phe Asp Glu Leu Trp Glu Arg Met Trp Ala Ser Ser Leu
65     70     75     80
Asp Val Pro Gly Pro Leu Val Asp Arg Leu Val Asp Ala Cys Arg Arg
85     90     95
His Asp Val Val Cys Val Ile Gly Val Asn Glu Arg Glu Ser Glu Arg
100    105    110
Pro Gly Ser Leu Tyr Asn Thr Met Leu Thr Leu Gly Pro Ser Gly Leu
115    120    125
Leu His Arg His Arg Lys Leu Met Pro Thr His His Glu Arg Leu Phe
130    135    140
His Gly Ile Gly Asp Gly Gln Asp Leu Gly Val Val Glu Thr Asp Ala
145    150    155    160
Gly Arg Ile Gly Gly Leu Ile Cys Trp Glu Asn Arg Met Pro Leu Ala
165    170    175
Arg Tyr Ala Val Tyr Gln Gly Gly Pro Gln Ile Trp Val Ala Pro Thr
180    185    190
Ala Asp Asp Ser Asp Gly Trp Leu Ala Ser Met Arg His Ile Ala Ile
195    200    205
Glu Ser Gly Ala Phe Val Val Ser Val Pro Gln Phe Ile Pro Ala Ser
210    215    220
Ala Phe Pro Asp Asp Phe Pro Val Glu Leu Pro Pro Gly Lys Glu Val

```

```

225                230                235                240
Phe Gly Arg Gly Gly Ala Ala Ile Val Glu Pro Thr Trp Gly Glu Val
                245                250                255
Ile Ala Gly Pro Leu Tyr Asp Arg Glu Gly Ile Val Phe Ala Asp Cys
                260                265                270
Asp Leu Arg Arg Gly Leu His Ala Lys Arg Trp Phe Asp Ser Val Gly
                275                280                285
His Tyr Ser Arg Ala Glu Val Leu Asp Gly Gly Val Glu Arg Val Pro
                290                295                300
Ala Pro Val Asp Gly Glu Ser Pro
305                310

```

<210> 71
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 71
atgccaaacg agaacaccaa cgccacattc aaagttgccg ctgtgcaggc ttgcctgtg      60
tttcttgatc gtgccgcaac aatcgacaag gcttgcgatt tgatcgccgc tgctggcggt      120
gaaggggcac gcttgattgt ctttccagaa gcattcatcc cgtcttatcc tgattgggta      180
tgggcaattc cttcgggtga agagggcgta ctcaatgagt tgtacgcaga tctgctatcc      240
aactcgggtca cgattcccag tgactcgacg gacaaactgt gcagagcagc caggcttgct      300
aatgcctacg tggatgatggg tatgagcgaa cgcaatgctg aggcaagcgg cgcgagcatg      360
tataacacgc tattgtatat tgatgcacag ggggagattc tgggcaagca tcggaagttg      420
gtgccaaacg gcggcgagcg gctagtcttg gcgcagggcg atggcagtac actgcaggtc      480
tatgatactc ccttagggaa actcgggtggc ttaatttgct gggagaatta tatgccactg      540
gcccgctata ccattgtatgc ctggggcaca caaatctatg tcgcggcaac gtgggatcgg      600
ggtcagccct ggctctctac tttagccac attgccaaag aaggcagggg gtatgtgatt      660
ggttggtgta tcgcgatgcg taaagacgat atcccagacc attatacaat gaaacagaag      720
ttttactcag atgcagatga gtggattaat attggcgata gtgcgattgt taatcccga      780
gggcaattta tcgctggacc ggtgcgcaag caggaagaga ttctctatgc ggagattgat      840
ccgcgcatgg tccaagggcc gaagtggatg ctgcacgtgg cgggacatta tgccaggccg      900
gatgtgttcg aactgattgt ccacacggat attcgaagga tgatcaaata ggaaaagaat      960
tcataa                                           966

```

<210> 72
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 72
Met Pro Asn Glu Asn Thr Asn Ala Thr Phe Lys Val Ala Ala Val Gln
1          5          10          15
Ala Ser Pro Val Phe Leu Asp Arg Ala Ala Thr Ile Asp Lys Ala Cys
20          25          30
Asp Leu Ile Ala Ala Ala Gly Gly Glu Gly Ala Arg Leu Ile Val Phe
35          40          45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
50          55          60
Ser Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Asp Leu Leu Ser
65          70          75          80
Asn Ser Val Thr Ile Pro Ser Asp Ser Thr Asp Lys Leu Cys Arg Ala
85          90          95
Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn

```

```

                100                105                110
Ala Glu Ala Ser Gly Ala Ser Met Tyr Asn Thr Leu Leu Tyr Ile Asp
                115                120                125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
                130                135                140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145                150                155                160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
                165                170                175
Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
                180                185                190
Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
                195                200                205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
                210                215                220
Ala Met Arg Lys Asp Asp Ile Pro Asp His Tyr Thr Met Lys Gln Lys
225                230                235                240
Phe Tyr Ser Asp Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
                245                250                255
Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
                260                265                270
Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
                275                280                285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu
                290                295                300
Leu Ile Val His Thr Asp Ile Arg Arg Met Ile Lys Ser Glu Lys Asn
305                310                315                320
Ser

```

<210> 73
 <211> 1035
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 73
atgacagcaa tagactcaac gtttaaagtc gccgccgttc aggctgcgcc ggtcttcttc      60
aatcgcgacg caaccgtgga gaaggcgtgc cggctgatca agtccgcggc agaggggaggc      120
gcgcgtctga tcgttttccc ggaagcgttc ataccggcct acccggactg ggtgtggacg      180
gtccctgccg gtgagcaagg cctgctcaac gacctctacg gccaactcgt cgaccagtcc      240
gtgacgattc ccagcgacat caccaccgag ttatgtaacg cggcacgggc agcaaacgcc      300
tatgtcgtga ttggtgtcaa cgagcgcaac gcggaggcaa gcaatggaag cctctacaac      360
tcgctcctct acatcgacgc aaacggcaaa attctcggta agcaccgcaa gctcgttccc      420
acaggcggag aacggctcgt gtggggcgag ggcgatggca gcacgctcga agcctacgac      480
acggagctgg gcaaactcgg cggctctcatt tgctgggaga actatatgcc gctggcacgc      540
tacgcgatgt acgcatgggg agtgcagctc tatgtcgccg cgacctggga ccgtggcggc      600
ccctggactg ccacgctgcg tcatgtcgcc aaggaaggtc agatgtacgt catcgggtgc      660
tgccaggccc tgcaacaagga tgacctgccg gagctagacg ggctgaagga gaagtactac      720
gccaacgcac gagagtggat caatgttggc gacagcgcta ttgtcggccc ggacggacaa      780
ttccttgtcg agcccgccg aatgcgggaa gacatcctct acgccgaggt ggacactcgc      840
aacttcgcgc gcccggaagt gatgttcgac gcggctggac actacgcgcg tcccgacatt      900
ttccaactca cagtgaaccg cgagcagcgg ccgatggtcc gcgtcgtcgg tgacagcagt      960
gaccagaagg agcggccgct cccggacgac ggacggctct ggtacgccta cagcaccaat     1020
cagcaccacg actga                                     1035

```

<210> 74
 <211> 344
 <212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 74

```

Met Thr Ala Ile Asp Ser Thr Phe Lys Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Val Phe Leu Asn Arg Asp Ala Thr Val Glu Lys Ala Cys Arg Leu
          20          25          30
Ile Lys Ser Ala Ala Glu Gly Gly Ala Arg Leu Ile Val Phe Pro Glu
          35          40          45
Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Thr Val Pro Ala Gly
          50          55          60
Glu Gln Gly Leu Leu Asn Asp Leu Tyr Gly Gln Leu Val Asp Gln Ser
65          70          75          80
Val Thr Ile Pro Ser Asp Ile Thr Thr Glu Leu Cys Asn Ala Ala Arg
          85          90          95
Ala Ala Asn Ala Tyr Val Val Ile Gly Val Asn Glu Arg Asn Ala Glu
          100          105          110
Ala Ser Asn Gly Ser Leu Tyr Asn Ser Leu Leu Tyr Ile Asp Ala Asn
          115          120          125
Gly Lys Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130          135          140
Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Ala Tyr Asp
145          150          155          160
Thr Glu Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
          165          170          175
Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Val Gln Leu Tyr Val
          180          185          190
Ala Ala Thr Trp Asp Arg Gly Gly Pro Trp Thr Ala Thr Leu Arg His
          195          200          205
Val Ala Lys Glu Gly Gln Met Tyr Val Ile Gly Cys Cys Gln Ala Leu
          210          215          220
His Lys Asp Asp Leu Pro Glu Leu Asp Gly Leu Lys Glu Lys Tyr Tyr
225          230          235          240
Ala Asn Ala Arg Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val Gly
          245          250          255
Pro Asp Gly Gln Phe Leu Val Glu Pro Val Arg Met Arg Glu Asp Ile
          260          265          270
Leu Tyr Ala Glu Val Asp Thr Arg Asn Phe Arg Gly Pro Lys Trp Met
          275          280          285
Phe Asp Ala Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Gln Leu Thr
          290          295          300
Val Asn Arg Glu Gln Arg Pro Met Val Arg Val Val Gly Asp Ser Ser
305          310          315          320
Asp Gln Lys Glu Arg Pro Leu Pro Asp Asp Gly Arg Leu Trp Tyr Ala
          325          330          335
Tyr Ser Thr Asn Gln His His Asp
          340

```

<210> 75

<211> 1125

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 75

```

atgagcacca ttgttaaagc cgctgcggtt caaatcagcc cagtctctcta cagccgcgag

```

60

```

gggacagtcg caaaagttgt gcggaagatc cacgaacttg gccaaaaggg ggtgcggttc 120
gccacgttcc cggagaccgt gggtccctac tatccatatt tttccgccgt ccagaccccc 180
attcaactat tgtccggaac cgagtacctg aagttgctcg accaaggcgt gaccgtgccg 240
tccacgacta ccgacgcaat cggggaggct gcccggaacg ccggcatggt tgtatctatc 300
ggcgtgaatg agcgtgacgg cgggaccctg tacaacgcgc agttgctctt cgatgcggat 360
gggaccttga ttacgcgtcg ccgcaagatc actcctacgc attacgagcg catgatctgg 420
ggccagggag atggttcggg tttgcgggcc gtcaagagcc aggttggtcg tattggccaa 480
cttgcatgct ttgagcacia caaccactg gcgcgttacg cgatgatggc cgatggcgag 540
caaatccatt cggccatgta tccaggttcc gcgttcggcg aggggttcgc ggaaaagatg 600
gaaatcaata tccgccagca tgcgttgagg tccgggtgct tcgttggtgaa tgcaacggcc 660
tggcttgacg ccagccagca ggcacaaatc atgaatgaca cgggttgcca aatcgggtccg 720
atctcgggag gttgctttac cagcatcgta acaccgacg gcacgtttct gggcgaacct 780
ctccggtcgg gtgagggcga ggatcatcgcc gatctcgatt tcaagctgat cgacaaacgc 840
aagatgttga tggactcgcg cggccactac agtcgcccg aattgctcag tctgctgac 900
gaccgcaccc ccaccgcgca cattcatgag cgaggtgcgc cgcagacgtc aggcgctgtg 960
caagaggcga cgaaagtggg ttccacacgc cgcctcctgc gtgacggaca atgggatcag 1020
ctcaatgcgg gagcggggcg acatacaggg aatggagaag cacagataga aatcatggcc 1080
cgggcccact cgggcacccc tggaattgaa gcgaaggag cctaa 1125

```

<210> 76

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 76

```

Met Ser Thr Ile Val Lys Ala Ala Val Gln Ile Ser Pro Val Leu
1      5      10      15
Tyr Ser Arg Glu Gly Thr Val Ala Lys Val Val Arg Lys Ile His Glu
20     25     30
Leu Gly Gln Lys Gly Val Arg Phe Ala Thr Phe Pro Glu Thr Val Val
35     40     45
Pro Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Ile Gln Leu Leu
50     55     60
Ser Gly Thr Glu Tyr Leu Lys Leu Leu Asp Gln Gly Val Thr Val Pro
65     70     75     80
Ser Thr Thr Thr Asp Ala Ile Gly Glu Ala Ala Arg Asn Ala Gly Met
85     90     95
Val Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn
100    105    110
Ala Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg
115    120    125
Lys Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp
130    135    140
Gly Ser Gly Leu Arg Ala Val Lys Ser Gln Val Gly Arg Ile Gly Gln
145    150    155    160
Leu Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met
165    170    175
Ala Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe
180    185    190
Gly Glu Gly Phe Ala Glu Lys Met Glu Ile Asn Ile Arg Gln His Ala
195    200    205
Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala
210    215    220
Ser Gln Gln Ala Gln Ile Met Asn Asp Thr Gly Cys Gln Ile Gly Pro
225    230    235    240
Ile Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Thr Phe
245    250    255
Leu Gly Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu

```

```

                260                265                270
Asp Phe Lys Leu Ile Asp Lys Arg Lys Met Leu Met Asp Ser Arg Gly
                275                280                285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
                290                295                300
Thr Ala His Ile His Glu Arg Gly Ala Pro Gln Thr Ser Gly Ala Val
305                310                315                320
Gln Glu Ala Thr Lys Val Gly Ser His Ala Pro Leu Leu Arg Asp Gly
                325                330                335
Gln Trp Asp Gln Leu Asn Ala Gly Ala Gly Arg His Thr Gly Asn Gly
                340                345                350
Glu Ala Gln Ile Glu Ile Met Ala Ala Ala His Ser Gly Thr Arg Gly
                355                360                365
Ile Glu Ala Lys Gly Ala
                370

```

<210> 77

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 77

```

atgccaaacc ccagcgatca tttcaaaatc gccgctgttc aggcctcgcc cgtgtttctg      60
gaccgggagg ccactgtgga aaaggcctgc cggttgatcg ccgaagccgc aaagcagggc      120
gtccgcctca tcgtctttcc ggaatcggtc atcccgcact acccgactg ggtatgggcc      180
gttcccccgga gaagggaag aatcctgaac cagctgtatt ctgaattcct ggccaatgcc      240
gtcgaatgttc ccggcgcggc gaccgaacaa cttgcccgag ctgcacgaat ggccggcgcc      300
tatgtgatta tgggcgtcac cgaaagagac acctcggccca gcggggccag cctctacaac      360
acctgtctct acttcagccc cgaaggcatc ctaatgggca aacaccggaa gctggttccc      420
acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac      480
actccgctgg gaaagatcgg cgggctgatc tgctgggaga actacatgcc cctggcccgg      540
tacacgatgt acgctgggg caccagatt tacatcgccg ccacctggga ccgcggggaa      600
ccgtggctct ccaccctgcg gcatatcgca aaggaaggaa gggctctacg catcggtgc      660
tgcacgccc tgcgccaggg ggatatcccg gaccggttcg agtacaaggg aaaattttat      720
tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaacct ggacggggaa      780
ttcatcgccg ggccggtgcg gacgaaggag gagatcctgt atgccgagat agacccccgg      840
cagatgcggg gcccgaagt gatgctcgat gtggccgggtc attacgcccg gccggatatc      900
ttcgagctca tcgtccaccg gaatccccac ccgatgatca aaatcgccga agacaggggc      960
acggggatcg cctcaagttt gattcgcccc cgccctaacc ttcccccatc aagggggagg     1020
aaatcggcaa gaagcaaacg caagcccaaa aaatga                                1056

```

<210> 78

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 78

```

Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
 1                5                10                15
Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
                20                25                30
Ile Ala Glu Ala Ala Lys Gln Gly Val Arg Leu Ile Val Phe Pro Glu
                35                40                45
Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50                55                60

```

```

Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
65      70      75      80
Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
      85      90      95
Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
      100     105     110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
      115     120     125
Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
      130     135     140
Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
145      150     155     160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
      165     170     175
Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
      180     185     190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
      195     200     205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
      210     215     220
Arg Gln Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gly Lys Phe Tyr
225      230     235     240
Ser Gly Ser Arg Glu Trp Ile Asn Glu Gly Asp Ser Ala Ile Val Asn
      245     250     255
Pro Asp Gly Glu Phe Ile Ala Gly Pro Val Arg Thr Lys Glu Glu Ile
      260     265     270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Arg Gly Pro Lys Trp Met
      275     280     285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile
      290     295     300
Val His Arg Asn Pro His Pro Met Ile Lys Ile Ala Glu Asp Arg Gly
305      310     315     320
Thr Gly Ile Ala Ser Ser Leu Ile Arg Pro Arg Pro Asn Leu Pro Pro
      325     330     335
Ser Arg Gly Arg Lys Ser Ala Arg Ser Lys Arg Lys Pro Lys Lys
      340     345     350

```

<210> 79
 <211> 990
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 79
atgacgaaga aaagcggccg cgattcgttt cgggtcgctg cgggtccaggc ctcgtccgtc      60
tacctggatc gggaacggag catcgagaaa gcgtgccggc tgatcgacga cgcgggacga      120
aacgacgccg acctcgtcgt gttccccgaa gccttcgtgc ccggataccc actgtgggtg      180
tggctcgttc cgccggggcg caccgcagac ttgcgctccg cttatgcgac gctccacgcc      240
aacgcgatca gcattccgga cgactccacc gatcggctgt ggcgccgccg aaaagacgcc      300
ggcgtcgccg tcgcgatcgg cgtcaacgaa cgcaacaccg aagcgagcgg catgagcctg      360
ttcaacacgc tgctctatat cggagcggac ggccggattc tcggaaaaca ccggaagctg      420
gtaccgaccg gcggcgaaac gctcgtctgg gcatctggcg acggcagcga cctcgaggtc      480
tactcgctgc cgcttcggtc cgtaagcgga ctgatctgct gggagcacta catgccgctc      540
gcccggtatg cgctcgccgc gtggggcgaa caggtgcacg tcgctccaac ctgggatcgt      600
ggcgagccgt ggctgtccac gctaaggcac atcgcgaaag aaggccgcgt tctcgtcgtc      660
ggctgctgtc aagccgtgcg caaggacgac atccctgaca cgctcgcgtt caagtccaaa      720
tacctcgtag acgtggacgg ctggatcaac ccaggtggca gcgtcatcat caatcctgac      780
ggcaaggtcg tcgcgggacc ggcgatggaa accgaaactg tactgtacgc ggaccttcgc      840
accgagcagc tcgtcggacc gcgctggcag ctcgacgtcg gcggacatta cgctcgctccg      900

```

gacgtcttcg agctcgtcgt ccacggcat ccgaagccgt tgattcggac agcgaccggt 960
 gtcaggcgcc gcaagcgtgc acgtcgctaa 990

<210> 80
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 80
 Met Thr Lys Lys Ser Gly Arg Asp Ser Phe Arg Val Ala Ala Val Gln
 1 5 10 15
 Ala Ser Ser Val Tyr Leu Asp Arg Glu Arg Ser Ile Glu Lys Ala Cys
 20 25 30
 Arg Leu Ile Asp Asp Ala Gly Arg Asn Asp Ala Asp Leu Val Val Phe
 35 40 45
 Pro Glu Ala Phe Val Pro Gly Tyr Pro Leu Trp Val Trp Leu Val Pro
 50 55 60
 Pro Gly Arg Thr Ala Asp Leu Arg Ser Ala Tyr Ala Thr Leu His Ala
 65 70 75 80
 Asn Ala Ile Ser Ile Pro Asp Asp Ser Thr Asp Arg Leu Cys Ala Ala
 85 90 95
 Ala Lys Asp Ala Gly Val Ala Val Ala Ile Gly Val Asn Glu Arg Asn
 100 105 110
 Thr Glu Ala Ser Gly Met Ser Leu Phe Asn Thr Leu Leu Tyr Ile Gly
 115 120 125
 Ala Asp Gly Arg Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Ser Gly Asp Gly Ser Asp Leu Glu Val
 145 150 155 160
 Tyr Ser Leu Pro Phe Gly Arg Val Ser Gly Leu Ile Cys Trp Glu His
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Ala Leu Ala Ala Trp Gly Glu Gln Val
 180 185 190
 His Val Ala Pro Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Leu Val Val Gly Cys Cys Gln
 210 215 220
 Ala Val Arg Lys Asp Asp Ile Pro Asp Thr Leu Ala Phe Lys Ser Lys
 225 230 235 240
 Tyr Leu Ala Asp Val Asp Gly Trp Ile Asn Pro Gly Gly Ser Val Ile
 245 250 255
 Ile Asn Pro Asp Gly Lys Val Val Ala Gly Pro Ala Met Glu Thr Glu
 260 265 270
 Thr Val Leu Tyr Ala Asp Leu Arg Thr Glu Gln Leu Val Gly Pro Arg
 275 280 285
 Trp Gln Leu Asp Val Gly Gly His Tyr Ala Arg Pro Asp Val Phe Glu
 290 295 300
 Leu Val Val His Arg His Pro Lys Pro Leu Ile Arg Thr Ala Thr Gly
 305 310 315 320
 Val Arg Arg Arg Lys Arg Ala Arg Arg
 325

<210> 81
 <211> 993
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 81
 atgaaagtcg tcaaagccgc cgctgtccag ttcagcccgg tgctctatag ccgcgaagcg 60
 accgtcgcca aggtcgctccg gaaaatccac gagctcggtc agaaaggcgt gcagttcgcc 120
 acctttcctg aaacggctcgt gccttattac ccttacttcg cggccgtcca gacgggcatc 180
 gagctcttgt cgggcaccga acatctgcgc ctgctcgaac aggccgtgac tgtgccctcc 240
 gctgcgaccg atgcaatcgg cgaagccgcg cgacaggccg gcatggtcgt gtccatcggc 300
 gtcaatgagc gtgacggcgg cacgctttac aacacgcaac tgctcttcga tgccgacggg 360
 acgctgatcc agcgcgcgcg caagatcacg ccgacccatt tcgaacgcat gatctggggg 420
 cagggagatg gctcgggctt gcgtgcagtc gacagcgacg tcggccgcat cggccagctc 480
 goatgcttcg agcacaacaa cccgcttgca cgttacgcaa tgatcgccga cggcgagcag 540
 atccattcag cgatgtaccc tggctcggcc tttggcgagg gcttcgccca gcgtatggag 600
 atcaacatcc gccagcatgc gctcgagtcc gccgctttcg tcgtcaacgc aacggcggtg 660
 cttgacgccc accagcaggc gcaaatcatg aaggacaccg gttgtggaat cggctccgatc 720
 tcggggcggt gcttcaccac gatcgcttct cctgacggta tgctgatggc cgatccgctt 780
 cgctcggggc aaggcgaagt gattgtcgat ctcgacttca cgcagatcga ccgccgcaag 840
 atgctgatgg actcggccgg ccactacaac cgccctgaac tgctgagtct gatgatcgac 900
 cgtacgccgg ctgcgcatgt tcacgaacgc gcttcgcgcc cgatgaccgt cgacgaccag 960
 agttccggcg atctgcgcac ccaggttgca tga 993

<210> 82

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 82
 Met Lys Val Val Lys Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Ala Lys Val Val Arg Lys Ile His Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Gln Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met

```

                245                250                255
Ala Asp Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
                260                265                270
Phe Thr Gln Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
                275                280                285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Ala
                290                295                300
Ala His Val His Glu Arg Ala Ser Arg Pro Met Thr Val Asp Asp Gln
305                310                315                320
Ser Ser Gly Asp Leu Arg Thr Gln Val Ala
                325                330

```

<210> 83
 <211> 1071
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 83
atgatgagtt cagcccgtgt aataaaactc gccgcagcac agctttcacc tgtgctgccg      60
ggggagtcca caaatagccg cgacggcacc attgccaaag tcgtcgcggc gattgcggag      120
gctgcgcgcg ccggcgcgca gctgatcgtg tttcccgaaa cgggtggtgcc gtattaccgc      180
tatttctcgt tcattacgcc ggcggtgacg atgggggagg agcatttgcg cttgtacgat      240
cagtctgtcg tgggtgccgag cgccgccact gatactgttg ccgccgctgc aaaaaaacac      300
agcatggttg tcgtgctcgg tattaacgaa cgcgatcacg gcacgctcta caacgcgcaa      360
ttaattttcg atgcgagcgg cgaattatta ttaaaacgcc gaaaaattac cccgacctat      420
cacgagcgca tgggtgtgggg tcagggcgac ggcagcggtt tgaaaaccgt cgacaccgcg      480
atcggccgtg tcggtgcgct cgcctgctgg gaacattaca acccattggc gcgttacagc      540
ctgatggccc agcacgaaga aattcattgc agtcaatttc cggggtcatt ggtcggggcca      600
attttcgccg agcaaattgga agtgacaatg cgccaccacg cgctcgaatc cggttgcttc      660
gtcgttaatg caacggcgtg gttatcgga ggcgaaattc aatcgatcag cagcgatccc      720
gcgatgcaaa aagcactgcg cggcgggttg tacaccgcaa ttatttcgcc cgaaggcaaa      780
catctgtgcg agccgctacg cgaaggtgaa ggtttgattt ttgccgaagc cgatatggcg      840
ctcattacca aacgcaaacg catgatggat tcgggttggtc attacgcgcg acccgaattg      900
ctgtoctgtg taatcgacca tcgcgccacc acaccattgc atagcgtcac cgcgagtgat      960
gccgcgcgcg taaaaaatac tcggagttcc gctcatgaat cagccgatag tgaaccatc     1020
cgcgagtcag ttaataacgg aactccaatc gcacggcttg cgcctagttg a           1071

```

<210> 84
 <211> 356
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 84
Met Met Ser Ser Ala Arg Val Ile Lys Leu Ala Ala Ala Gln Leu Ser
 1                5                10                15
Pro Val Leu Pro Gly Glu Ser Thr Asn Ser Arg Asp Gly Thr Ile Ala
                20                25                30
Lys Val Val Ala Ala Ile Ala Glu Ala Ala Arg Ala Gly Ala Gln Leu
                35                40                45
Ile Val Phe Pro Glu Thr Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe
                50                55                60
Ile Thr Pro Ala Val Thr Met Gly Ala Glu His Leu Arg Leu Tyr Asp
65                70                75                80
Gln Ser Val Val Val Pro Ser Ala Ala Thr Asp Thr Val Ala Ala Ala
                85                90                95

```

Ala Lys Lys His Ser Met Val Val Val Leu Gly Ile Asn Glu Arg Asp
 100 105 110
 His Gly Thr Leu Tyr Asn Ala Gln Leu Ile Phe Asp Ala Ser Gly Glu
 115 120 125
 Leu Leu Leu Lys Arg Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met
 130 135 140
 Val Trp Gly Gln Gly Asp Gly Ser Gly Leu Lys Thr Val Asp Thr Ala
 145 150 155 160
 Ile Gly Arg Val Gly Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu
 165 170 175
 Ala Arg Tyr Ser Leu Met Ala Gln His Glu Glu Ile His Cys Ser Gln
 180 185 190
 Phe Pro Gly Ser Leu Val Gly Pro Ile Phe Ala Glu Gln Met Glu Val
 195 200 205
 Thr Met Arg His His Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala
 210 215 220
 Thr Ala Trp Leu Ser Glu Ala Gln Ile Gln Ser Ile Ser Ser Asp Pro
 225 230 235 240
 Ala Met Gln Lys Ala Leu Arg Gly Gly Cys Tyr Thr Ala Ile Ile Ser
 245 250 255
 Pro Glu Gly Lys His Leu Cys Glu Pro Leu Arg Glu Gly Glu Gly Leu
 260 265 270
 Ile Phe Ala Glu Ala Asp Met Ala Leu Ile Thr Lys Arg Lys Arg Met
 275 280 285
 Met Asp Ser Val Gly His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu
 290 295 300
 Ile Asp His Arg Ala Thr Thr Pro Leu His Ser Val Thr Ala Ser Asp
 305 310 315 320
 Ala Ala Ala Val Lys Asn Thr Arg Ser Ser Ala His Glu Ser Ala Asp
 325 330 335
 Ser Glu Thr Ile Arg Glu Ser Val Asn Asn Gly Thr Pro Ile Ala Arg
 340 345 350
 Leu Ala Pro Ser
 355

<210> 85
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 85
 atgggtcttg ttcattcagaa atacaagggtt gcggtggttc aggcggcgcc ggtctttctc 60
 gacctgatg cgacggtgga caagacgatc gccctgatcg agcaggccgc agcacagggc 120
 gcgaagctga tcgcgtttcc cgagaccttc attcccggat atccgtggca gatctggctt 180
 ggggcgccc cctgggcgat cggccgtggc ttcgtgcagc gctatttcga taactcgttg 240
 tcatttgaca gccgcaggc cgaaaaaatt cgcaaggccg tcaagcgcgc caagctgacc 300
 gcggtgatcg gogtctccga acgcgacggc ggcagcctct atatcgcca atggctgatc 360
 ggtcccgaag gcgagaccat tgcgaagcgc cgcaagctgc ggccgaccca tgccgaacgc 420
 accgtgttcg ggcagggcga cggcagcgac ctgcgcgtcc atgatcgcg cgcagctggga 480
 cggtcgggtg caatgtgctg ctgggagcat ctgcagccgc tgtcgaaata cgcgatgtac 540
 gccagaacg agcaggttca cgtcggcgcc tggccgagct tctcattgta cgaccattc 600
 gcccatgcgc ttggctggga agtaaaacac gcggcgagca aggtttatgc tgtcgagggc 660
 tcatgtttct tctcggccc gtgcgcggtg gtctcgcagg ccatgatcga cgagctctgc 720
 gattcccccg aaaagcacgc cttcctgcac gctggcggcg gccacgcggt aatctatggg 780
 ccggacggga gttcgtctgc cgacaaactt ccaccgatc agggaggcat tctgtatgcc 840
 gatatacatc toggcatgat cggcgtggga aagaacgccg ccgacccgcg aggaactat 900
 tccaggccgg acgtcacgcg cgtgctgctc aacacttccc gcgccaatcg cgtcgagcat 960
 ttttcattgc cgatcgatgc cgaggtcatg agcgaaatca gacttcaggc ctga 1014

<210> 86
 <211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 86
 Met Gly Leu Val His Gln Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Ile Ala Leu
 20 25 30
 Ile Glu Gln Ala Ala Ala Gln Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp Gln Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ser Phe Asp Ser Pro Gln Ala Glu Lys Ile Arg Lys Ala Val Lys Arg
 85 90 95
 Ala Lys Leu Thr Ala Val Ile Gly Val Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Gly Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Ala Asp Val Gly
 145 150 155 160
 Arg Leu Gly Ala Met Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Gly Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Phe
 210 215 220
 Leu Gly Pro Cys Ala Val Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Ser Pro Glu Lys His Ala Phe Leu His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Asp Lys Leu Pro Pro
 260 265 270
 Asp Gln Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Thr Ser Arg Ala Asn Arg Val Glu His
 305 310 315 320
 Phe Ser Leu Pro Ile Asp Ala Glu Val Met Ser Glu Ile Arg Leu Gln
 325 330 335
 Ala

<210> 87
 <211> 1062
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 87

atggcggaat	cgaagctgaa	ggtcgccgca	attcaagttg	cgcccgtgtt	catggatcgc	60
gatgccacga	tcgcccgcgc	ctgcgagcgg	atcgccgaag	ccgcccgcgc	cggcgcggag	120
ttggtggtct	ttcccgcaggc	attcgtgccc	gggtatcccg	actggatctg	ggtggcgcgg	180
ccaagccaac	gcaaactgct	caatgatctt	tacgcgcacc	tcgtctcgca	gtcggtcgac	240
gtgccgtcgg	cctccgtgga	tcgtttgcgc	gacgcggctc	gcgacggcgg	ggtcacgggtg	300
gtgatcggcg	tcaacgagcg	caacaccgaa	gcgagcggcg	cgagcctcta	caacaccgcg	360
ctcgtgatcg	gtccactggg	gcagctgata	ggccgccacc	gcaagcttgt	gccgaccggg	420
ccggagcgca	tggtgtgggc	gcagggcgac	ggcagcacgc	tcgacgtcta	cgacacaccc	480
gtcggcaagc	tttcgacgtt	gatctgctgg	gagaactaca	tgccgctcgc	gcgctacgcc	540
atggcggcgt	ggggcgcgcg	catccacgtc	gccggcacgt	gggaccgcgg	cgagccgtgg	600
atctcgacca	tgcgctcatgt	ggcgacggag	ggccgcgtat	tcgtgattag	ctgttgcatg	660
gcgctgcgca	aacgagacat	tcccgcggag	ctcgagttcg	cgatgctcta	tcccgcgggg	720
cgcgaaatgga	tcaacgccgg	tgattcgtct	gtcgtgaatc	ccgctggcca	gatcatcgct	780
gggcccgttcg	acgagcagga	aggaatcctc	tacgccgagc	tcgagcgcaa	tcagatgacc	840
ggtccgcgtt	ggatgttcga	cgccgcgggc	cattacgcgc	gaccggacgt	cttccaactc	900
acggtaaacc	gctccccgcg	cccgatgctg	cgggaggcgg	gggcaaagac	gagtgaaggca	960
aacacgagag	atgccgtacc	catggacagc	acgccctcga	gatcgcggcc	ccgcgcgggtg	1020
gcgcgaaagg	ccgcacgcac	cggtcgctcc	aagcggcggt	ga		1062

<210> 88

<211> 353

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 88

Met	Ala	Glu	Ser	Lys	Leu	Lys	Val	Ala	Ala	Ile	Gln	Val	Ala	Pro	Val
1				5					10					15	
Phe	Met	Asp	Arg	Asp	Ala	Thr	Ile	Ala	Arg	Ala	Cys	Glu	Arg	Ile	Ala
			20					25					30		
Glu	Ala	Ala	Arg	Ala	Gly	Ala	Glu	Leu	Val	Val	Phe	Pro	Glu	Ala	Phe
			35				40					45			
Val	Pro	Gly	Tyr	Pro	Asp	Trp	Ile	Trp	Val	Ala	Arg	Pro	Ser	Gln	Arg
	50				55						60				
Lys	Leu	Leu	Asn	Asp	Leu	Tyr	Ala	His	Leu	Val	Ser	Gln	Ser	Val	Asp
65					70				75					80	
Val	Pro	Ser	Ala	Ser	Val	Asp	Arg	Leu	Arg	Asp	Ala	Ala	Arg	Asp	Gly
				85					90					95	
Gly	Val	Thr	Val	Val	Ile	Gly	Val	Asn	Glu	Arg	Asn	Thr	Glu	Ala	Ser
			100					105					110		
Gly	Ala	Ser	Leu	Tyr	Asn	Thr	Ala	Leu	Val	Ile	Gly	Pro	Leu	Gly	Gln
			115				120					125			
Leu	Ile	Gly	Arg	His	Arg	Lys	Leu	Val	Pro	Thr	Gly	Pro	Glu	Arg	Met
			130			135					140				
Val	Trp	Ala	Gln	Gly	Asp	Gly	Ser	Thr	Leu	Asp	Val	Tyr	Asp	Thr	Pro
145					150				155						160
Val	Gly	Lys	Leu	Ser	Thr	Leu	Ile	Cys	Trp	Glu	Asn	Tyr	Met	Pro	Leu
			165					170						175	
Ala	Arg	Tyr	Ala	Met	Ala	Ala	Trp	Gly	Ala	Arg	Ile	His	Val	Ala	Gly
			180				185					190			
Thr	Trp	Asp	Arg	Gly	Glu	Pro	Trp	Ile	Ser	Thr	Met	Arg	His	Val	Ala
		195				200					205				
Thr	Glu	Gly	Arg	Val	Phe	Val	Ile	Ser	Cys	Cys	Met	Ala	Leu	Arg	Lys
	210				215					220					
Arg	Asp	Ile	Pro	Ala	Glu	Leu	Glu	Phe	Ala	Met	Leu	Tyr	Pro	Asp	Gly
225					230				235						240

Arg Glu Trp Ile Asn Ala Gly Asp Ser Leu Val Val Asn Pro Ala Gly
 245 250 255
 Gln Ile Ile Ala Gly Pro Leu His Glu Gln Glu Gly Ile Leu Tyr Ala
 260 265 270
 Glu Leu Glu Arg Asn Gln Met Thr Gly Pro Arg Trp Met Phe Asp Ala
 275 280 285
 Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln Leu Thr Val Asn Arg
 290 295 300
 Ser Pro Arg Pro Met Leu Arg Glu Ala Gly Ala Lys Thr Ser Glu Ala
 305 310 315 320
 Asn Thr Arg Asp Ala Val Pro Met Asp Ser Thr Pro Ser Arg Ser Arg
 325 330 335
 Pro Arg Ala Val Ala Arg Lys Ala Ala Arg Thr Gly Arg Ser Lys Arg
 340 345 350
 Arg

<210> 89
 <211> 918
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 89
 atgaataacca aagaagtaaa ggtcgcagcc gctcaatttg cccacacattt tctgaatttg 60
 agcaaaacgg tggaaaaaac ctgcaacttg atttccgaag caggcaaaaaa tggagcaaaag 120
 ctcatgtgat ttccggaagc cttcctctct gggtatcccg attgggtctg gtttaattccc 180
 aatggaaatt caacaatgct ggatgattta tatcaggaat tggttgagaa cgctgtaaca 240
 atccctgatt caacaacaca gaaactctgt caggcagcaa aagatgccgg ggtatatgtc 300
 gcagtcggta tccatgaaag aaatgcagaa gcaagtggct tcacactttt caataccctt 360
 ctatacatta atgatcaagg cagcatcatt ggaaaacacc gaaaactgat cccaacaggg 420
 ggcgaacgcc tggctctggg gcagggtaat ggggatacgc ttgctgcatt cgatacacac 480
 tttggcaaat tgggaggatt gctttgctgg gaaaactaca tgcccctggc tcggcaagct 540
 atgtacgcag ttgggactga agtttatgtt gcccacactt gggactccag tgagaattgg 600
 ttgctgagta tgcgccatat agccagagag ggcggcatgt ttgtgatcaa tgtttgccag 660
 gctgtccgaa aagacgatat tcctgaccgc tatgcattca agcaactcta ttctggtaat 720
 tcagaatgga tcaatagcgg caacagttgc atcatcaatc cgcgcggtga aatcattgcc 780
 ggaccatcct caaacaggca agaaatactc tacgcagatt tagatctgag tttgattaca 840
 aaatctaaac gcatgttcga tgttaccggg cattatgccc ggccggatgt gtttagatat 900
 gaaatcaaaa aaagctag 918

<210> 90
 <211> 305
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 90
 Met Asn Thr Lys Glu Val Lys Val Ala Ala Ala Gln Phe Ala Pro His
 1 5 10 15
 Phe Leu Asn Leu Ser Lys Thr Val Glu Lys Thr Cys Asn Leu Ile Ser
 20 25 30
 Glu Ala Gly Lys Asn Gly Ala Lys Leu Ile Val Phe Pro Glu Ala Phe
 35 40 45
 Leu Ser Gly Tyr Pro Asp Trp Val Trp Leu Ile Pro Asn Gly Asn Ser
 50 55 60
 Thr Met Leu Asp Asp Leu Tyr Gln Glu Leu Val Glu Asn Ala Val Thr

65					70					75				80
Ile	Pro	Asp	Ser	Thr	Thr	Gln	Lys	Leu	Cys	Gln	Ala	Ala	Lys	Asp
				85					90					95
Gly	Val	Tyr	Val	Ala	Val	Gly	Ile	His	Glu	Arg	Asn	Ala	Glu	Ala
			100					105					110	
Gly	Phe	Thr	Leu	Phe	Asn	Thr	Leu	Leu	Tyr	Ile	Asn	Asp	Gln	Gly
		115				120						125		
Ile	Ile	Gly	Lys	His	Arg	Lys	Leu	Ile	Pro	Thr	Gly	Gly	Glu	Arg
	130					135					140			
Val	Trp	Gly	Gln	Gly	Asn	Gly	Asp	Thr	Leu	Ala	Ala	Phe	Asp	Thr
145					150					155				160
Phe	Gly	Lys	Leu	Gly	Gly	Leu	Leu	Cys	Trp	Glu	Asn	Tyr	Met	Pro
			165					170					175	
Ala	Arg	Gln	Ala	Met	Tyr	Ala	Val	Gly	Thr	Glu	Val	Tyr	Val	Ala
			180					185					190	
Thr	Trp	Asp	Ser	Ser	Glu	Asn	Trp	Leu	Leu	Ser	Met	Arg	His	Ile
		195				200						205		
Arg	Glu	Gly	Gly	Met	Phe	Val	Ile	Asn	Val	Cys	Gln	Ala	Val	Arg
	210					215					220			
Asp	Asp	Ile	Pro	Asp	Arg	Tyr	Ala	Phe	Lys	Gln	Leu	Tyr	Ser	Gly
225					230					235				240
Ser	Glu	Trp	Ile	Asn	Ser	Gly	Asn	Ser	Cys	Ile	Ile	Asn	Pro	Arg
			245					250					255	
Glu	Ile	Ile	Ala	Gly	Pro	Ser	Ser	Asn	Arg	Gln	Glu	Ile	Leu	Tyr
			260					265					270	
Asp	Leu	Asp	Leu	Ser	Leu	Ile	Thr	Lys	Ser	Lys	Arg	Met	Phe	Asp
	275						280					285		
Thr	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Phe	Arg	Tyr	Glu	Ile	Lys
	290					295					300			
Ser														
305														

<210> 91
 <211> 939
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 91					60
atgaccaaaa	tgcgtgtcat	tcaagaacct	ccggtctatc	tgaatctgag	taaatcgatg
gacagagcgg	tcgacttgat	tgccaatgct	gcaagcaagg	ggtgtgagtt	gatttgtttt
cccgaagcct	ggcttgacag	ttacccacc	ttcgtctggc	gtcttgccgc	gggcagcgga
atgggaaaaa	ctgatgagct	ttacgcgcgt	ttgctcgcca	actcggtcga	ccgtagcaaa
gaggggctta	gaccattgca	ggaggccgca	aaggagcatg	gcgttgatcat	tgtgctgggt
tatcaagagg	tggatggcgc	gggaagcagc	agcacgatct	tcaacagctg	tgcgattatt
gatgcggacg	ggcgactggc	caacaatcat	cgcaagtga	tgcccaccaa	tccggagagg
atgggtttggg	gtttttggcg	cggttcaggc	ctgaacgtcg	ttgacaccgc	ggtgggcagg
atcggcacgc	tgatttgctg	ggaaaactac	atgccgttag	cgcgctacgc	gctgtatgtc
caaaacatcg	aaatctatgt	tgccccgact	tgggacagtg	gtgccatgtg	gcaggcgacc
ctgcagcata	tcgcgcgcga	aggtggctgc	tgggtcatcg	gatgtgcaac	gtcgctggaa
gcctctgaca	tcccggacga	cgttcccat	cgggatgagc	tattcccgaa	caaagacgaa
tgggtaaacc	ctggcgatgc	ggtggtttat	aagccatttg	gcgccattgt	ggccggcccc
atgcatcagg	aaaaggggct	tctcatcgca	gagttggacg	tgcgcgctgt	tcagtcgtca
cgtcggaagt	tcgatgcgag	cgggcactac	gctcgccccg	atgtcttcaa	actgcatgtg
aatcgcaccg	cgatgcggcc	agttgatttc	acgaattag		939

<210> 92
 <211> 312
 <212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 92

```

Met Thr Lys Ile Ala Val Ile Gln Glu Pro Pro Val Tyr Leu Asn Leu
 1          5          10
Ser Lys Ser Met Asp Arg Ala Val Asp Leu Ile Ala Asn Ala Ala Ser
 20          25          30
Lys Gly Cys Glu Leu Ile Val Phe Pro Glu Ala Trp Leu Ala Gly Tyr
 35          40          45
Pro Thr Phe Val Trp Arg Leu Ala Pro Gly Ser Gly Met Gly Lys Thr
 50          55          60
Asp Glu Leu Tyr Ala Arg Leu Leu Ala Asn Ser Val Asp Arg Ser Lys
 65          70          75          80
Glu Gly Leu Arg Pro Leu Gln Glu Ala Ala Lys Glu His Gly Val Val
 85          90          95
Ile Val Leu Gly Tyr Gln Glu Val Asp Gly Ala Gly Ser Ser Ser Thr
 100          105          110
Ile Phe Asn Ser Cys Ala Ile Ile Asp Ala Asp Gly Arg Leu Ala Asn
 115          120          125
Asn His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
 130          135          140
Phe Gly Asp Gly Ser Gly Leu Asn Val Val Asp Thr Ala Val Gly Arg
 145          150          155          160
Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
 165          170          175
Ala Leu Tyr Val Gln Asn Ile Glu Ile Tyr Val Ala Pro Thr Trp Asp
 180          185          190
Ser Gly Ala Met Trp Gln Ala Thr Leu Gln His Ile Ala Arg Glu Gly
 195          200          205
Gly Cys Trp Val Ile Gly Cys Ala Thr Ser Leu Glu Ala Ser Asp Ile
 210          215          220
Pro Asp Asp Val Pro His Arg Asp Glu Leu Phe Pro Asn Lys Asp Glu
 225          230          235          240
Trp Val Asn Pro Gly Asp Ala Val Val Tyr Lys Pro Phe Gly Gly Ile
 245          250          255
Val Ala Gly Pro Met His Gln Glu Lys Gly Leu Leu Ile Ala Glu Leu
 260          265          270
Asp Val Ala Ala Val Gln Ser Ser Arg Arg Lys Phe Asp Ala Ser Gly
 275          280          285
His Tyr Ala Arg Pro Asp Val Phe Lys Leu His Val Asn Arg Thr Ala
 290          295          300
Met Arg Pro Val Asp Phe Thr Asn
305          310

```

<210> 93

<211> 978

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 93

```

atgcccacatca tcaaagccgc tgccgtgcaa atcagcccgg tgctttacag tcgcgaaggc 60
accgtggaca aggtctgtca acagatcatc gacctcggtc ggcaaggcgt gcagttcgcc 120
gtctttccgg aaacggtggt gccttactac ccgtactttt cgtttgtgca gccggccttt 180
gccatgggag cacagcacct caagttgctg gatcaatcgg tgacagtgcc gtcggccgcc 240
accttgGCCa tcggtgaagc ttgcaagcaa gcaggggatag tgggtgtccat cggcgtcaac 300

```

```

gaacgcgatg gcggtacgat ctacaacgcg caattactct tcgatgccga cggcagcctg 360
attcagcatc gccgcaaaat caccgccacc tatcacgaac gcatgggtctg ggggcaaggc 420
gatgggttccg gcctgcgcgc catcgacagt gcagtggggc gcattggctc cctggcctgt 480
tgggagcatt acaaccgcgt ggctcgttat gccttgatgg ccgatggcga gcagatccac 540
gccgcgatgt ttcccggtc gctgggtgggc gacatttttg ccgagcagat cgaagtcacc 600
atccgccatc acgccttgga gtccggctgt ttcgtggtca acgccaccgc ctggctggac 660
gccgatcagc agggccaaat catgcaagac accggttgca gcctcggccc gatctcgggt 720
ggctgcttca ccgccatcgt ttcccctgaa ggcaagttgc tcggtgagcc gctgcgttcc 780
ggcgaagggg tggatgatcg cgatctcgat ctggcactga tcgataagcg taaacggatg 840
atggattcgg tcgggcatta cagtcgcccg gaactgctca gcctgttgat cgaccgcacg 900
cccacagcgc atgtgcata acgcagcgcg cactgggtgg ctgtcgctac cgaggagttc 960
gatcatgcaa accaatga

```

<210> 94

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 94

```

Met Pro Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1           5           10           15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Asp Leu
          20           25           30
Gly Arg Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
          35           40           45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
          50           55           60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala
          65           70           75           80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Ile Val Val Ser
          85           90           95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
          100          105          110
Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln His Arg Arg Lys Ile Thr
          115          120          125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
          130          135          140
Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
          145          150          155          160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
          165          170          175          180
Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
          180          185          190
Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
          195          200          205
Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
          210          215          220
Gly Gln Ile Met Gln Asp Thr Gly Cys Ser Leu Gly Pro Ile Ser Gly
          225          230          235          240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Glu
          245          250          255
Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Leu Ala
          260          265          270
Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
          275          280          285
Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr Ala His
          290          295          300
Val His Glu Arg Ser Ala His Leu Val Ala Val Ala Thr Glu Glu Phe

```

305
Asp His Ala Asn Gln
325

315

320

<210> 95
<211> 966
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 95
atgtccaacg agaataacat tgctacattc aaagttgccg cagtccaggc cacacctgtg 60
tttcttgatc gtgaagcaac catcgacaaa gcttgccgct tgattgccac tgctggcagt 120
gaaggagcgc gcctgattgt gtttccagaa gcattcatcc caacttatcc tgaatgggta 180
tgggggtattc cctcogggtga gcaagggtta ctcaacgaac tctatgcaga gttgtccacc 240
aatgcggtca ccattcccag cgatgcgact gacaggctgt gcgaggctgc gcagcttgcg 300
aatgcctacg tagtgatggg catgagcgaa cggaacgtcg aggcgagtggt cgcaagcctg 360
tataatacgc tggtgtacat aaatgcgagc ggggagattt tagggaaaca tcgaaagctg 420
gtgccaacgg gcggcgaaac cctgggtatgg gcgcagggtg atggcagtag gctgcaggtc 480
tacgatactc cattgggaaa actcgggtggc ttaatttgct gggaaaatta tatgccgctg 540
gcacgggtatg ctatgtatgc ctggggaaaca caaatctatg tcgcggcaac gtgggatcgc 600
ggtcaaccct ggctttctac attaaggcat atcgccaaag aaggcagggt atacgtgatt 660
ggttgctgta tcgcgatgcg taaagacgat attccagatc gttacaccat gaagcaaaaa 720
tattatgctg aaatggatga atggatgaat gttggtgaca gtgtgattgt caatcccag 780
gggcacttta ttgccggggc tgtgcgcaag caggaagaaa ttctctacgc ggagattgat 840
cctcgcatgg tgcaaggccc gaagtggatg ctcgatgtgg cagggcatta tgcgagaccg 900
gatgtgttcc agttgacggt gcatacggat gtgaggcgga tgatgcgggt ggaagatgat 960
tcataa 966

<210> 96
<211> 321
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 96
Met Ser Asn Glu Asn Asn Ile Ala Thr Phe Lys Val Ala Ala Val Gln
1 5 10 15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
20 25 30
Ala Leu Ile Ala Thr Ala Gly Ser Glu Gly Ala Arg Leu Ile Val Phe
35 40 45
Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
50 55 60
Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ala Glu Leu Leu Thr
65 70 75 80
Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
85 90 95
Ala Gln Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
100 105 110
Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asn
115 120 125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
130 135 140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145 150 155 160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn

Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
 165 170 175
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 180 185 190
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 195 200 205
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Thr Met Lys Gln Lys
 210 215 220
 Tyr Tyr Ala Glu Met Asp Glu Trp Met Asn Val Gly Asp Ser Val Ile
 225 230 235
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 240 245 250
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 255 260 265
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 270 275 280
 Leu Thr Val His Thr Asp Val Arg Arg Met Met Arg Val Glu Asp Asp
 285 290 300
 305 310 315 320
 Ser

<210> 97
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 97
 atgggcatcg aacatccgaa atacaagggtc gccgtggtgc aagctgcgcc cgcctggctc 60
 gacctcgacg cgtcgatcga caagacgatc gggctgatcg aggaggcggc gaagaaaggc 120
 gccaaagctga tcgctttccc cgaagccttc attccggct acccttggca catctggctc 180
 gactcaccgc cctgggcat cgcccgcggt ttctgtgcagc gctatttcga caattcgctc 240
 gcctacgaca gccacaggc ggaaaggctg cgacaggccg tgcggaaggc caagctcacc 300
 gccgtgatcg gcctgtccga gcgcgacggc ggcagcctct atctcgcgca gtggctgatc 360
 gggcccgcagc gtgagaccat cgcaaagcgc cgcaagctgc ggccgaccca tgccgagcgc 420
 accgtctatg gcgaaggcga cggcagcgat ctgcgcgtcc ctgcagccgc tgctgaaatt cgccatgtac 480
 cggtcggcg cgctgtgctg ctgggagcat ctgcagccgc tctcgctcta cgatcccttc 540
 gccagaacg agcaggtaca tgtcgcggcc tggccgagct tctcgctcta cgatcccttc 600
 gcgcctgcgc tgggcgcgga ggtgaacaac gccgcctccc gcatctatgc ggtggaaggc 660
 tcctgcttcg tgcctgcacc gtgcgcgacg gtctcgagg ccatgatcga cgagctctgc 720
 gatcgccggc acaagcacgc gctgctgcat gccggcggcg gcttcgccgc gatctacggg 780
 cccgacggca gccagatcgg cgacaagctg ccgcccagc aggagggcct gctgatcgcc 840
 gagatcgatc tgggcgcgat cggcgctcgcc aagaacgcgg ccgatcccgc cgggcattat 900
 tcgcggccgc acgtcacgc gctcctgctc aacaggaagc cgaacaagcg cgtggagcag 960
 ttcgcgctgc ccgtcgacac ggtcgagccc gtcgacgtcg cggcggcagc aagctga 1017

<210> 98
 <211> 338
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 98
 Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Thr Ile Gly Leu

<210>	99
<211>	1014
<212>	DNA
<213>	Unknown

<400>	99								
atgcctgaca	agagaatcgt	cgcgcgccgc	gcgggtccaga	tagcacccgga	cctcgaaacgg				60
cccggtgcca	cgctcgagaa	ggtcctcgag	acgatcgacg	acgccgcacg	ccaggggcgtg				120
cagctcatcg	tcttccccga	gaccttcctg	ccctactacc	cgtacttttc	gttcgtgcgg				180
gcgcgcggtg	catcgggtgc	agagcacatg	cggctctatg	acgaagcggt	ggtcgtgcgc				240
gggccgggtg	cgcatgcggt	ggccgagcgg	gcacggcgcc	acggcatggt	cgtagtcgtc				300
ggcgtgaacg	agcgcgatca	cggcagctta	tacaacgcac	aactgatctt	cgataccgac				360
ggcgagtctc	tgctcaagcg	cgcgaagatc	acgccgacgt	ttcagcaacg	gatgatctgg				420
ggcatggggc	acgcagcccg	ctgaaaggta	gcgaaaacgc	gtatcggccg	ggtgggtgca				480
ctcgcttgct	gggaacacta	caacccgctt	gcacgttatg	cactgatgac	ccagcacgaa				540
gagattcatt	gcagccagtt	tcccggtctg	ctggtcggac	ccatcttcgg	tgaacagatc				600

```

gaagtgacca tccggcatca cgcactggaa tccggctgct tcgtgatcaa ttccaccggc 660
tggtgaccg agccgcagat cgagtcgatc acgaaagatc cgggcctgca gaaggcgctt 720
cgcggcggct gcaacacggc gatcatctcg cccgaaggcc agcatctcgc cccgcgcgtg 780
cgtgagggcg agggcatggt catcgctgac ctggacatgt cgctgatcac caaacgcaaa 840
cgcatgatgg attctgtcgg ccactacgcg cggcccgaac tgctgagcct cgccatcaac 900
gaccggccgg cggtcacgtc ggcacccacg aacagcttct catcttcaac cgggggattg 960
caccttgaac gcgaacgaga ccttgtcggc cgtgagccgg caattgatga ctga 1014

```

<210> 100

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 100

```

Met Pro Asp Lys Arg Ile Val Arg Ala Ala Ala Val Gln Ile Ala Pro
1          5          10          15
Asp Leu Glu Arg Pro Gly Gly Thr Leu Glu Lys Val Leu Glu Thr Ile
20          25          30
Asp Asp Ala Ala Arg Gln Gly Val Gln Leu Ile Val Phe Pro Glu Thr
35          40          45
Phe Leu Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Ala Pro Val Ala
50          55          60
Ser Gly Ala Glu His Met Arg Leu Tyr Asp Glu Ala Val Val Val Pro
65          70          75          80
Gly Pro Val Thr His Ala Val Ala Glu Arg Ala Arg Arg His Gly Met
85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
100          105          110
Ala Gln Leu Ile Phe Asp Thr Asp Gly Glu Leu Leu Leu Lys Arg Arg
115          120          125
Lys Ile Thr Pro Thr Phe His Glu Arg Met Ile Trp Gly Met Gly Asp
130          135          140
Ala Ala Gly Leu Lys Val Ala Glu Thr Arg Ile Gly Arg Val Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
165          170          175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
180          185          190
Gly Pro Ile Phe Gly Glu Gln Ile Glu Val Thr Ile Arg His His Ala
195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Glu
210          215          220
Pro Gln Ile Glu Ser Ile Thr Lys Asp Pro Gly Leu Gln Lys Ala Leu
225          230          235          240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Gln His Leu
245          250          255
Ala Pro Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
260          265          270
Met Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Arg Pro Ala
290          295          300
Val Thr Ser Ala Pro Met Asn Ser Phe Ser Ser Thr Gly Gly Leu
305          310          315          320
His Leu Glu Arg Glu Arg Asp Leu Val Gly Arg Glu Pro Ala Ile Asp
325          330          335
Asp

```

<210> 101
 <211> 1065
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 101
 atggcgacag tccatccgaa atttaaagta gccgcggtcc aggcggcccc ggcctttctc 60
 gacctcgacg cgtcgggtgga aaaagcgggtg cgcctgattg atgaagccgg cgccgctggg 120
 gcccggtctca tcgcgtttcc agagactttt atccccgggt atccgtgggt gatctggctc 180
 ggtgctccgg cctgggcat catgcgcggc ttctgtctccc gctatttcga caactcgctg 240
 cagtaaggca ccccggaagc cgaccggctg cgggcagcgg ccaaacgcaa caaatgttc 300
 gtcgcgctcg gactgtcaga gcgcgacggc ggaggtctct acatcgcccc atggattatc 360
 ggacccgacg gcgagacggg cgcaacgcgc cgcaagctca agcctactca cgccgagcgg 420
 acgggtgttcg gcgaaggcga tggctcgcac cttgcgggtcc acgaacttga tatcgggagg 480
 gtcgggtgcg tgtgctgttg ggagcacctg cagccactgt cgaagtagcg gatgtatgcg 540
 cagaacgagc aagttcatat cgcggcgttg ccgagctttt cgctttacga tccgttcgcg 600
 catgcgcttg gcgcgaggt caacaacgcg gcgagcaaga tctacgcggg cgaaggctca 660
 tgctttgtga ttgcgccatg cgcgaccgtt tcccaggcga tgatcgacga attgtgtgac 720
 tcgcccagaga agcatcagtt cctgcacgtc ggcggcgggt tcgccgtgat ctatggtccc 780
 gacggcgcgc cactcgccaa gccactggcg cccgatcagg aggggtctct ttacgaggat 840
 atcgacctcg gcatgatttc ggtcgcgaaa gcggcgcccg atccggctgg acattacgcg 900
 cgcccggaag tgaccctgt gttgttcaac aatcgctcgt ggaaccgggt ggagacactc 960
 gcgctgccgg tcgaccagga ggcagaggcg ggagcaggcg gcaaaccctgc gcccaagtca 1020
 ccgagtgtcg ctgcgttcac actgacgcag gcggcagccg agtag 1065

<210> 102
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 102
 Met Ala Thr Val His Pro Lys Phe Lys Val Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Ala Phe Leu Asp Leu Asp Ala Ser Val Glu Lys Ala Val Arg Leu
 20 25 30
 Ile Asp Glu Ala Gly Ala Ala Gly Ala Arg Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Gln Tyr Gly Thr Pro Glu Ala Asp Arg Leu Arg Ala Ala Ala Lys Arg
 85 90 95
 Asn Lys Met Phe Val Ala Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Glu Thr Val Ala
 115 120 125
 Thr Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser His Leu Ala Val His Glu Leu Asp Ile Gly Arg
 145 150 155 160
 Val Gly Ala Leu Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
 165 170 175
 Ala Met Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ala Trp Pro Ser

Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Arg Gly Leu Ile
 20 25 30
 Arg Glu Ala Gly Glu Lys Gly Val Asp Leu Leu Ala Phe Gly Glu Thr
 35 40 45
 Trp Leu Thr Gly Tyr Pro Tyr Trp Lys Asp Ala Pro Trp Ser Arg Glu
 50 55 60
 Tyr Asn Asp Leu Arg Ala Arg Tyr Val Ala Asn Gly Val Met Ile Pro
 65 70 75 80
 Gly Pro Glu Thr Asp Ala Leu Cys Gln Ala Ala Glu Ala Gly Val
 85 90 95
 Asp Val Ala Ile Gly Val Val Glu Leu Glu Pro Gly Ser Leu Ser Ser
 100 105 110
 Val Tyr Cys Thr Leu Leu Phe Ile Ser Arg Glu Gly Glu Ile Leu Gly
 115 120 125
 Arg His Arg Lys Leu Lys Pro Thr Asp Ser Glu Arg Arg Tyr Trp Ser
 130 135 140
 Glu Gly Asp Ala Thr Gly Leu Arg Val Tyr Glu Arg Pro Tyr Gly Arg
 145 150 155 160
 Leu Ser Gly Leu Asn Cys Trp Glu His Leu Met Met Leu Pro Gly Tyr
 165 170 175
 Ala Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp Pro Asn
 180 185 190
 Met Ala Ser Ser Ala Ser Glu Leu Leu Ser Arg Ala Tyr Ala Tyr Gln
 195 200 205
 Ala Gly Cys Tyr Val Leu Cys Ala Gly Gly Leu Gly Pro Ala Pro Gly
 210 215 220
 Glu Leu Pro Asp Gly Ile Ala Ala Glu Ser Leu Asp His Leu Thr Gly
 225 230 235 240
 Glu Ser Cys Ile Ile Asp Pro Trp Gly Lys Val Ile Ala Gly Pro Val
 245 250 255
 Ser Cys Glu Glu Thr Leu Ile Thr Ala Arg Val Ser Thr Ala Ser Ile
 260 265 270
 Tyr Arg Arg Lys Ser Leu Thr Asp Val Gly Gly His Tyr Ser Arg Pro
 275 280 285
 Asp Val Phe Arg Phe Glu Val Asp Arg Ser Glu Arg Pro Arg Val Val
 290 295 300
 Phe Arg Asp Gly Asp Val Asp Asp Arg Gly
 305 310

<210> 105

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 105

atgaccattg	tcaaagccgc	tgccgtccag	attgcccccg	ttctctacag	ccgtgaaggc	60
actgtagaaa	aggtcgttaa	caagattcgc	gaactcggcg	agaaggcggt	gcagttcgcc	120
gttttccttg	aaaccgtcgt	accgtactac	ccgtactttt	cctttgtgca	gagccctttc	180
aaaatggggt	ccgagcacta	caaattgctc	gaccaggccg	ttgtcgtgcc	gtcggcgacc	240
accgatgcca	tcggcaaaag	ggccaaggaa	gccaacatgg	tggtgtccat	cggcgtcaac	300
gaacgcgatg	gcagcaccct	ctacaacacg	cagttgctgt	ttgatgccga	cggcactttg	360
attcaggccc	gtcgcaagat	ttcaccgacc	taccacgaac	gcacgatctg	gggcatgggc	420
gacgggttccg	gcctgcgcgc	caccgacagc	gcggtcgggc	gcacgcggca	attggcctgc	480
tggaacatt	acaatccgct	ggcgcggtac	gccttgatcg	aagacggcga	acagatccac	540
gcctcgatgt	accggggtc	gttcgcaggt	cctttattca	ctcgccagat	ggaagtcagc	600
atccgatgc	atgccctgga	atcggcgtgc	ttcgtggtca	actcgaccgc	gtggtgttac	660
ccggaacagc	aagcccagat	catggccgac	accggttgcg	agatcgggcc	gatctccggc	720
ggctgctaca	ccgcgatcat	cgaccacacg	ggtgaagtcg	tcggcgccact	gaccgaaggc	780

gagggcgaa	tgattgccga	catcgatctg	tccagatcg	aaatccgtaa	acgtcagatg	840
gacggccgtg	gtcactacag	ccgtccggaa	atcctgagcc	tgaacatcga	ccgtacgccg	900
catcgccatg	ttcacgaacg	caacgaccag	cagaaaccgg	gtgtgatcga	cactgctgaa	960
gaaaccgggc	gttga					975

<210>	106
<211>	324
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	106																
Met	Thr	Ile	Val	Lys	Ala	Ala	Ala	Val	Gln	Ile	Ala	Pro	Val	Leu	Tyr		
1				5					10					15			
Ser	Arg	Glu	Gly	Thr	Val	Glu	Lys	Val	Val	Asn	Lys	Ile	Arg	Glu	Leu		
			20					25					30				
Gly	Glu	Lys	Gly	Val	Gln	Phe	Ala	Val	Phe	Pro	Glu	Thr	Val	Val	Pro		
		35					40					45					
Tyr	Tyr	Pro	Tyr	Phe	Ser	Phe	Val	Gln	Ser	Pro	Phe	Lys	Met	Gly	Ser		
	50					55					60						
Glu	His	Tyr	Lys	Leu	Leu	Asp	Gln	Ala	Val	Val	Val	Pro	Ser	Ala	Thr		
65				70						75					80		
Thr	Asp	Ala	Ile	Gly	Lys	Ala	Ala	Lys	Glu	Ala	Asn	Met	Val	Val	Ser		
				85					90					95			
Ile	Gly	Val	Asn	Glu	Arg	Asp	Gly	Ser	Thr	Leu	Tyr	Asn	Thr	Gln	Leu		
			100					105					110				
Leu	Phe	Asp	Ala	Asp	Gly	Thr	Leu	Ile	Gln	Ala	Arg	Arg	Lys	Ile	Ser		
		115					120					125					
Pro	Thr	Tyr	His	Glu	Arg	Met	Ile	Trp	Gly	Met	Gly	Asp	Gly	Ser	Gly		
	130					135					140						
Leu	Arg	Ala	Thr	Asp	Ser	Ala	Val	Gly	Arg	Ile	Gly	Gln	Leu	Ala	Cys		
145				150					155					160			
Trp	Glu	His	Tyr	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Leu	Ile	Glu	Asp	Gly		
				165					170					175			
Glu	Gln	Ile	His	Ala	Ser	Met	Tyr	Pro	Gly	Ser	Phe	Ala	Gly	Pro	Leu		
			180					185					190				
Phe	Thr	Arg	Gln	Met	Glu	Val	Ser	Ile	Arg	Met	His	Ala	Leu	Glu	Ser		
		195					200					205					
Ala	Cys	Phe	Val	Val	Asn	Ser	Thr	Ala	Trp	Leu	Tyr	Pro	Glu	Gln	Gln		
	210					215					220						
Ala	Gln	Ile	Met	Ala	Asp	Thr	Gly	Cys	Glu	Ile	Gly	Pro	Ile	Ser	Gly		
225				230					235					240			
Gly	Cys	Tyr	Thr	Ala	Ile	Ile	Asp	Pro	Gln	Gly	Glu	Val	Val	Gly	Ala		
				245					250					255			
Leu	Thr	Glu	Gly	Glu	Gly	Glu	Val	Ile	Ala	Asp	Ile	Asp	Leu	Phe	Gln		
			260					265					270				
Ile	Glu	Ile	Arg	Lys	Arg	Gln	Met	Asp	Gly	Arg	Gly	His	Tyr	Ser	Arg		
		275					280					285					
Pro	Glu	Ile	Leu	Ser	Leu	Asn	Ile	Asp	Arg	Thr	Pro	His	Arg	His	Val		
	290					295					300						
His	Glu	Arg	Asn	Asp	Gln	Gln	Lys	Pro	Gly	Val	Ile	Asp	Thr	Ala	Glu		
305					310					315					320		
Glu	Thr																

<210>	107
<211>	981
<212>	DNA
<213>	Unknown

<220>

<223> Obtained from an environmental sample

<400> 107

```

atggccatca ttgcgcagc agccgtacag atcagcccgg ttcttttacag ccgcgaaggc      60
accgtggaca aggtctgcc gcagatcatc acccttggca aacaggggtgt gcagttcgcc      120
gtgttcccgg aaacgggtggt gccgtactac ccctattttt cctttgtgca gccggcggttc      180
gccatgggtg cgcaacacct caaattgcta gatcaatctg taaccgtgcc atcggccgcc      240
accctggcga ttggcgaagc gtgcaagcaa gcaggaatgg tcgtttccat cggagtcaat      300
gaacgcgatg gcggtacgat ttacaacgcg caattactct tcgatgctga cggcacgctg      360
attcagcatc ggcgcaaaat caccgccgac taccacgagc gcatgggtctg ggggcagggc      420
gatggttccg gtctgcgcgc catcgacagc gcggtcgggc gcatcggctc cctggcatgc      480
tgggaacatt acaaccgcgt ggcccgttac gccttgatgg cagacggcga acagatccac      540
gccgcgatgt ttcccgggttc cctgggtgggt gacatcttcg ccgagcagat cgaggtcacc      600
atccgccatc acgcattgga gtcaggatgc ttcgtggtca atgcaacagc ctggctggat      660
gcggatcagc agggccaaat aatgcaggac acaggttgcg gccttggtcc catctcgggc      720
ggctgcttca ccgcgatcgt atcgccggaa gggaagctac ttggagagcc gcttcgctcc      780
ggggaaggcg tagtgattgc cgacctgat acggccttga tcgacaagcg caaacgggatg      840
atggattcag taggtcatta cagtcgtccc gagctgctca gcctattgat cgatcgatcg      900
ccgactgcgc atgttcatga acgcgccggc tttgtttcga gcaacgccgg tttgcaggag      960
gtcgcccatg cagaccaatg a                                     981

```

<210> 108

<211> 326

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 108

```

Met Ala Ile Ile Arg Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Thr Leu
20     25     30
Gly Lys Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
50     55     60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala
65     70     75     80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val Val Ser
85     90     95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
100    105    110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln His Arg Arg Lys Ile Thr
115    120    125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
130    135    140
Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
145    150    155    160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
165    170    175
Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
180    185    190
Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
195    200    205
Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
210    215    220
Gly Gln Ile Met Gln Asp Thr Gly Cys Gly Leu Gly Pro Ile Ser Gly

```

```

225          230          235          240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Glu
          245          250          255
Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Thr Ala
          260          265          270
Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
          275          280          285
Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Ser Pro Thr Ala His
          290          295          300
Val His Glu Arg Ala Gly Phe Val Ser Ser Asn Ala Gly Leu Gln Glu
305          310          315          320
Val Ala His Ala Asp Gln
          325

```

<210> 109
 <211> 1092
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 109
atggccatca ttgcgcgagc agccgtacag atcagcccgg ttctttacag ccgcgaaggc      60
accgtggaca ggggtctgcc gcagatcatc acccttggca aacaagggtgt gcagttcgcc      120
gtgttcccg aaacgggtgg gccgtactac ccctattttt cctttgtgca gccggcattt      180
gcgatgggtg cacaacacct caaattgctc gatcaatctg taaccgtgcc atcggcgcgc      240
accctggcga ttggcgaagc gtgcaagcaa gcaggaatgg tcgtttccat cggcgtcaat      300
gaacgcgatg gcggtacgat ttacaacgcg caattactct tcgatgctga cggcactctg      360
attcagcatc ggcgcaaaat caccgacgac taccacgagc gcatggtctg ggggcagggc      420
gatggttccg gtctgcgcgc catcgacagc gcggtcgggc gcacgcgctc cctggcatgc      480
tggaacatt acaaccogct ggcccgttac gccttgatgg cagacggcga acagatccac      540
gccgcgatgt ttcccggttc cctgggtgggt gacatcttcg ccgagcagat cgaggtcacc      600
atccgccatc acgcattgga atcaggatgc ttctgtgtca atgcaacagc ttggctggat      660
gcgcatcagc agggccaaat aatgcaggac acaggttgcg gccttgggtcc catctcgggc      720
ggctgcttca ccgcgatcgt atcgccggaa gggaagctac ttggagagcc gcttcgctca      780
ggggaaggcg tagtgattgc cgacctcgat atggccttga tcgacaagcg caaacggatg      840
atggattoag taggtcatta cagtcgtccc gagctgtcca gcctattgat cgatcgatcg      900
ccgactgcgc attttcatga acgcgcgggg ctttgttccg agcgacgcgc gtttgcagga      960
ggtcgcgcgc gcagaccaat gaattgctcg ctgacctgca aatccaaggc ctgcgttggc     1020
cggccgcgca aatggcttgt cgcgccaagg cggcgccggt ccttcagacc acaaggcgct     1080
gagcctaggt aa                                     1092

```

<210> 110
 <211> 363
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 110
Met Ala Ile Ile Arg Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
  1          5          10          15
Ser Arg Glu Gly Thr Val Asp Arg Val Cys Gln Gln Ile Ile Thr Leu
          20          25          30
Gly Lys Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
          35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
          50          55          60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala

```

65					70					75					80
Thr	Leu	Ala	Ile	Gly	Glu	Ala	Cys	Lys	Gln	Ala	Gly	Met	Val	Val	Ser
				85					90					95	
Ile	Gly	Val	Asn	Glu	Arg	Asp	Gly	Gly	Thr	Ile	Tyr	Asn	Ala	Gln	Leu
			100					105					110		
Leu	Phe	Asp	Ala	Asp	Gly	Thr	Leu	Ile	Gln	His	Arg	Arg	Lys	Ile	Thr
		115					120					125			
Pro	Thr	Tyr	His	Glu	Arg	Met	Val	Trp	Gly	Gln	Gly	Asp	Gly	Ser	Gly
	130					135					140				
Leu	Arg	Ala	Ile	Asp	Ser	Ala	Val	Gly	Arg	Ile	Gly	Ser	Leu	Ala	Cys
145				150						155					160
Trp	Glu	His	Tyr	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Leu	Met	Ala	Asp	Gly
			165						170					175	
Glu	Gln	Ile	His	Ala	Ala	Met	Phe	Pro	Gly	Ser	Leu	Val	Gly	Asp	Ile
		180						185					190		
Phe	Ala	Glu	Gln	Ile	Glu	Val	Thr	Ile	Arg	His	His	Ala	Leu	Glu	Ser
		195					200					205			
Gly	Cys	Phe	Val	Val	Asn	Ala	Thr	Ala	Trp	Leu	Asp	Ala	Asp	Gln	Gln
	210					215					220				
Gly	Gln	Ile	Met	Gln	Asp	Thr	Gly	Cys	Gly	Leu	Gly	Pro	Ile	Ser	Gly
225				230						235					240
Gly	Cys	Phe	Thr	Ala	Ile	Val	Ser	Pro	Glu	Gly	Lys	Leu	Leu	Gly	Glu
			245						250					255	
Pro	Leu	Arg	Ser	Gly	Glu	Gly	Val	Val	Ile	Ala	Asp	Leu	Asp	Met	Ala
		260						265					270		
Leu	Ile	Asp	Lys	Arg	Lys	Arg	Met	Met	Asp	Ser	Val	Gly	His	Tyr	Ser
	275						280					285			
Arg	Pro	Glu	Leu	Leu	Ser	Leu	Leu	Ile	Asp	Arg	Ser	Pro	Thr	Ala	His
	290					295						300			
Phe	His	Glu	Arg	Ala	Gly	Leu	Cys	Ser	Glu	Arg	Arg	Arg	Phe	Ala	Gly
305					310					315					320
Gly	Arg	Ala	Cys	Arg	Pro	Met	Asn	Cys	Ser	Leu	Thr	Cys	Lys	Ser	Lys
			325						330					335	
Ala	Cys	Val	Gly	Arg	Pro	Arg	Lys	Trp	Leu	Val	Ala	Pro	Arg	Arg	Arg
		340						345					350		
Arg	Ser	Phe	Arg	Pro	Gln	Gly	Ala	Glu	Pro	Arg					
		355					360								

<210> 111

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 111

atgccccaaa	cagtacgtgc	cgcagcagtc	cagatcgcg	ccgacctgac	gtcacgcgcc	60
ggcaccgtcg	agcgggtcct	caatgcaatc	gccgaagctg	ctgacaaagg	cgccgagctg	120
atcgtatttc	ccgagacctt	cgtgcccttg	tatccctatt	tcagtttctg	tctgccacct	180
gtccagcaag	gccctgagca	tcttcgtctt	tatgaggaag	cagtcacggt	accatcagca	240
gaaacacggg	ccgtcgcgga	cgcgcgcgcg	aaacgcaatg	cggttatcgt	ccttggcgct	300
aatgagcgcg	accacggctc	gctctataac	actcagctga	tcttcgacgc	ggatggcagc	360
ctgaaactca	agcgtcgcaa	gatcacgccg	acctatcacg	aacggatgat	ctggggccaa	420
ggcgtatggc	ccggcctgaa	ggttgtcgac	actgccgtcg	gtcgcgtggg	tgccctggca	480
tgctggggagc	attacaatcc	tctggcccgc	tatactttga	tgggccagca	tgaggaaatt	540
cacgcctctc	atttcccggg	ctcactggtc	ggcccgatat	tcggcgcagca	aatcgaagtc	600
accatgcgcc	accacgcgtt	ggaatcgggc	tgtttcgtgg	tcaatgccac	cggctggctg	660
agcgaggagc	agatcgcatc	tattcatccg	gacccgcct	tgcaaaagg	cctgogcgat	720
ggctgcatga	cctgcacatc	cacgccggaa	ggacgccatg	tcgtaccgcc	gctgacctcg	780
ggcgaaggca	tcctgatcgg	cgatctggac	atcgcggtca	ttaccaagcg	caagcggatg	840

```

atggattcgg tcggacacta tgctcggcct gaactgctgc accttggtcca tgacacgacg      900
cccgcacgcg cacgcgagca ggtcggcctt tcaggcgatt ttcccgatgc ggagcaagac      960
aagctatttg aggaggttca taatgcgtga      990

```

<210> 112
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 112
 Met Pro Lys Thr Val Arg Ala Ala Ala Val Gln Ile Ala Pro Asp Leu
 1 5 10 15
 Thr Ser Arg Ala Gly Thr Val Glu Arg Val Leu Asn Ala Ile Ala Glu
 20 25 30
 Ala Ala Asp Lys Gly Ala Glu Leu Ile Val Phe Pro Glu Thr Phe Val
 35 40 45
 Pro Trp Tyr Pro Tyr Phe Ser Phe Val Leu Pro Pro Val Gln Gln Gly
 50 55 60
 Pro Glu His Leu Arg Leu Tyr Glu Glu Ala Val Thr Val Pro Ser Ala
 65 70 75 80
 Glu Thr Arg Ala Val Ala Asp Ala Ala Arg Lys Arg Asn Ala Val Ile
 85 90 95
 Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn Thr Gln
 100 105 110
 Leu Ile Phe Asp Ala Asp Gly Ser Leu Lys Leu Lys Arg Arg Lys Ile
 115 120 125
 Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ala
 130 135 140
 Gly Leu Lys Val Val Asp Thr Ala Val Gly Arg Val Gly Ala Leu Ala
 145 150 155 160
 Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Thr Leu Met Ala Gln
 165 170 175
 His Glu Glu Ile His Ala Ser His Phe Pro Gly Ser Leu Val Gly Pro
 180 185 190
 Ile Phe Gly Glu Gln Ile Glu Val Thr Met Arg His His Ala Leu Glu
 195 200 205
 Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser Glu Glu Gln
 210 215 220
 Ile Ala Ser Ile His Pro Asp Pro Ala Leu Gln Lys Gly Leu Arg Asp
 225 230 235 240
 Gly Cys Met Thr Cys Ile Ile Thr Pro Glu Gly Arg His Val Val Pro
 245 250 255
 Pro Leu Thr Ser Gly Glu Gly Ile Leu Ile Gly Asp Leu Asp Met Arg
 260 265 270
 Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ala
 275 280 285
 Arg Pro Glu Leu Leu His Leu Val His Asp Thr Thr Pro Ala Arg Ala
 290 295 300
 Arg Glu Gln Val Gly Leu Ser Gly Asp Phe Pro Asp Ala Glu Gln Asp
 305 310 315 320
 Lys Leu Phe Glu Glu Val His Asn Ala
 325

<210> 113
 <211> 993
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 113

```

atgacgaagg aacgcgccgc gcgcagcctg cgcgcagctg ccatacagct tgaagccgaa      60
gtcggcgaca tcgccgcaa tctcgcacgc atcgaggcga tggtcgagga ggctgcgggc      120
aaggcgccgc aactgatcgc cattccggag ttctgcacct cccgcatgcc cttcgatgca      180
cgcgtgcacg acgccgtgct gccgccggac aacttcgtgg tcgatgcctt tcgccgcatg      240
gcagcgacgc acaactgccg gctcggcggc tccatgctca ttgccgacgg tggcgagatc      300
tacaaccgct accacttcgt cgaacccgac ggcagcgtgc atctgcacga caaggatctg      360
ccgacgatgt gggagaacgc cttctacacc ggccggctccg acgacggcgt cttcgacacc      420
ggcatcggcg gcgtcggcgc cgcggtgtgc tgggaactgg tacgcaccgg caccgtgcga      480
cgcatgctcg gtcgcgtcga cgtcgccatg accggcacgc attggtggac gatgccgcac      540
aactggggca gcgccgtcgc gcgcacgctg gccgcgatga cgcagtacaa ccgctacatg      600
tccgagaatg caccaccgga attcgcccgc cgcctgggtg tgccgggtgt gcaggcctcg      660
cactgcgga gtttcgcac cggtttcttg ctgctgccag gcagcggggc tgcaactgcc      720
tatgacaccg agtacgtcgg cgccacacag atcgtcgatg ccgatggcca catcctcgcc      780
caccgtcgca cgcaggaagg ccccggtgtc gtcgtcgccg acatcacgct cgggtgccgc      840
acgcccgagc tgccactgga agaccgcttc tggattcccg agctgccgct cttcctcaag      900
gcctactggc accaccagaa cctgtgcggc aagtccctact accgtcgcgt cggccgcgat      960
gccggcctgg cggcggcgga gcgttcggca tga      993

```

<210> 114

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 114

```

Met Thr Lys Glu Arg Ala Ala Arg Ser Leu Arg Ala Ala Ala Ile Gln
 1          5          10          15
Leu Glu Ala Glu Val Gly Asp Ile Ala Ala Asn Leu Ala Arg Ile Glu
 20          25          30
Ala Met Val Glu Glu Ala Ala Gly Lys Gly Ala Glu Leu Ile Ala Ile
 35          40          45
Pro Glu Phe Cys Thr Ser Arg Met Pro Phe Asp Ala Arg Val His Asp
 50          55          60
Ala Val Leu Pro Pro Asp Asn Phe Val Val Asp Ala Phe Arg Arg Met
 65          70          75          80
Ala Ala Thr His Asn Cys Arg Leu Gly Gly Ser Met Leu Ile Ala Asp
 85          90          95
Gly Gly Glu Ile Tyr Asn Arg Tyr His Phe Val Glu Pro Asp Gly Ser
100          105          110
Val His Leu His Asp Lys Asp Leu Pro Thr Met Trp Glu Asn Ala Phe
115          120          125
Tyr Thr Gly Gly Ser Asp Asp Gly Val Phe Asp Thr Gly Ile Gly Gly
130          135          140
Val Gly Ala Ala Val Cys Trp Glu Leu Val Arg Thr Gly Thr Val Arg
145          150          155          160
Arg Met Leu Gly Arg Val Asp Val Ala Met Thr Gly Thr His Trp Trp
165          170          175
Thr Met Pro His Asn Trp Gly Ser Ala Val Ala Arg Thr Leu Ala Ala
180          185          190
Met Thr Gln Tyr Asn Arg Tyr Met Ser Glu Asn Ala Pro Thr Glu Phe
195          200          205
Ala Arg Arg Leu Gly Val Pro Val Leu Gln Ala Ser His Cys Gly Ser
210          215          220
Phe Arg Thr Gly Phe Leu Leu Leu Pro Gly Ser Gly Arg Ala Leu Pro
225          230          235          240

```

<400>	116															
Met	Asn	Gln	Ile	Ile	Lys	Ala	Ala	Ala	Val	Gln	Cys	Ser	Pro	Val	Leu	
1				5					10					15		
Tyr	Ser	Gln	Ala	Gly	Thr	Val	Lys	Lys	Ile	Cys	Asp	Thr	Ile	Leu	Glu	
			20					25					30			
Leu	Gly	Gln	Gln	Gly	Val	Gln	Phe	Ala	Val	Phe	Pro	Glu	Thr	Val	Val	
		35					40					45				
Pro	Tyr	Tyr	Pro	Tyr	Phe	Ser	Phe	Val	Gln	Pro	Pro	Phe	Ala	Met	Gly	
	50					55					60					
Lys	Glu	His	Leu	Lys	Leu	Leu	His	Glu	Ser	Val	Val	Val	Pro	Ser	Ala	
65				70						75				80		
Ala	Thr	Thr	Leu	Ile	Gly	Gln	Ala	Cys	Lys	Glu	Ala	Asn	Met	Val	Val	
				85					90					95		

Ser Ile Gly Ile Asn Glu Arg Ala Gly Gly Thr Ile Tyr Asn Ala Gln
 100 105 110
 Leu Leu Phe Asp Ala Asp Gly Ser Ile Ile Gln His Arg Arg Lys Ile
 115 120 125
 Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser
 130 135 140
 Gly Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala
 145 150 155 160
 Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Phe Ala Leu Met Ala Asp
 165 170 175
 Gly Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Gln
 180 185 190
 Ile Phe Ala Asp Gln Ile Ser Ala Thr Ile Gln His His Ala Leu Glu
 195 200 205
 Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Pro Glu Gln
 210 215 220
 Gln Gln Gln Ile Met Gln Asp Thr Gly Cys Glu Leu Gly Pro Ile Ser
 225 230 235 240
 Gly Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Phe Leu Ser
 245 250 255
 Glu Pro Ile Thr Gln Gly Glu Gly Tyr Val Ile Ala Asp Leu Asp Phe
 260 265 270
 Ser Leu Ile Glu Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr
 275 280 285
 Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Arg Pro Thr Ser
 290 295 300
 Val Leu His Glu Leu Lys Leu Glu Asn Pro Ser Asn Asn Ser Ile Glu
 305 310 315 320
 Lys Val Ser Glu Phe Ala Glu Val His Ala
 325 330

<210> 117

<211> 957

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 117

atgactcaat	ccaggataat	tcgtgctgcg	gcagcgcaga	tcgctccgga	tttgacaggtt	60
ccaggtaaca	cgatcgacaa	agtttgccgc	accatcagcg	aggcggccgc	aaaaggcgta	120
cagattattg	ttttccctga	aacottggtg	ccttattacc	cttacttctc	ttacatttca	180
ccgcccattc	aacagggcaa	agaacatttg	cggtgtgatg	accatgcagt	ggttgtgccc	240
ggctcggaag	ccgaggcaat	ttcagctcct	gccgcccac	acaatatggt	ggtggttttg	300
ggtgtgaacg	agcgcgatca	cggcacactt	tacaacgcac	aaattatttt	caacagcgac	360
ggaaagattc	tggtgaagcg	ccgaaaaatt	acaccaactt	atcacgagcg	gatggtgtgg	420
gggcagggtg	acgcttcagg	cttgaagggtg	ggtgattccg	cagtgggccc	tgtgggtgca	480
ttggcctggt	gggaacacta	caacccttgg	gctcgctatt	gtttgatggc	ccagcacgaa	540
gaaattcaact	gtgcgcagtt	tcccgggtca	ttggtggggc	aagtttttgc	cgaccaaattg	600
gaagtgacca	ttcgtcacca	cgcaacttgag	tcgggctggt	ttgtcatcaa	cagcaccgct	660
tggttttctg	aagaacaggt	tcaaagtatt	tcacccgaca	gcgcattgca	gaaagggctt	720
agaggcgggt	gtttcacggc	cattgtcagc	cctgagggaa	agctgtttgg	tgagccgctc	780
accgagggtg	agggcatggt	gatcgccgac	ctcgacatgg	cgttggttac	gaaacgcaaa	840
cgcatgatgg	attcagtggg	ccattatgcg	cgccccgagt	tggtgagttt	gctggttcgg	900
gatgaggctt	caagcccat	gaaaaaaatt	caggaggttc	aacatgctga	gtactga	957

<210> 118

<211> 318

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 118

```

Met Thr Gln Ser Arg Ile Ile Arg Ala Ala Ala Ala Gln Ile Ala Pro
 1          5          10          15
Asp Leu Gln Val Pro Gly Asn Thr Ile Asp Lys Val Cys Arg Thr Ile
          20          25          30
Ser Glu Ala Ala Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
          35          40          45
Leu Val Pro Tyr Tyr Pro Tyr Phe Ser Tyr Ile Ser Pro Pro Ile Gln
          50          55          60
Gln Gly Lys Glu His Leu Arg Leu Tyr Asp His Ala Val Val Val Pro
65          70          75          80
Gly Ser Glu Thr Glu Ala Ile Ser Ala Leu Ala Ala Gln His Asn Met
          85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
          100          105          110
Ala Gln Ile Ile Phe Asn Ser Asp Gly Lys Ile Leu Leu Lys Arg Arg
          115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp
          130          135          140
Ala Ser Gly Leu Lys Val Val Asp Ser Ala Val Gly Arg Val Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Cys Leu Met
          165          170          175
Ala Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Leu Val
          180          185          190
Gly Gln Val Phe Ala Asp Gln Met Glu Val Thr Ile Arg His His Ala
          195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Ala Trp Leu Ser Glu
          210          215          220
Glu Gln Val Gln Ser Ile Ser Ser Asp Ser Ala Leu Gln Lys Gly Leu
225          230          235          240
Arg Gly Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu
          245          250          255
Ala Glu Pro Leu Thr Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
          260          265          270
Met Ala Leu Val Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Val Arg Asp Glu Ala Ser
          290          295          300
Ser Pro Met Lys Lys Ile Gln Gly Val Gln His Ala Glu Tyr
305          310          315

```

<210> 119

<211> 984

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 119

```

atggatacac tcaaagttgg attggttcag atggccccc tctggttgaa ccgggataaa      60
accctgatca aagttgagga atacatgcag aaagcaggca aacagggctg caacctggta      120
gcttttggtg aagcgtggt tcccggtac cccttctggg tggaacgcac agagggcgcc      180
agattcaatt ccaaagtcca gaaagaactc ttgcacatt acctgatca ggcggtgcag      240
atcgaagccg gccaccttga tcctctccag gcattagccc aacaatacaa gatggctgtg      300
tacgtgggga cgattgaacg cccgcctgag cggagcggcc acagcctgta ctgctcccta      360

```

```

atatttatag acccagaagg cgagatcggc tcggttcacc gcaagttgat gccacccat 420
gaggaacgcc tggctctggc aactggcgat gggcacggcc tgcgaacaca ttctctgggc 480
gcctttaccg ttggcggact caactgctgg gaaaactgga tgccgctctc ccgcacagct 540
ctttatgcc aaggagagga tcttcatggt gctgcctggc ccgggagtca gcgcaatact 600
tatgatataa ccaaattcat tgccaaggaa tctcgctctt atgtgatctc cgtatccggg 660
atgatgaaaa aagaaaatat cctctctgaa attccccaca gccaatgat gctggaaaaat 720
agcgaggata ttatggctga tggcggatcc tgtctggctg gaccagatgg agaatggatc 780
atcgagccca tcgtcggaga ggaaaccctg gtaactgctg aactatcaca tcagcgggtc 840
agagaagaaa gacagaattt cgacccaaca ggctactaca gtccggcctga tgtgacccgc 900
ctggtagtcg accgcaggcg ccagcagatc ctggagatca ccccgacga aaaaggaaga 960
tcggatgaaa atcaatccct ttaa 984

```

<210> 120
 <211> 327
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 120

Met	Asp	Thr	Leu	Lys	Val	Gly	Leu	Val	Gln	Met	Ala	Pro	Ile	Trp	Leu	1	5	10	15
Asn	Arg	Asp	Lys	Thr	Leu	Ile	Lys	Val	Glu	Glu	Tyr	Met	Gln	Lys	Ala	20	25	30	
Gly	Lys	Gln	Gly	Cys	Asn	Leu	Val	Ala	Phe	Gly	Glu	Ala	Leu	Val	Pro	35	40	45	
Gly	Tyr	Pro	Phe	Trp	Val	Glu	Arg	Thr	Glu	Gly	Ala	Arg	Phe	Asn	Ser	50	55	60	
Lys	Val	Gln	Lys	Glu	Leu	Phe	Ala	His	Tyr	Leu	Asp	Gln	Ala	Val	Gln	65	70	75	80
Ile	Glu	Ala	Gly	His	Leu	Asp	Pro	Leu	Gln	Ala	Leu	Ala	Gln	Gln	Tyr	85	90	95	
Lys	Met	Ala	Val	Tyr	Val	Gly	Thr	Ile	Glu	Arg	Pro	Pro	Glu	Arg	Ser	100	105	110	
Gly	His	Ser	Leu	Tyr	Cys	Ser	Leu	Ile	Phe	Ile	Asp	Pro	Glu	Gly	Glu	115	120	125	
Ile	Gly	Ser	Val	His	Arg	Lys	Leu	Met	Pro	Thr	His	Glu	Glu	Arg	Leu	130	135	140	
Val	Trp	Ser	Thr	Gly	Asp	Gly	His	Gly	Leu	Arg	Thr	His	Ser	Leu	Gly	145	150	155	160
Ala	Phe	Thr	Val	Gly	Gly	Leu	Asn	Cys	Trp	Glu	Asn	Trp	Met	Pro	Leu	165	170	175	
Ser	Arg	Thr	Ala	Leu	Tyr	Ala	Met	Gly	Glu	Asp	Leu	His	Val	Ala	Ala	180	185	190	
Trp	Pro	Gly	Ser	Gln	Arg	Asn	Thr	Tyr	Asp	Ile	Thr	Lys	Phe	Ile	Ala	195	200	205	
Lys	Glu	Ser	Arg	Ser	Tyr	Val	Ile	Ser	Val	Ser	Gly	Met	Met	Lys	Lys	210	215	220	
Glu	Asn	Ile	Leu	Ser	Glu	Ile	Pro	His	Ser	Gln	Leu	Met	Leu	Glu	Asn	225	230	235	240
Ser	Glu	Asp	Ile	Met	Ala	Asp	Gly	Gly	Ser	Cys	Leu	Ala	Gly	Pro	Asp	245	250	255	
Gly	Glu	Trp	Ile	Ile	Glu	Pro	Ile	Val	Gly	Glu	Glu	Thr	Leu	Val	Thr	260	265	270	
Ala	Glu	Leu	Ser	His	Gln	Arg	Val	Arg	Glu	Glu	Arg	Gln	Asn	Phe	Asp	275	280	285	
Pro	Thr	Gly	His	Tyr	Ser	Arg	Pro	Asp	Val	Thr	Arg	Leu	Val	Val	Asp	290	295	300	
Arg	Arg	Arg	Gln	Gln	Ile	Leu	Glu	Ile	Thr	Pro	Asp	Glu	Lys	Gly	Arg	305	310	315	320

Ser Asp Glu Asn Gln Ser Leu
325

<210> 121
<211> 1158
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 121
atgagcaaaa aagttctagg cggcagagaa aaagtaaaag ttgcagtagt tcaggctgcg 60
cccgtttttca tggacaagga gaagacgatt gaaaaggctt gcaagctaata aaaagaagcg 120
gggagaaatc gagccgagct catagcgttc tcagagtcatt tcatccccgt ctatcctgca 180
tactataaccg tcggctatga aaccoccttct caagaatgga gagattacgt gattgcgcta 240
caggataaact ccgtgctgat tccgagcgag gataccgagg tactcggaca ggctgcaaaag 300
gagggcagggg cttatgcagt aataggatgc agcgagatgg acgaccgtcc gggaagccga 360
acagttttaca acacgctoct cttcatcggc aaagacggca aggtcatggg aaggcataga 420
aaactcaaac ccacgttcac ggagagaata tactggggag agggagatgc tggagacata 480
aaggttttttg ataccgagat cggcaggatc ggaggcctcg tatgctggga gaaccatatg 540
actctagtca gggccgcgat gatacacagg ggagaggagt ttcatatcgc ggtctggccg 600
ggaaactgga aggggtgcgga aaacaagctt ctccaagcag ataataagccc agggaggcgcc 660
ctctgcaacc ttcaatctct cattaaagta cagcctttg aggccggggc gtttgtgctg 720
agcgcttgcg gctttttgac gccagaggat ttcccggaaa ggtggcatta tataagggat 780
ggtaaccata ttaactgcga ctgggcaactg ggcggaagct caatcgtcaa tcccgcgggc 840
cgttatctcg tcgagcctaa ctttgagaag gatgcaatcc tctatgcgga ttgttatgca 900
aaccagataa aagcagtaaa agcgggtttt gattcccttg gccactattc ccgctgggat 960
attgcccac tggcgataag gcaggaagcc tggaatccag aggtttcttt gatcgattcc 1020
tcttcgactg aagttgagct tccggcagac gagcttcgaa ggatttcgga gaagtttgaa 1080
gtaactgcgg ataagttgga atctttgctt gaggaattg gaaagattaa aaagcccagg 1140
aaacaagccg gttcctaa 1158

<210> 122
<211> 385
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 122
Met Ser Lys Lys Val Leu Gly Gly Arg Glu Lys Val Lys Val Ala Val
1 5 10 15
Val Gln Ala Ala Pro Val Phe Met Asp Lys Glu Lys Thr Ile Glu Lys
20 25 30
Ala Cys Lys Leu Ile Lys Glu Ala Gly Arg Asn Arg Ala Glu Leu Ile
35 40 45
Ala Phe Ser Glu Ser Phe Ile Pro Val Tyr Pro Ala Tyr Tyr Thr Val
50 55 60
Gly Tyr Glu Thr Pro Ser Gln Glu Trp Arg Asp Tyr Val Ile Ala Leu
65 70 75 80
Gln Asp Asn Ser Val Leu Ile Pro Ser Glu Asp Thr Glu Val Leu Gly
85 90 95
Gln Ala Ala Lys Glu Ala Gly Ala Tyr Ala Val Ile Gly Cys Ser Glu
100 105 110
Met Asp Asp Arg Pro Gly Ser Arg Thr Val Tyr Asn Thr Leu Leu Phe
115 120 125
Ile Gly Lys Asp Gly Lys Val Met Gly Arg His Arg Lys Leu Lys Pro
130 135 140
Thr Phe Thr Glu Arg Ile Tyr Trp Gly Glu Gly Asp Ala Gly Asp Ile

$\langle 210 \rangle$	124
$\langle 211 \rangle$	329

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 124
Met Ser Thr Phe Lys Ile Ala Thr Val Gln Ser Ala Pro Val Phe Met
1 5 10 15
Asp Arg Glu Ala Thr Ile Asp Lys Thr Cys Glu Leu Ile Ala Glu Ala
20 25 30
Ala Gln Asp Asp Val Arg Leu Val Val Phe Pro Glu Ala Phe Ile
35 40 45
Pro Thr Tyr Pro Asp Trp Val Trp Arg Ile Pro Pro Gly Gln His Gln
50 55 60
Met Leu Ala Asp Leu Tyr Gly Glu Leu Leu Glu Gln Ser Val Thr Ile
65 70 75 80
Pro Ser Leu Ala Thr Glu Arg Leu Cys Gln Ala Ala Lys Lys Ala Gly
85 90 95
Val Tyr Val Ala Val Gly Leu Asn Glu Arg Asn Thr Glu Ala Ser Asn
100 105 110
Ala Thr Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala Glu Gly Asn Leu
115 120 125
Leu Gly Lys His Arg Lys Leu Val Pro Thr Ala Pro Glu Arg Met Val
130 135 140
Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Glu Thr Ser Phe
145 150 155 160
Gly Lys Leu Ser Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala
165 170 175
Arg Tyr Ala Leu Tyr Ala Trp Gly Val Gln Leu Tyr Leu Ala Pro Thr
180 185 190
Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His Ile Ala Lys
195 200 205
Glu Gly Arg Val Tyr Val Val Gly Cys Ser Ile Ala Leu Arg Lys Glu
210 215 220
Asp Ile Pro Asp Arg Phe Glu Phe Lys Ala Lys Tyr Tyr Ala Glu Ala
225 230 235 240
Gly Glu Trp Ile Asn Lys Gly Asp Ser Val Ile Val Gly Pro Asp Gly
245 250 255
Glu Leu Ile Ala Gly Pro Leu His Lys Glu Gln Gly Ile Leu Tyr Ala
260 265 270
Glu Leu Asp Thr Arg Gln Met His Ala Pro Lys Trp Asn Leu Asp Val
275 280 285
Ala Gly His Tyr Ala Arg Pro Asp Val Phe Arg Leu Thr Val Ser Lys
290 295 300
Asp Gly His Pro Met Leu Gly Val Ala Gln Gly Pro Lys His Glu Pro
305 310 315 320
Gln Asp Lys Thr Glu Val Leu Glu Gly
325

<210> 125
<211> 1050
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 125
atgacaactg taaaaaagac ggtacgcgca gcagcgatcc agatcgacc tgacctcgac 60
agtgcaggcg gtacgctgga caaggtttgc acggccattc aaaaggcggc ggcacaaggc 120

```

gctggagctgg tggttttttcc cgaaaccttc ttgccctact atccttactt ttcattcgtg 180
cggccgccct tgcgcatcgg cccggaacac ttgctgctat atgaacgcgc agtggcggtg 240
ccaggcccggtg tgaccgatgc cgtctctgcc gtgcgcgcga gccacggcgt ggtgggtggtg 300
ctcggcggtca atgaacgcga ccatggcacg ctgtacaaca cccaactggt gttcgacgcg 360
aatggcggaac tgggtgttgaa acgcagaaaa atcacgccga cttatcacga gcggatgac 420
tgggggtcaag gcgacggcag cggactcaaa gtagtgcaaa cggcggtcgg cgggctaggc 480
gcgctagcct gttgggaaca ctacaaccca ctggcccggt atgcattgat ggcgcaacac 540
gaagaaatcc attgcgcca gtttcccggt tccatggtcg ggcaaatatt cgccgaccag 600
atggaagtga cgatacgcca tcacgctctc gtagtcggct gcttcgtggt gaatgccaca 660
ggctggctga ccgatgcgca aatcacatcg atcacgccgg accccgcgct acaaaaggca 720
ttacgtggcg gttgctgcac cgccatcgtc tcgccggaag gtgtgctcct ggcagagccg 780
ctacgcagcg gcgaaggcat ggtgatcgcc gatctcgata tggcactcat caccaaacgc 840
aaacggatga tggattcggg cggccactat gcgcggcccg aattgttaag cctgcttgctc 900
gacgaccggc gcaaggtacc ggtatccgcg ctatttgccg acagcaaccc tgccaacggg 960
cacacagttt tcaccccatc cgacatacca acccttggga gcgcacatca tgcaaacagt 1020
taccaaaccg aaccagcaac tgatcactga 1050

```

<210> 126

<211> 349

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 126

```

Met Thr Thr Val Lys Lys Thr Val Arg Ala Ala Ala Ile Gln Ile Ala
1      5      10      15
Pro Asp Leu Asp Ser Ala Gly Gly Thr Leu Asp Lys Val Cys Thr Ala
20     25     30
Ile Gln Lys Ala Ala Ala Gln Gly Ala Glu Leu Val Val Phe Pro Glu
35     40     45
Thr Phe Leu Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Pro Pro Phe
50     55     60
Ala Ser Gly Pro Glu His Leu Leu Leu Tyr Glu Arg Ala Val Ala Val
65     70     75     80
Pro Gly Pro Val Thr Asp Ala Val Ser Ala Val Ala Arg Ser His Gly
85     90     95
Val Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr
100    105    110
Asn Thr Gln Leu Val Phe Asp Ala Asn Gly Glu Leu Val Leu Lys Arg
115    120    125
Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly
130    135    140
Asp Gly Ser Gly Leu Lys Val Val Gln Thr Ala Val Gly Arg Leu Gly
145    150    155    160
Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu
165    170    175
Met Ala Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met
180    185    190
Val Gly Gln Ile Phe Ala Asp Gln Met Glu Val Thr Ile Arg His His
195    200    205
Ala Leu Glu Ser Ala Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr
210    215    220
Asp Ala Gln Ile Thr Ser Ile Thr Pro Asp Pro Ala Leu Gln Lys Ala
225    230    235    240
Leu Arg Gly Gly Cys Thr Ala Ile Val Ser Pro Glu Gly Val Leu
245    250    255
Leu Ala Glu Pro Leu Arg Ser Gly Glu Gly Met Val Ile Ala Asp Leu
260    265    270
Asp Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly

```

```

      275      280      285
His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Val Asp Asp Arg Arg
      290      295      300
Lys Val Pro Val Ser Ala Leu Phe Ala Asp Ser Asn Pro Ala Asn Gly
305      310      315      320
His Thr Val Phe Thr Pro Ser Asp Ile Pro Thr Leu Gly Ser Ala His
      325      330      335
His Ala Asn Ser Tyr Gln Thr Glu Pro Ala Thr Asp His
      340      345

```

<210> 127
 <211> 1005
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 127
atgatagcac ggaagacaat aaggggcgcg gcggtgcaga tagcgctgt gatggaagat      60
cggaaggcga cgaccgacaa ggtgtgcgcc tacattcagg aagcaggcga gaatggagcc      120
gaaattgttg tgtttcctga aaccttcatt cccaattatc cctatttctc ttttgtaaaa      180
cctccgtgtg tggcaggtaa ggatcacctt acctgttatg accaagcggg ggaaatccct      240
agccctacta ccgaccaagt ggggtctatg gccaaaaaat ggggaatcgt agtgggtgtg      300
ggcgtgaacg aaagaagcca cggcactttg tacaatgcc aaattgtctt tgacgctact      360
ggtgatattg tattggtgag acgcaaaatc acccctacct atcatgaacg gatgatctgg      420
ggacagggag atggcagtg attaaaagca gtagacacag ctgtgggaag agtgggcgct      480
ttggcgtgtt gggaacacta taatccactt gcgcgctacg cccttatggg agaccatgag      540
gaaattcatt gcagccaatt ccctggctct atggtcggcc ccattttcgg tgaccagata      600
gaagtgcaga ttgcacca ca tgcgttggaa tcgggtgtgt ttgtcatcaa ttccacaggt      660
tggctgtttg aagagcaaat ccaagccatc accgatgatc cgaaactgca caaagcattg      720
aaagacggct gtatgaccgc cattatttct cccgaaggcg tgcatttgac caaacctta      780
acagaaggcg aaggcatcat ctacgcctat ctggacatga aactcataga caagcgga      840
cggatgatgg actcggtagg acactatgca cgtccagagt tgctctcttt gcatatcaac      900
aatgcagagc aaaaaccagc cgtttacacc tctcctctta ccaaaacgga aaccaaagaa      960
gacgtaaaaa gctatgatcg caacaaagaa cagcttatcg tctga      1005

```

<210> 128
 <211> 334
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 128
Met Ile Ala Arg Lys Thr Ile Arg Ala Ala Ala Val Gln Ile Ala Pro
  1      5      10      15
Val Met Glu Asp Arg Lys Ala Thr Thr Asp Lys Val Cys Ala Tyr Ile
      20      25      30
Gln Glu Ala Gly Glu Asn Gly Ala Glu Ile Val Val Phe Pro Glu Thr
      35      40      45
Phe Ile Pro Asn Tyr Pro Tyr Phe Ser Phe Val Lys Pro Pro Val Leu
      50      55      60
Ala Gly Lys Asp His Leu Thr Leu Tyr Asp Gln Ala Val Glu Ile Pro
      65      70      75      80
Ser Pro Thr Thr Asp Gln Val Gly Ser Met Ala Lys Lys Trp Gly Ile
      85      90      95
Val Val Val Leu Gly Val Asn Glu Arg Ser His Gly Thr Leu Tyr Asn
      100      105      110
Ala Gln Ile Val Phe Asp Ala Thr Gly Asp Ile Val Leu Val Arg Arg

```

```

      115              120              125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130              135              140
Gly Ser Gly Leu Lys Ala Val Asp Thr Ala Val Gly Arg Val Gly Ala
145              150              155              160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
      165              170              175
Val Asp His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Met Val
      180              185              190
Gly Pro Ile Phe Gly Asp Gln Ile Glu Val Thr Ile Arg His His Ala
      195              200              205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Phe Glu
      210              215              220
Glu Gln Ile Gln Ala Ile Thr Asp Asp Pro Lys Leu His Lys Ala Leu
225              230              235              240
Lys Asp Gly Cys Met Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu
      245              250              255
Thr Lys Pro Leu Thr Glu Gly Glu Gly Ile Ile Tyr Ala Tyr Leu Asp
      260              265              270
Met Lys Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275              280              285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu His Ile Asn Asn Ala Glu Gln
      290              295              300
Lys Pro Ala Val Tyr Thr Ser Pro Leu Thr Lys Thr Glu Thr Lys Glu
305              310              315              320
Asp Val Lys Ser Tyr Asp Arg Asn Lys Glu Gln Leu Ile Val
      325              330

```

<210> 129
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 129
atgtcagaaa agcgaattat taaagcggct gcagttcaaa tcacaccaga ttttgaatcg      60
catgatggaa ccgtaaagaa ggttttgaat gtaattgatg aagcgggtgc taaaggtgta      120
cagatcattg tattccctga aacctttatt ccatattacc catatttttc tttcatcact      180
ccaccagtga ctgctggcgc ggagcatttg cggctctatg aaaaaagtgt cgtgatacct      240
ggtcccgtta ctcaagccat ttccgaacgt gcacgcatga ataatatggg tgttgacttt      300
ggtgtaaatg agcgtgataa cggcagtcta tataacaccc agattatttt tgatgctacc      360
ggtgagatgc ttctgaagag aagaaaaatc acacctacct atcatgagcg catgatttgg      420
gggcaaggag atgcttcagg cctgaaggtc gtcgatacgg ctattgggcg agtcggagca      480
ttggcatgct gggagcacta taaccctttg gctagataca gcctcatgac acagcatgaa      540
gaaattcact gtgctcaatt tccaggctcc atggttggtc agatcttcgc agatcaaatg      600
gatgtcacga ttctcatca tgccttgagg tcaggttgct tcgtcatcaa ctccactggc      660
tggttaactg atgatcagat caaatctatc accgacgatc ccaaaatgca gaaagcttta      720
agaggtgggt gcaacacggc cattatttct ccagaaggga atcattttaac cgagcctttg      780
cgagaagggt aaggcatggt gattgctgat cttgatattg cactcatcac caaacgaaaa      840
agaatgatgg actcagttgg ccaactacgc agaccagaac tgttgagctt agcgatcaat      900
gatgctccgg ctactccttc attccagatg aacgaacatc gtcttaaatc agtgcaatta      960
cctatcgcag aggagcttaa aaatgacaac aagcttagca gtggacagta a      1011

```

<210> 130
 <211> 336
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 130

```

Met Ser Glu Lys Arg Ile Ile Lys Ala Ala Ala Val Gln Ile Thr Pro
 1          5          10          15
Asp Phe Glu Ser His Asp Gly Thr Val Lys Lys Val Cys Asn Val Ile
          20          25          30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
          35          40          45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Thr
          50          55          60
Ala Gly Ala Glu His Leu Arg Leu Tyr Glu Lys Ser Val Val Ile Pro
65          70          75          80
Gly Pro Val Thr Gln Ala Ile Ser Glu Arg Ala Arg Met Asn Asn Met
          85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
          100          105          110
Thr Gln Ile Ile Phe Asp Ala Thr Gly Glu Met Leu Leu Lys Arg Arg
          115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
          130          135          140
Ala Ser Gly Leu Lys Val Val Asp Thr Ala Ile Gly Arg Val Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
          165          170          175
Thr Gln His Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
          180          185          190
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala
          195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Asp
          210          215          220
Asp Gln Ile Lys Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu
225          230          235          240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Asn His Leu
          245          250          255
Thr Glu Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
          260          265          270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Ala Pro Ala
          290          295          300
Thr Pro Ser Phe Gln Met Asn Glu His Arg Leu Lys Ser Val Gln Leu
305          310          315          320
Pro Ile Ala Glu Glu Leu Lys Asn Asp Asn Lys Leu Ser Ser Gly Gln
          325          330          335

```

<210> 131

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 131

```

atgtcagaaa agcgaattat taaagcggct gcagttcaaa tcacaccaga ttttgaatcg      60
catgatggaa ccgtaaagaa ggtttgtaat gtaattgatg aagcgggtgc taaaggtgta      120
cagatcattg tattccctga aacctttatt ccatattacc catatttttc tttcatcact      180
ccaccagtga ctgctggcgc ggagcatttg cggctctatg aaaaaagtgt cgtgatacct      240
gggtcccgta ctcaagacat ttccgaacgt gcacgcgatga ataatatggt tgttgacttt      300
gggtgtaaag agcgtgataa cggcagtcta tataacaccc agattatatt tgatgctacc      360

```

```

ggtgagatgc ttctgaagag aagaaaaatc acacctacct atcatgagcg catgatttgg 420
gggcaaggag atgcttcagg cctgaagggtc gtcgatacgg ctattggggcg agtcggagca 480
ttggcatgct gggagcacta taaccctttg gctagataca gcctcatgac acagcatgaa 540
gaaattcact gtgctcaatt tccagggtcc atgggttggtc agatccttcgc agatcaaatg 600
gatgtcacga ttcgtcatca tgccttggag tcagggttgct tcgtcatcaa ctccactggc 660
tggttaactg atgatcagat caaatctatc accgacgac ccaaaatgca gaaagcttta 720
agaggtggtt gcaacacggc cattatttct ccagaaggga atcattttaac cgagcctttg 780
cgagaagggtg aaggcatggt gattgctgat cttgatatgg cactcatcac caaacgaaaa 840
agaatgatgg actcagttgg ccactacgcc agaccagaac tgttgagctt agcgatcaat 900
gatgctccgg ctactccttc attccagatg aacgaacatc gtcttaaatc agtgcaatta 960
cctatcgtag aggagcttaa aaatgacaac aagcttagca gtggacagta a 1011

```

<210> 132

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 132

```

Met Ser Glu Lys Arg Ile Ile Lys Ala Ala Ala Val Gln Ile Thr Pro
  1           5           10           15
Asp Phe Glu Ser His Asp Gly Thr Val Lys Lys Val Cys Asn Val Ile
      20           25           30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
      35           40           45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Thr
      50           55           60
Ala Gly Ala Glu His Leu Arg Leu Tyr Glu Lys Ser Val Val Ile Pro
      65           70           75
Gly Pro Val Thr Gln Asp Ile Ser Glu Arg Ala Arg Met Asn Asn Met
      85           90           95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
      100          105          110
Thr Gln Ile Ile Phe Asp Ala Thr Gly Glu Met Leu Leu Lys Arg Arg
      115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130          135          140
Ala Ser Gly Leu Lys Val Val Asp Thr Ala Ile Gly Arg Val Gly Ala
      145          150          155
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
      165          170          175
Thr Gln His Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
      180          185          190
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala
      195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Asp
      210          215          220
Asp Gln Ile Lys Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu
      225          230          235
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Asn His Leu
      245          250          255
Thr Glu Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
      260          265          270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Ala Pro Ala
      290          295          300
Thr Pro Ser Phe Gln Met Asn Glu His Arg Leu Lys Ser Val Gln Leu
      305          310          315          320

```

Pro Ile Ala Glu Glu Leu Lys Asn Asp Asn Lys Leu Ser Ser Gly Gln
 325 330 335

<210> 133
 <211> 1026
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 133
 atgtcgacca agcggatcgt acgcgcgcgt gccgttcagc tggcaccgga tctggagcgg 60
 ccggagggca cactggagaa ggtttgcgcg gccatcgaca aggcggcggg ggacgggtgtg 120
 cagctcatcg tcttccccga gaccttcgta ccgtactacc cgtacttctc tttcgtgcgt 180
 gcgcgggtcg cgatgggtgc cgagcacatg cggttatacg agcgcgcggt agcgggtgccc 240
 ggtccagtaa cgccaccgt ggccggagcgg gcaaaagcgc acgcgatggt cgtcgtgctg 300
 ggtgtaaacy agcgcgatca cggctcactg tataacgcgc aactgatctt cgacgagacc 360
 ggccgtctcg tctcaaacg ccgcaagatc actccgacct atcacgagcg catggtgtgg 420
 gggcagggcg acggcagcgg ccttaagggt gtagacaccg gtatcggcag gatcggagcc 480
 ctgcctgct gggagcacta caaccgcctc gcgcgctatg cgctcatggc gcagcacgaa 540
 gagattcatt gcgcgcagtt tccgggctcg atggtggggc cgatcttcgc ggatcagatc 600
 gaggtcacga tccgccatca cgcgctggag tccggctgct tcgtcgtcaa tgcgaccggc 660
 tggctgacac ccgaacagat cgcgtcgatc acaccggacg cgggtctgca aaaggcaatc 720
 agcgggggct gcaacaccgc gatcatctcg ccggagggcg tgcacctggc cccgccgttg 780
 cgagaaggtg agggcatggt cgtggccgac ctgcacatgg cgctcatcac caaacgcaaa 840
 cgcattgatg attcgggtggg tcactacgct cgcccgaggt tgctcagcct gcgcacgat 900
 agccgcgcg cttcgcgat gtcgtcacia atggaaatac ccgggagctt gcatgaaatc 960
 accagccacg atgtccagcc agcaactgat gaccgagctc cagtcctccg gcttgagggt 1020
 ggctga 1026

<210> 134
 <211> 341
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 134
 Met Ser Thr Lys Arg Ile Val Arg Ala Ala Ala Val Gln Leu Ala Pro
 1 5 10 15
 Asp Leu Glu Arg Pro Glu Gly Thr Leu Glu Lys Val Cys Ala Ala Ile
 20 25 30
 Asp Lys Ala Ala Gly Asp Gly Val Gln Leu Ile Val Phe Pro Glu Thr
 35 40 45
 Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Ala Pro Val Ala
 50 55 60
 Met Gly Ala Glu His Met Arg Leu Tyr Glu Arg Ala Val Ala Val Pro
 65 70 75 80
 Gly Pro Val Thr Ala Thr Val Ala Glu Arg Ala Lys Ala His Ala Met
 85 90 95
 Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
 100 105 110
 Ala Gln Leu Ile Phe Asp Glu Thr Gly Arg Leu Val Leu Lys Arg Arg
 115 120 125
 Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp
 130 135 140
 Gly Ser Gly Leu Lys Val Val Asp Thr Gly Ile Gly Arg Ile Gly Ala
 145 150 155 160
 Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met

<400> 136
Met Ser Asp Lys Arg Ile Ile Lys Ala Ala Ala Val Gln Ile Thr Pro

1	5	10	15
Asp Phe Asp Ser Ala Asp Gly Thr Val Lys Lys Val Cys Lys Val Ile			
20	25	30	
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr			
35	40	45	
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Thr			
50	55	60	
Ala Gly Ala Glu His Leu Lys Leu Tyr Glu Lys Ser Val Val Ile Pro			
65	70	75	80
Gly Pro Val Thr Gln Ala Ile Ala Glu Arg Ala Arg Val Asn Gln Met			
85	90	95	
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn			
100	105	110	
Thr Gln Leu Ile Phe Asp Thr Asn Gly Glu Leu Leu Leu Lys Arg Arg			
115	120	125	
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp			
130	135	140	
Ala Ser Gly Leu Lys Val Val Glu Thr Glu Ile Ala Arg Val Gly Ala			
145	150	155	160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met			
165	170	175	
Thr Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val			
180	185	190	
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala			
195	200	205	
Leu Glu Ser Gly Cys Phe Val Ile Asn Ala Thr Gly Trp Leu Thr Asp			
210	215	220	
Ala Gln Ile Gln Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu			
225	230	235	240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu			
245	250	255	
Thr Glu Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asn Leu Asp			
260	265	270	
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His			
275	280	285	
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Lys Pro Ala			
290	295	300	
Thr Thr Thr Phe Ser Met Thr Glu Gly Arg Thr Gln Thr Glu Pro Phe			
305	310	315	320
Arg Ile Ala Glu Glu Lys Asn Asp Asp Lys Leu Ser Thr Gly Asn			
325	330	335	

<210> 137

<211> 978

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 137

atggctattg	tcaaggccgc	ggcgggtgcag	atcagtcg	tgctctacag	tcgcgcgcgc	60
acagtgga	aggctgctgc	gaagatccgc	gagctggg	gacgagggg	cgagttcgcc	120
gtcttcccc	agaccgtcat	tccctactat	ccctacttct	cttctgtgca	gccccctac	180
accagggcca	ccgaacacct	gcgcctgctc	gaggaatcgg	tgaccgtgcc	ctccgccgaa	240
accgacgcga	tcgccaaggc	cgctcgcgag	gcgggcatgg	tcgtctccat	cggcgtcaac	300
gagcgcgacg	gcggaacct	ctacaacacc	caactcctct	tcgacgccga	cggcactctc	360
atccagcgcc	gcgcgaagat	cacccccacc	tatcacgaac	gcatgggtctg	ggggcagggg	420
gacggctcag	gtctgcgcgc	cgctcgacagt	gcggtcggcc	gcatcgccca	gctcgcctgc	480
tgggagcact	accagccact	ggcccgttac	gccctcatcg	ctgacggcga	gcagatccac	540
gccgcgatgt	accccggcgc	cttcggcgcc	gatctgttcg	ccgagcagat	cgaggtcaac	600

```

atccgccagc acgccctgga atccgccagc ttcgtcgtca acgccaccgc ctggctcgac 660
gccgatcagc agggccagat cgccaaggac accggaggcc cggtcocggc cttctccggt 720
ggctttcttca ccgccatcgt cgaccccgaa ggccgtatca tcggcgaccc cctcaccagc 780
ggcgaaggcg aagtgatcgc cgacctcgat ctgcgtctca tcaaccgccc caagcgctc 840
atggacgcca gtggacacta ccagccgccc gaaattctta gcttcacatt gaccggtgca 900
ccggcgccctt atgtcaagag cgcggcgtgc cggggaaccc cgggtacgac cgtggccgag 960
gagggacggt ccgcttag                                     978

```

<210> 138

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 138

```

Met Ala Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1           5           10           15
Ser Arg Ala Gly Thr Val Asp Lys Val Val Ala Lys Ile Arg Glu Leu
      20           25           30
Gly Arg Arg Gly Val Glu Phe Ala Val Phe Pro Glu Thr Val Ile Pro
      35           40           45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Tyr Thr Gln Ala Thr
      50           55           60
Glu His Leu Arg Leu Leu Glu Glu Ser Val Thr Val Pro Ser Ala Glu
      65           70           75           80
Thr Asp Ala Ile Ala Lys Ala Ala Arg Glu Ala Gly Met Val Val Ser
      85           90           95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr Gln Leu
      100          105          110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys Ile Thr
      115          120          125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
      130          135          140
Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu Ala Cys
      145          150          155          160
Trp Glu His Tyr Gln Pro Leu Ala Arg Tyr Ala Leu Ile Ala Asp Gly
      165          170          175
Glu Gln Ile His Ala Ala Met Tyr Pro Gly Ala Phe Gly Gly Asp Leu
      180          185          190
Phe Ala Glu Gln Ile Glu Val Asn Ile Arg Gln His Ala Leu Glu Ser
      195          200          205
Ala Ser Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
      210          215          220
Ala Gln Ile Ala Lys Asp Thr Gly Gly Pro Val Pro Ala Phe Ser Gly
      225          230          235          240
Gly Phe Phe Thr Ala Ile Val Asp Pro Glu Gly Arg Ile Ile Gly Asp
      245          250          255
Pro Leu Thr Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp Leu Ala
      260          265          270
Leu Ile Asn Arg Arg Lys Arg Leu Met Asp Ala Ser Gly His Tyr Gln
      275          280          285
Pro Pro Glu Ile Leu Ser Phe Thr Leu Thr Gly Ala Pro Ala Pro Tyr
      290          295          300
Val Lys Ser Ala Ala Cys Arg Gly Thr Pro Gly Thr Thr Val Ala Glu
      305          310          315          320
Glu Gly Arg Ser Ala
      325

```

<210> 139

<211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 139
 atgaaaacaa cggttaccgt tgcctgcggt caggccgccc ccgtatttat ggatttagaa 60
 ggcaccgtag ataaaaaat caccctcatc tctgaagccg cacagaaagg cgcggagctc 120
 atcgcttttc cggagacctg gatacccggt tacccggtgt tcttatggct gaactcgccc 180
 gccacaaata tgcccctggt ttatcagtat catcagaact ctctgggtgct ggacagtaac 240
 caggcgaagc gaattgcgga tgcggcacgg cagaataaca tcactgtcgc tctgggcttc 300
 agcgaacgag atcatggaag cctctatatc gcacagtggc tgattggcag cgacggggag 360
 accattggca tccggcgcaa gctcaaggcc acgcacgtgg agcgtacgct gtccggcgaa 420
 agcgacggct cctccctgac caccctgggag acacctctgg gtaacgtcgg ggccctctgc 480
 tgctgggagc acctgcagcc gctgtcccgc tatgcaatgt attcccagca tgaggagatc 540
 cacatcgctg cctggcccag ttccagtctc tacaccagtg caacggccgc actgggtcct 600
 gacgtcaata cggcggcttc acgcctctat gccgcggagg ggcagtgcct cgtgatagcc 660
 ccgtgtgccg tggtttctga tgaaatgatt gatttactct gtcctgatga tgaccggaga 720
 gcgttactca gtgccggagg gggacatgcc cgtatttacg gcccgacgg aagagaactc 780
 gtcacccttc tcggggaaaa tgaggaagga ctgottatcg ctgagctcga ctctgctgcg 840
 attacctttg ccaaactggc ggcagaccgg gttggccact attcccgtcc tgacgtgacc 900
 cgctcctttt ttaatccttc agccaacaag actgtgatta aacgacattc gcctcctgag 960
 ttaattgccg agcagactgc agaagaagag gaggagtag 999

<210> 140
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 140
 Met Lys Thr Thr Val Thr Val Ala Cys Val Gln Ala Ala Pro Val Phe
 1 5 10 15
 Met Asp Leu Glu Gly Thr Val Asp Lys Thr Ile Thr Leu Ile Ser Glu
 20 25 30
 Ala Ala Gln Lys Gly Ala Glu Leu Ile Ala Phe Pro Glu Thr Trp Ile
 35 40 45
 Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asn Ser Pro Ala Thr Asn Met
 50 55 60
 Pro Leu Val Tyr Gln Tyr His Gln Asn Ser Leu Val Leu Asp Ser Thr
 65 70 75 80
 Gln Ala Lys Arg Ile Ala Asp Ala Ala Arg Gln Asn Asn Ile Thr Val
 85 90 95
 Ala Leu Gly Phe Ser Glu Arg Asp His Gly Ser Leu Tyr Ile Ala Gln
 100 105 110
 Trp Leu Ile Gly Ser Asp Gly Glu Thr Ile Gly Ile Arg Arg Lys Leu
 115 120 125
 Lys Ala Thr His Val Glu Arg Thr Leu Phe Gly Glu Ser Asp Gly Ser
 130 135 140
 Ser Leu Thr Thr Trp Glu Thr Pro Leu Gly Asn Val Gly Ala Leu Cys
 145 150 155 160
 Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met Tyr Ser Gln
 165 170 175
 His Glu Glu Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu Tyr Thr
 180 185 190
 Ser Ala Thr Ala Ala Leu Gly Pro Asp Val Asn Thr Ala Ala Ser Arg
 195 200 205

Leu Tyr Ala Ala Glu Gly Gln Cys Phe Val Ile Ala Pro Cys Ala Val
 210 215 220
 Val Ser Asp Glu Met Ile Asp Leu Leu Cys Pro Asp Asp Arg Arg
 225 230 235 240
 Ala Leu Leu Ser Ala Gly Gly His Ala Arg Ile Tyr Gly Pro Asp
 245 250 255
 Gly Arg Glu Leu Val Thr Pro Leu Gly Glu Asn Glu Glu Gly Leu Leu
 260 265 270
 Ile Ala Glu Leu Asp Ser Ala Ala Ile Thr Phe Ala Lys Leu Ala Ala
 275 280 285
 Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu Phe
 290 295 300
 Asn Pro Ser Ala Asn Lys Thr Val Ile Lys Arg His Ser Pro Pro Glu
 305 310 315 320
 Leu Ile Ala Glu Gln Thr Ala Glu Glu Glu Glu
 325 330

<210> 141
 <211> 1026
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 141
 atggtgttca aggcagcgac tgttcatgca gctccggtat tcatggacaa ggaagcgctcg 60
 atagataagg ctatcgacct catcaagaag gccggtcagg aagggattaa gcttctgggtt 120
 tttccggaaa cgtttattcc gggctatccg tattttatcg aatgctatcc gccgcttgcg 180
 caggtggaag cgctcgccca gtacactgac gcttccgtgg agatcgacgg cccggaagtc 240
 acccggtctc agcaggtagc caaggcggca ggcgttgacg tcgtcatggg catcagcgaa 300
 cgaatggctg agacccgaac ctgcttcaac tcgcaggtgt tcattgacgt cgacggcacg 360
 ctgctcggcg tgcacgcaa gctgcagcgg acttatgccg agcgcaaggt atggggcacag 420
 ggcggtgggt atacgctgag gacctacaag agctcgcttg gcgtgctcgg cggtcttgcc 480
 tgctgggagc acacgatgaa cctcgcgcgg caggccctga tcatgcagag cgagcagatc 540
 catgcggtcg catggcccgg actatcgacg atgcgaggtt tcgagcccgt ggccgatatc 600
 cagatcgacg ccatgatgaa gactcacgcg cttaccgcac agtgctgggt gctttcggcc 660
 ggcaatcccg tcgaccggac ctgcctcgac tggatggaaa agaacatcgg accgcaggat 720
 tacgtcaccg agggcgggcg atggagcgcc gttatccatc cgttcaacag ctatctcggc 780
 ggccctcaca cgggccttga ggaaaagctg gtcgtcgggc agatcaatct ggacgatctc 840
 aagttcgtca aagtcctggc cgacagcaaa gggcactatg ctcggccgga aatcctgaaa 900
 cttggcgtca accaaaagca gatttggcct gatgaacatt tgctggcgcg gcaggatgtg 960
 accgagttgc tggaggcgga tatcatcgaa tacccttgc aactgttgca agaccgcgcg 1020
 caatag 1026

<210> 142
 <211> 341
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 142
 Met Val Phe Lys Ala Ala Thr Val His Ala Ala Pro Val Phe Met Asp
 1 5 10 15
 Lys Glu Ala Ser Ile Asp Lys Ala Ile Asp Leu Ile Lys Lys Ala Gly
 20 25 30
 Gln Glu Gly Ile Lys Leu Leu Val Phe Pro Glu Thr Phe Ile Pro Gly
 35 40 45
 Tyr Pro Tyr Phe Ile Glu Cys Tyr Pro Pro Leu Ala Gln Val Glu Ala

50	55	60
Leu Ala Gln Tyr Thr Asp	Ala Ser Val Glu Ile Asp Gly Pro Glu Val	
65	70	75
Thr Arg Leu Gln Gln Val	Ala Lys Ala Ala Gly Val Ala Val Val Met	80
	85	90
Gly Ile Ser Glu Arg Met Ala Glu Thr Arg Thr Cys Phe Asn Ser Gln		95
	100	105
Val Phe Ile Asp Val Asp Gly Thr Leu Leu Gly Val His Arg Lys Leu		110
	115	120
Gln Pro Thr Tyr Ala Glu Arg Lys Val Trp Ala Gln Gly Gly Gly Tyr		125
	130	135
Thr Leu Arg Thr Tyr Lys Ser Ser Leu Gly Val Leu Gly Gly Leu Ala		140
	145	150
Cys Trp Glu His Thr Met Asn Leu Ala Arg Gln Ala Leu Ile Met Gln		155
	165	170
Ser Glu Gln Ile His Ala Ala Ala Trp Pro Gly Leu Ser Thr Met Arg		175
	180	185
Gly Phe Glu Pro Val Ala Asp Ile Gln Ile Asp Ala Met Met Lys Thr		190
	195	200
His Ala Leu Thr Ala Gln Cys Trp Val Leu Ser Ala Gly Asn Pro Val		205
	210	215
Asp Arg Thr Cys Leu Asp Trp Met Glu Lys Asn Ile Gly Pro Gln Asp		220
	225	230
Tyr Val Thr Glu Gly Gly Trp Ser Ala Val Ile His Pro Phe Asn		235
	245	250
Ser Tyr Leu Gly Gly Pro His Thr Gly Leu Glu Glu Lys Leu Val Val		255
	260	265
Gly Glu Ile Asn Leu Asp Asp Leu Lys Phe Val Lys Val Trp Leu Asp		270
	275	280
Ser Lys Gly His Tyr Ala Arg Pro Glu Ile Leu Lys Leu Gly Val Asn		285
	290	295
Gln Lys Gln Ile Trp Pro Asp Glu His Leu Leu Ala Arg Gln Asp Val		300
	305	310
Thr Glu Leu Leu Glu Ala Asp Ile Ile Glu Tyr Pro Leu Gln Leu Leu		315
	325	330
Gln Asp Arg Ala Gln		335
	340	

<210> 143

<211> 1122

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 143

atgacgatca	ttgcaggcgc	ggttcattgcg	gcgcgggtat	tcattggatgt	cgatgccact	60
atcgacaagg	catgcgaaat	catttcgcaag	gcaggcaaag	acggaatcga	gcttctcgtc	120
ttccctgagg	ttttcgtacc	cggctacccc	tacttcattcg	agtgttatcc	gaccttgaac	180
caaaccgctg	cgctggccgc	ctatacggat	gcctcgatcg	aggttccagg	cccgggaagtc	240
cggcgcttgc	aggtggccgc	acatcaggcc	ggcgtgatgg	ttgtgatggg	cgtagcgag	300
cgctcgcgcg	gatctcgcac	ctgcttcaac	agccagggtg	tcattcgaccg	tgacggcacc	360
ttgctgggcg	tgacccgcaa	actccagccg	acctatgtcg	agcgcattcgt	ctggggccag	420
ggcggcggac	acaccctcaa	ggtatttcgac	agcacactgg	gcaagggtggg	cggactggcc	480
tgctgggagc	acacgatgaa	cctcgcgcgc	catgcgttga	tcgcccaggg	tatccagatc	540
catgccgccc	cctggcctgg	gctttcgaca	atggccgggt	tcgaagcggg	ggctgacgtc	600
cagatcgacg	cgatgatgaa	aactcatcgc	ttgagcgcgc	aatgctttgt	cgtatcgcc	660
gcaaaccctg	tggatcagac	ctgcctggag	tggtgggaga	aacacctcgg	ccgcagcaa	720
ctcgttaccg	ccggcgagg	ctgggtcgca	atcgtccatc	ctttctgtgg	ttatatcgcc	780
gccctcaca	ccggtgccga	ggagaaggtt	ctggtaggcg	aatcaatct	ggacgacctc	840

```

aagcagggtca aggtatgggt tgattccgca ggtcattatg cgcgcccga agtcgtgcaa 900
ttgcgcgacg ccctggagag ccgtggcaat tatcgcgttg cgctgaccg cgacgccgac 960
accttgcgtgc cgctggaaga ccgcgtgcgc tttgcgcgcc agcagaacgc cgacctcttc 1020
atctcgatcc acgccgacgc caacgccaac cacgatgcgc gcggggctgg cttcacttcg 1080
aaggttga aa acctttccac gggcatttta ccaggcgatt ga 1122

```

<210> 144
 <211> 373
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 144
Met Thr Ile Ile Ala Gly Ala Val His Ala Ala Pro Val Phe Met Asp
 1           5           10           15
Val Asp Ala Thr Ile Asp Lys Ala Cys Glu Ile Ile Arg Lys Ala Gly
          20           25           30
Lys Asp Gly Ile Glu Leu Leu Val Phe Pro Glu Val Phe Val Pro Gly
          35           40           45
Tyr Pro Tyr Phe Ile Glu Cys Tyr Pro Thr Leu Asn Gln Thr Ala Ala
          50           55           60
Leu Ala Ala Tyr Thr Asp Ala Ser Ile Glu Val Pro Gly Pro Glu Val
          65           70           75           80
Arg Arg Leu Gln Val Ala Ala His Gln Ala Gly Val Met Val Val Met
          85           90           95
Gly Val Ser Glu Arg Leu Arg Gly Ser Arg Thr Cys Phe Asn Ser Gln
          100          105          110
Val Phe Ile Asp Arg Asp Gly Thr Leu Leu Gly Val His Arg Lys Leu
          115          120          125
Gln Pro Thr Tyr Val Glu Arg Ile Val Trp Gly Gln Gly Gly Gly His
          130          135          140
Thr Leu Lys Val Phe Asp Ser Thr Leu Gly Lys Val Gly Gly Leu Ala
          145          150          155          160
Cys Trp Glu His Thr Met Asn Leu Ala Arg His Ala Leu Ile Ala Gln
          165          170          175
Gly Ile Gln Ile His Ala Ala Ala Trp Pro Gly Leu Ser Thr Met Ala
          180          185          190
Gly Phe Glu Ala Val Ala Asp Val Gln Ile Asp Ala Met Met Lys Thr
          195          200          205
His Ala Leu Ser Ala Gln Cys Phe Val Val Ser Ala Ala Asn Pro Val
          210          215          220
Asp Gln Thr Cys Leu Glu Trp Met Glu Lys His Leu Gly Pro Gln Gln
          225          230          235          240
Leu Val Thr Ala Gly Gly Gly Trp Ser Ala Ile Val His Pro Phe Cys
          245          250          255
Gly Tyr Ile Ala Ala Pro His Thr Gly Ala Glu Glu Lys Val Leu Val
          260          265          270
Gly Glu Ile Asn Leu Asp Asp Leu Lys Gln Val Lys Val Trp Val Asp
          275          280          285
Ser Ala Gly His Tyr Ala Arg Pro Glu Val Val Gln Leu Arg Asp Ala
          290          295          300
Leu Glu Ser Arg Gly Asn Tyr Arg Val Ala Leu Thr Arg Asp Ala Asp
          305          310          315          320
Thr Phe Val Pro Leu Glu Asp Arg Val Arg Phe Ala Arg Gln Gln Asn
          325          330          335
Ala Asp Leu Phe Ile Ser Ile His Ala Asp Ala Asn Ala Asn His Asp
          340          345          350
Ala Arg Gly Ala Gly Phe Thr Ser Lys Val Glu Asn Leu Ser Thr Gly
          355          360          365

```

Ile Leu Pro Gly Asp
370

<210> 145
<211> 1014
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 145
atgggcatca cccacccgaa ctacaaggtc gcagtggtcc aggctgcgcc ggtctggttg 60
aacctcgagg caacggtcga gaagacaatc aggtatatg aagaggcggc caaggctgga 120
gcgaagctga tagcgtttcc ggaaacctgg attccgggct atccatggca catttggtac 180
ggaacgcccg catgggcaat cggtaagggc ttctgtccagc gctatttcga caactcgctc 240
agctatgaca gcccgctcgc gcgagcagtc gctgacgccg cagcaaagag caagatcacg 300
gttggttctcg gcctctccga gcgagcaggt ggaagcctat acatcgcgca atggctgac 360
ggaccagatg gcgagaccat cgcgaagcgg cgcaagctgc gtccgaccca cgtcgagcgc 420
acgggtgttcg gtgacgggtga cggcagccac atcgccgtgc atgaccgatc cgatctgggc 480
cggctcgggg cggtgtgctg ctgggagcac gtgcagccgt tgacgaaatt cgcgatgtac 540
gcgcagaacg agcaggttca cgtggcagca tggccgagct tctcgatgta cgaacccttt 600
gcgcatgcgc tgggttggga gacgaacaac gcggtcagca aggtctacgc ggtcgaggga 660
tcgtgcttcg tgctcgctcc ctgtgccgtt atttcgcaag cgatggtgga cgagatgtgc 720
gacactcccg acaagcgcga gcttggtcac gccggcggcg gccacgcggt gatttacggc 780
cctgacggaa gcccgctcgc agaaaagctc ggggaaaacg aagaggggct tctctacgcg 840
acgggtcaatc ttgctgcgat cggggttgcc aagaatgccg cggatccggc cgggcactat 900
tcgcgtccg acgttctaag gctgctattc aacaagagcc cggcccgaag agtggagcat 960
tttgcgctgc cgcacgagca gctcgagatc ggggcaggcc cgtctggcga ctga 1014

<210> 146
<211> 337
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 146
Met Gly Ile Thr His Pro Asn Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Val Trp Leu Asn Leu Glu Ala Thr Val Glu Lys Thr Ile Arg Tyr
20 25 30
Ile Glu Glu Ala Ala Lys Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
35 40 45
Thr Trp Ile Pro Gly Tyr Pro Trp His Ile Trp Ile Gly Thr Pro Ala
50 55 60
Trp Ala Ile Gly Lys Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Leu Ala Arg Gln Ile Ala Asp Ala Ala Lys
85 90 95
Ser Lys Ile Thr Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly
130 135 140
Asp Gly Asp Gly Ser His Ile Ala Val His Asp Arg Ser Asp Leu Gly
145 150 155 160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Val Gln Pro Leu Thr Lys
165 170 175

Phe Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Met Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Thr
 195 200 205
 Asn Asn Ala Val Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Val Ile Ser Gln Ala Met Val Asp Glu Met Cys
 225 230 235 240
 Asp Thr Pro Asp Lys Arg Glu Leu Val His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Glu Lys Leu Gly Glu
 260 265 270
 Asn Glu Glu Gly Leu Leu Tyr Ala Thr Val Asn Leu Ala Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Leu Arg Leu Leu Phe Asn Lys Ser Pro Ala Arg Arg Val Glu His
 305 310 315 320
 Phe Ala Leu Pro His Glu Gln Leu Glu Ile Gly Ala Gly Pro Ser Gly
 325 330 335
 Asp

<210> 147
 <211> 1098
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 147
 atgaccacg acgagaccac tgcccggagg ctggcagctg tgcattgccgc gcctgtgttc 60
 atggacaccg acgcgaccat cgacaagggtg atcggcttcg tcgaacaggc cggccgcgaa 120
 ggcattcgaac tcctgggtgtt ccccagagacc ttctgtgcctg gttacccta ctggatcgag 180
 tgctatccgc cgtgcagca ggtggccgccc aacgcgcagt acacggacgc ctccgtcgag 240
 gtgcctgtgc cggagatcaa gggggtgcag gcggcctgtg cccgcgctgg cgtcgaagtc 300
 gtctctcgcg tcagcgagcg actcaggggt accaggacat gcttcaactc ccagggtgttc 360
 atcgacgccc acgggagcct gctcggcggtg caccgcaagc tgcagccgac gtacgtggag 420
 cgcattcgtg gggcccaggg cggaggcgcg accctgtcgg tgttcggctc ccgctccggc 480
 cggatcggcg gtctggcctg ctgggagcac acgatgaacc tggctcgtca ggcactgctt 540
 gagcaggagc agcagatcca cgcggcgcg tggcctgccc tgtcgacgat ggcgggggttc 600
 gagaccgtcg cggacgcccc gatcgaggcc atgatgaaga cccatgcgct cacggcacag 660
 gtgttcgtca tctgcgcgtc caaccgggtc gacggcactt gcctggaatg gatgcgggac 720
 aacctcgggt aacagaagt cgtgaccgcc ggagggggct ggtccgcggt catccacccc 780
 ttcaactcct tcctcggcgg gccgcatacc ggtttgagg agaagctcgt cagcgcgacg 840
 atcgaattct ccgacatccg cttggtcaag gcctgggttg attcgaagg gcactacgcg 900
 cggcccagg tcctgcgact cgcggtcgac cgcaagccac tgtggcacga cgagtgcgag 960
 gtgccgggac aggcgcaggt acgcacccgc gctgcttctc tggcagtga ggagcaccgc 1020
 gtggtgctgc ctccagggggc ggcgcggccc gctccgcaag actgggacac ctctgcggcg 1080
 caggagctga cttcctga 1098

<210> 148
 <211> 365
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 148

```

Met Thr Gln His Glu Thr Thr Ala Arg Arg Leu Ala Ala Val His Ala
 1      5      10      15
Ala Pro Val Phe Met Asp Thr Asp Ala Thr Ile Asp Lys Val Ile Gly
 20      25      30
Phe Val Glu Gln Ala Gly Arg Glu Gly Ile Glu Leu Leu Val Phe Pro
 35      40      45
Glu Thr Phe Val Pro Gly Tyr Pro Tyr Trp Ile Glu Cys Tyr Pro Pro
 50      55      60
Leu Gln Gln Val Ala Ala Asn Ala Gln Tyr Thr Asp Ala Ser Val Glu
 65      70      75      80
Val Pro Gly Pro Glu Ile Lys Arg Val Gln Ala Ala Cys Ala Arg Ala
 85      90      95
Gly Val Glu Val Val Leu Gly Val Ser Glu Arg Leu Arg Gly Thr Arg
100      105      110
Thr Cys Phe Asn Ser Gln Val Phe Ile Asp Ala Asp Gly Ser Leu Leu
115      120      125
Gly Val His Arg Lys Leu Gln Pro Thr Tyr Val Glu Arg Ile Val Trp
130      135      140
Ala Gln Gly Gly Gly Ala Thr Leu Ser Val Phe Gly Ser Arg Ser Gly
145      150      155      160
Arg Ile Gly Gly Leu Ala Cys Trp Glu His Thr Met Asn Leu Ala Arg
165      170      175
Gln Ala Leu Leu Glu Gln Glu Gln Ile His Ala Ala Ala Trp Pro
180      185      190
Ala Leu Ser Thr Met Ala Gly Phe Glu Thr Val Ala Asp Ala Gln Ile
195      200      205
Glu Ala Met Met Lys Thr His Ala Leu Thr Ala Gln Val Phe Val Ile
210      215      220
Cys Ala Ser Asn Pro Val Asp Gly Thr Cys Leu Glu Trp Met Arg Asp
225      230      235      240
Asn Leu Gly Glu Gln Lys Phe Val Thr Ala Gly Gly Gly Trp Ser Ala
245      250      255
Val Ile His Pro Phe Asn Ser Phe Leu Gly Gly Pro His Thr Gly Leu
260      265      270
Glu Glu Lys Leu Val Ser Ala Thr Ile Asp Phe Ser Asp Ile Arg Leu
275      280      285
Val Lys Ala Trp Val Asp Ser Lys Gly His Tyr Ala Arg Pro Glu Val
290      295      300
Leu Arg Leu Ala Val Asp Arg Lys Pro Leu Trp His Asp Glu Cys Glu
305      310      315      320
Val Pro Gly Gln Ala Gln Val Arg Thr Arg Ala Ala Ser Leu Ala Val
325      330      335
Gln Glu His Pro Val Val Leu Pro Gln Gly Ala Ala Arg Pro Ala Pro
340      345      350
Gln Asp Trp Asp Thr Ser Ala Ala Gln Glu Leu Thr Ser
355      360      365

```

<210> 149

<211> 942

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 149

```

atgacgaagc ttgagaaggt ggtcgcggcg gcgggtccagg cgacgcgcgga gttcctcgac      60
cgcgaggcga ccgtcgagaa ggccgtgcgg ctgatcaagg aagcggccgg ggagggcgcc      120
ggcctgatcg tggtccccga gacgttcac cgcacgtacc cggactgggt ctggcgcgcg      180
ccggcctggg acggcccatc cgcggacctg tacgcaatgc tgctggagaa cgcggtggag      240
atccccgggc cgggtgacgga gaccctgggg aaggcggcga agcaggccaa ggccttcgtg      300

```

```

tcgatgggcg tcaacgagcg cgagccgggc ggcgggacga tctacaacac gcaggtcacg 360
ttcggaccog acgggagcgt gtcgggcaag caccgcaagc tgatgccgac cggcggcgag 420
cgcctggtgt gggggatggg cgacgggtcg atgctccagg tctatgacac gccgttcggc 480
cgctggggcg ggctgatctg ctgggagaac tacatgccgc tcgcgcgcta ctgatgtac 540
gccaagggcg tggacgtcta cgttgcgcgc acgtgggaca acagcgacat gtgggtggcg 600
acgctccgcc acatcgccaa ggagggggcg ctgtacgtga tcggcgtggc gccgctgctg 660
cgcggggtcg acgtccccga cgacgtgccg gggaaggccg agctgtgggg cggcgatgac 720
gactggatgt cgcgcggtt ctccaccatc gtcgcgcggg gcggcgaggt gctggccggg 780
ccgctgacgg aggaggaagg catcctctac gcgagatcg acccggcgag agcccgttcg 840
tcacggcacc agttcgatcc ggtggggcac tactcgcgcc ccgacgtgtt tcggctcgtc 900
gtggacgagt cgccaagcc ccagacgtcc ggcccgggct ag 942

```

<210> 150

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 150

```

Met Thr Lys Leu Glu Lys Val Val Ala Ala Val Gln Ala Thr Pro
1      5      10      15
Glu Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Val Arg Leu Ile
20      25      30
Lys Glu Ala Ala Gly Glu Gly Ala Gly Leu Ile Val Phe Pro Glu Thr
35      40      45
Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Arg Ala Pro Ala Trp Asp
50      55      60
Gly Pro Ser Ala Asp Leu Tyr Ala Met Leu Leu Glu Asn Ala Val Glu
65      70      75      80
Ile Pro Gly Pro Val Thr Glu Thr Leu Gly Lys Ala Ala Lys Gln Ala
85      90      95
Lys Ala Phe Val Ser Met Gly Val Asn Glu Arg Glu Pro Gly Gly Gly
100     105     110
Thr Ile Tyr Asn Thr Gln Val Thr Phe Gly Pro Asp Gly Ser Val Leu
115     120     125
Gly Lys His Arg Lys Leu Met Pro Thr Gly Gly Glu Arg Leu Val Trp
130     135     140
Gly Met Gly Asp Gly Ser Met Leu Gln Val Tyr Asp Thr Pro Phe Gly
145     150     155     160
Arg Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg
165     170     175
Tyr Ser Met Tyr Ala Lys Gly Val Asp Val Tyr Val Ala Pro Thr Trp
180     185     190
Asp Asn Ser Asp Met Trp Val Ala Thr Leu Arg His Ile Ala Lys Glu
195     200     205
Gly Arg Leu Tyr Val Ile Gly Val Ala Pro Leu Leu Arg Gly Ser Asp
210     215     220
Val Pro Asp Asp Val Pro Gly Lys Ala Glu Leu Trp Gly Gly Asp Asp
225     230     235     240
Asp Trp Met Ser Arg Gly Phe Ser Thr Ile Val Ala Pro Gly Gly Glu
245     250     255
Val Leu Ala Gly Pro Leu Thr Glu Glu Glu Gly Ile Leu Tyr Ala Glu
260     265     270
Ile Asp Pro Ala Arg Ala Arg Ser Ser Arg His Gln Phe Asp Pro Val
275     280     285
Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Val Val Asp Glu Ser
290     295     300
Pro Lys Pro Gln Thr Ser Gly Pro Gly
305     310

```

<210> 151
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 151
 atgagagtcg ttaaagccgc cggggtccaa ctgaaaccag tcctttatag ccgtgaggga 60
 acagtcgata acgtcgtcaa gaagatccac gagctgggcc aacaaggagt gcagttcgca 120
 acgttcccgg aaaccgtggt gccttactat ccgtactttt cgatcgtgca gtccggctat 180
 caaatccttg ccggcgggtga gttcctaaag ctgcttgatc agtcagtgc cgtgccatct 240
 cttgccaccg aagcgatcgg cgaggcctgc aggcaagcgg gcgtcgttgt ctccatcggc 300
 gtcaacgagc gtgacggggg aactctgtac aatacgcaac ttctctttga tgccgacggc 360
 acgttgattc aaagacgacg caagatcacg cccacccatt acgagcgcac ggtctggggc 420
 cagggcgatg gctcaggttt acgggcggtt gacagcaagg tcgcgcgcat tgggtcaactg 480
 gcttggtttt agcactacaa cccgcttgcg cgttacgcca tgatggccga tggcgagcaa 540
 atccactctg cgatgttccc gggctccatg ttccggcgatg cgttttcaga gaaggtggaa 600
 atcaacgtaa ggcagcatgc aatggagtct ggatgctttg tcgtctgcgc tacggcctgg 660
 ctggatgccg accaacaggc acaaatcatg aaggacacag gctgcgagat cgttccgatc 720
 tcgggcggtt gcttcaccgc tatcgtgaca cccgacggga cgctgatagg cgaacccatc 780
 cactcggggc aaggcggttg tattgccgac ctcgatttca agctcatcga caagcggaag 840
 cagtggttg acacgcgcgg ccactacagc cggccagaat tgctcagcct cctaattgat 900
 cggaactcca cggcacacat acacgaacgg aacgagcaac cgaagtcggc cgttgagcaa 960
 gactcgaga atgtattcac cgctattgct taa 993

<210> 152
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 152
 Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Lys Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Gly Thr Val Asp Asn Val Val Lys Lys Ile His Glu Leu
 20 25 30
 Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Ala
 50 55 60
 Gly Gly Glu Phe Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
 65 70 75 80
 Leu Ala Thr Glu Ala Ile Gly Glu Ala Cys Arg Gln Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Val Ala Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Phe Pro Gly Ser Met Phe Gly
 180 185 190

```

Asp Ala Phe Ser Glu Lys Val Glu Ile Asn Val Arg Gln His Ala Met
      195                200                205
Glu Ser Gly Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
      210                215                220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Glu Ile Gly Pro Ile
      225                230                235                240
Ser Gly Gly Cys Phe Thr Ala Ile Val Thr Pro Asp Gly Thr Leu Ile
      245                250                255
Gly Glu Pro Ile His Ser Gly Glu Gly Val Cys Ile Ala Asp Leu Asp
      260                265                270
Phe Lys Leu Ile Asp Lys Arg Lys His Val Val Asp Thr Arg Gly His
      275                280                285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
      290                295                300
Ala His Ile His Glu Arg Asn Glu Gln Pro Lys Ser Ala Val Glu Gln
      305                310                315                320
Asp Ser Gln Asn Val Phe Thr Ala Ile Ala
      325                330

```

<210> 153
 <211> 1074
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 153
atgccaaacg caagaaagat tgttgaggcc gtggcccaag ttgcacagga attcttcgac      60
actgaagcga atctcggtaa agcgatagcg gcgattcaca atgctgcgaa gcaaggcgca      120
gatatcgctcg tcttcgccga atgctatttg ggccaatata catattgggc gcaattttac      180
gacaactctg ccaagaacta ttccaagggt tggacggccc tgtacgacgg tgcgatcact      240
gtgggtggcg atgaatgccg ggctattgct gctgcgggcta gacagtccaa gattcatgtc      300
gtcatggggtt gcaatgagct atccgaccga gccggcgggcg caacggtata caacagcctc      360
ttgttttttcg accgaaaggg cgagttgata ggctcgacacc ggaaattgat gccgtcgatg      420
cacgagcggtt tgatccatgg cacaggcgac ggaagagact tgaatgttta cgataccgat      480
atcggtatgt tgggtggggtt gatttgctgg gagcaccata tgtcgctctc gaagtatgcc      540
atggcgacta tgggtgaaga agttcatgtt gcaagctggc ctgggatgtg gcgcggagga      600
gacgcggcaa tcggtgagag gatggtcgaa gcggatcttg gggcgccggtt tgtttgtgac      660
gccgaatttg cgatccgaga atatgcggca gagacaggaa atttcgttct aagcgcgtct      720
ggatatttttc cgaaggacaa tatatccgat gagtggcgcg aagcgattcc aaaccttcaa      780
gcgcagtggg ctgtggggcg gagttctatc gtggcaccgg ggggctccta tctggtccca      840
ccactcatta atgaggagaa gatcctctgc gccgaactcg atttcaatct caggcgtott      900
tggaagacct ggatcgatcc gattggtoac tattcgcgtc ccgatgttta tagcctgcaa      960
ctgcataacg ttgctggggc tgagtattcc tatcaggccg tagatttgaa gcgcacgcca     1020
aagccccaat cgctgtgggt agatgcgtcc gaggaagacg gtgcgctgaa ttga      1074

```

<210> 154
 <211> 357
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 154
Met Pro Asn Ala Arg Lys Ile Val Gly Ala Val Ala Gln Val Ala Gln
  1              5              10              15
Glu Phe Phe Asp Thr Glu Ala Asn Leu Gly Lys Ala Ile Ala Ala Ile
      20              25              30
His Asn Ala Ala Lys Gln Gly Ala Asp Ile Val Val Phe Ala Glu Cys

```

<400>	155								
atgggcatcg	aacatccgaa	atacaagggtg	gccgtggtgc	aggccgcgcc	ggcctggctc				60
gatctcgacg	gctogatcaa	gaaggcgatt	gcgctgatcg	aggaagcggc	cgccaagggc				120
gctaagctga	tcgctttccc	cgaaaccttc	attcccggct	atccctggca	catctggctg				180
gactcgccgg	cctgggcgat	cgccgcgcgc	tttgtgcagg	gctacttcga	taactcgctg				240
gcctacgaca	gcccgcgaagc	cgaaaagctg	cgcgcgcgcg	tcaagaaggc	caagctcact				300
gccgtgattg	gcctgtcgga	gcgcgacggc	ggcagcctct	atatagcgca	atggctgatt				360
ggccctgatg	gcgagaccat	cgcaaaacgc	agaaagctgc	ggccaacgca	cgcggaacgc				420
accgtttttt	gcgagggtga	cggcagcgac	cttgccctgc	acgacgggcc	cggaatcggg				480
cggctgggag	cgctgtgctg	ctggggcgac	ctgcaaccgc	tttcgaaata	cgcgatgtat				540
gcgcagaacg	aacaggtcca	tgtcgcgtca	tggccaggct	tctcgtctct	cgcaccttc				600

```

gcgccggcgcg tcggcgccga ggtcaacaat gcggcttccc gcgtctacgc ggctcgagggc 660
tcgtgcttcg tgctggcgcc gtgcgccacg gtttcgcaag ccatgatcga cgagctgtgt 720
gaccggccgg acaagcatgc gctgttgac gcgggtggcg gacacgccgc gatttacggc 780
ccggacggca gctcgatcgc ggagaagctg ccgcaggacg cggagggcct gttgatcgcc 840
gagatcgatc tcggggcgat cgggggttgcc aagaatgcag ccgaccggcg cggtcattat 900
tcgcggccgg acgtgacgcg actcctgctg aacaagaacc ggatgcgaag ggctcgaggag 960
tttgcgctgc cggtcgatcc ggctcgcaacg accgaggagg agcaagtcgc gacgccgtcg 1020
aggcccagcc aggccgcgta a 1041

```

<210> 156
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 156

Met	Gly	Ile	Glu	His	Pro	Lys	Tyr	Lys	Val	Ala	Val	Val	Gln	Ala	Ala
1				5					10					15	
Pro	Ala	Trp	Leu	Asp	Leu	Asp	Gly	Ser	Ile	Lys	Lys	Ala	Ile	Ala	Leu
			20					25					30		
Ile	Glu	Glu	Ala	Ala	Ala	Lys	Gly	Ala	Lys	Leu	Ile	Ala	Phe	Pro	Glu
			35					40					45		
Thr	Phe	Ile	Pro	Gly	Tyr	Pro	Trp	His	Ile	Trp	Leu	Asp	Ser	Pro	Ala
			50					55				60			
Trp	Ala	Ile	Gly	Arg	Gly	Phe	Val	Gln	Arg	Tyr	Phe	Asp	Asn	Ser	Leu
					70					75					80
Ala	Tyr	Asp	Ser	Pro	Gln	Ala	Glu	Lys	Leu	Arg	Ala	Ala	Val	Lys	Lys
					85					90				95	
Ala	Lys	Leu	Thr	Ala	Val	Ile	Gly	Leu	Ser	Glu	Arg	Asp	Gly	Gly	Ser
			100						105				110		
Leu	Tyr	Ile	Ala	Gln	Trp	Leu	Ile	Gly	Pro	Asp	Gly	Glu	Thr	Ile	Ala
			115					120					125		
Lys	Arg	Arg	Lys	Leu	Arg	Pro	Thr	His	Ala	Glu	Arg	Thr	Val	Phe	Gly
			130					135				140			
Glu	Gly	Asp	Gly	Ser	Asp	Leu	Ala	Val	His	Asp	Arg	Pro	Gly	Ile	Gly
					150					155					160
Arg	Leu	Gly	Ala	Leu	Cys	Cys	Trp	Glu	His	Leu	Gln	Pro	Leu	Ser	Lys
				165						170				175	
Tyr	Ala	Met	Tyr	Ala	Gln	Asn	Glu	Gln	Val	His	Val	Ala	Ser	Trp	Pro
			180						185				190		
Ser	Phe	Ser	Leu	Tyr	Asp	Pro	Phe	Ala	Pro	Ala	Leu	Gly	Ala	Glu	Val
			195					200				205			
Asn	Asn	Ala	Ala	Ser	Arg	Val	Tyr	Ala	Val	Glu	Gly	Ser	Cys	Phe	Val
			210			215						220			
Leu	Ala	Pro	Cys	Ala	Thr	Val	Ser	Gln	Ala	Met	Ile	Asp	Glu	Leu	Cys
					230					235					240
Asp	Arg	Pro	Asp	Lys	His	Ala	Leu	Leu	His	Ala	Gly	Gly	Gly	His	Ala
				245						250				255	
Ala	Ile	Tyr	Gly	Pro	Asp	Gly	Ser	Ser	Ile	Ala	Glu	Lys	Leu	Pro	Gln
			260					265					270		
Asp	Ala	Glu	Gly	Leu	Leu	Ile	Ala	Glu	Ile	Asp	Leu	Gly	Ala	Ile	Gly
			275				280					285			
Val	Ala	Lys	Asn	Ala	Ala	Asp	Pro	Ala	Gly	His	Tyr	Ser	Arg	Pro	Asp
			290			295					300				
Val	Thr	Arg	Leu	Leu	Leu	Asn	Lys	Asn	Arg	Met	Arg	Arg	Val	Glu	Glu
					310					315					320
Phe	Ala	Leu	Pro	Val	Asp	Pro	Val	Ala	Thr	Thr	Glu	Glu	Glu	Gln	Val
				325					330					335	
Ala	Thr	Pro	Ser	Arg	Pro	Ser	Gln	Ala	Ala						

340

345

<210> 157
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 157
 atgagagtcg ttaaagctgc tgcggtccaa ctgagtcgcc tgctgtatag ccgtgaggga 60
 acagtagaaa aggtcggttcg gaagatccac gagcttggcg atcaaggagt cgagttcgcc 120
 acgttcccgg agaccgtagt gccctactat ccgtacttct cggccgtcca gacgccgatt 180
 cagaacatgc acggcccggg gcacctgaag ttgctcgagc aatcggtgac cgtcccgtcg 240
 cccgccaccg acgcgatcgg cgacgcctgc cgccacgccg gcgtcgctcg ctcgatcggc 300
 gtcaacgaac gcgatggcgg cacgatctac aacacgcagc tcctgttcga cgccgacggc 360
 accttgatcc agcgcggcgg aaagatcacg ccgaccttct acgaacgaat ggtctgggga 420
 caggggtgacg gttcggggct gcgcgccgtc gacagccgcg taggacgcat cggccagctc 480
 gcctgtttcg agcactacaa cccgctggcg cgctacgccca tgatggccga cggcgagcag 540
 attcactccg cgatgtaccc cggctccatc tttggagacg cattcgcgca gaaaatcgag 600
 atcaacatcc gccagcacgc gctcgagtcc ggtgcgttcg tcgtcaacgc caccgcctgg 660
 ctcgatgccg accagcaggc gcgatcatg aaggataccg gctgcaccat cgaaccgatc 720
 tcgggcccgtt gcttcaccgc catcgtcacc ccggacggga ccctgctggg cgaagcgata 780
 cgttcggggg agggagtggg ggtcgccgat ctgcacttca cgctgatcga caggcgcaag 840
 caagtgatgg actctcgtgg tcactacagt cggccggagt tgctcagcct tctgatcgac 900
 cgcacaccca ccgcacacct acacgaacgc gaagcgcacc ccagagcaag tgaggactgg 960
 caaggttccg agagtctgcg cgccatgcag gcctcggcac cgaaggtctg a 1011

<210> 158
 <211> 336
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 158
 Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
 20 25 30
 Gly Asp Gln Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Ile Gln Asn Met His
 50 55 60
 Gly Pro Glu His Leu Lys Leu Leu Glu Gln Ser Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Gly Asp Ala Cys Arg His Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr Phe Tyr Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Arg Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ile Phe Gly

<400> 160															
Met	Ser	Ser	Thr	Val	Thr	Val	Ala	Ile	Ile	Gln	Ala	Ala	Pro	Val	Tyr
1				5				10					15		
Tyr	Asp	Leu	Pro	Ala	Thr	Leu	Asp	Lys	Ala	Ala	Lys	Leu	Val	Ala	Asp
			20					25					30		
Ala	Ala	Ala	Gln	Gly	Ala	Thr	Leu	Ile	Val	Phe	Gly	Glu	Thr	Trp	Phe
		35					40					45			

Pro Gly Tyr Pro Ala Trp Leu Asp Tyr Cys Pro Asn Val Ala Leu Trp
 50 55 60
 Asn His Pro Pro Thr Lys Gln Val Phe Glu Arg Leu His Arg Asn Ser
 65 70 75 80
 Ile Ala Val Pro Ser Lys Glu Leu Asp Phe Leu Gly Ala Leu Ala Arg
 85 90 95
 Lys His Gln Val Val Leu Val Leu Ser Ile Asn Glu Arg Val Glu Gln
 100 105 110
 Gly Ala Gly His Gly Thr Leu Tyr Asn Thr Leu Leu Thr Ile Asp Ala
 115 120 125
 Asp Gly Thr Leu Ala Asn His His Arg Lys Leu Met Pro Thr Tyr Thr
 130 135 140
 Glu Arg Met Val Trp Gly Met Gly Asp Gly Val Gly Leu Gln Ala Val
 145 150 155 160
 Asp Thr Ala Val Gly Arg Val Gly Gly Leu Ile Cys Trp Glu His Trp
 165 170 175
 Met Pro Leu Ala Arg Gln Thr Met His Ile Ser Gly Glu Gln Ile His
 180 185 190
 Ile Ser Val Phe Pro Thr Val His Glu Met His Gln Ile Ala Ser Arg
 195 200 205
 Gln Tyr Ala Phe Glu Gly Arg Thr Phe Val Leu Thr Val Gly Gly Ile
 210 215 220
 Leu Ala Ala Gln Asp Leu Pro Ala Glu Leu Glu Arg Pro Ala Asp Leu
 225 230 235 240
 Pro Pro Thr Gln Leu Val Gln Arg Gly Gly Ser Ala Ile Ile Ala Pro
 245 250 255
 Asp Gly Arg Tyr Leu Ala Gly Pro Val Tyr Asn Glu Glu Thr Ile Leu
 260 265 270
 Thr Ala Thr Leu Asp Leu Gly Glu Ile Ile Arg Glu Ser Met Thr Leu
 275 280 285
 Asp Val Thr Gly His Tyr Ala Arg Pro Asp Val Phe Asp Leu Thr Val
 290 295 300
 Lys Arg Ser Arg Pro
 305

<210> 161
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 161
 atgaccacca tccgcgcgcgc cgccgtgcag tttagcccgg tgctgtactc gcgccaggcc 60
 accgtcgaca agctgtgccg caccctgctg gaactgggcc gcgaaggggg gcagttcgcg 120
 gtattcccgg aaaccgtggg gcgtactac ccatattttt ccttcgtgca gccaccgttc 180
 gccatgggca aacaacacct gttgctgctc gagcaatccg tcaactgtgcc ctctgacgtc 240
 acccggcaga tcggtgaggg ctgccgggaa gcggggatcg tcgccagcat cggcgtcaac 300
 gaacgcgacg gcggcactat ttataacgcg cagttgctgt tcgatgccga cggcagcctg 360
 attcagcagc ggcgcaagat caccocgacc tatcacgaac gcatggctctg ggggcagggc 420
 gatggttccg gcctgcgcgc cgtggacagt gcggtggggc gtatcggttc cctggcctgc 480
 tgggaacatt acaaccccct ggcgcgctac gcgctgatgg ccgatggcga acagattcat 540
 gtggcgatgt ttcccggctc cctggctcggc gacatctttg ccgagcagat cgaagtacc 600
 atccgccacc acgccctgga aagcggtctc ttctgtgtca acgccacggc ttggctggat 660
 gccgaccagc agggccggat catgcaggac accggctgcg agttggggcc gatttccggc 720
 ggctgtttta ccgcgatcat ttcccgggag ggcaagggtc tcggcgagcc gctgcgcagc 780
 ggcaagggg tggtcattgc tgacctcgac ctggccctga tcgacaagcg caaacgcatg 840
 atggattcgg tcggtcacta cagccgcccg gaactgctca gcctgcttat cgaccgcagc 900
 ccgaccgcc acgtgcatga acttgccgcc gcgcttaatc ctgccaggga gtctgatcca 960
 ctagtgtcga cctgcaggcg cgcgagctcc agcttttgtt cccttttag 1008

<210> 162
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 162
 Met Thr Thr Ile Arg Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Gln Ala Thr Val Asp Lys Leu Cys Arg Thr Leu Leu Glu Leu
 20 25 30
 Gly Arg Glu Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Ala Met Gly Lys
 50 55 60
 Gln His Leu Leu Leu Leu Glu Gln Ser Val Thr Val Pro Ser Asp Val
 65 70 75 80
 Thr Arg Gln Ile Gly Glu Ala Cys Arg Glu Ala Gly Ile Val Ala Ser
 85 90 95
 Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
 100 105 110
 Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Gln Arg Arg Lys Ile Thr
 115 120 125
 Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
 130 135 140
 Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
 145 150 155 160
 Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
 165 170 175
 Glu Gln Ile His Val Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
 180 185 190
 Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
 195 200 205
 Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
 210 215 220
 Gly Arg Ile Met Gln Asp Thr Gly Cys Glu Leu Gly Pro Ile Ser Gly
 225 230 235 240
 Gly Cys Phe Thr Ala Ile Ile Ser Pro Glu Gly Lys Val Leu Gly Glu
 245 250 255
 Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Leu Ala
 260 265 270
 Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
 275 280 285
 Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Ser Pro Thr Ala His
 290 295 300
 Val His Glu Leu Ala Ala Ala Leu Asn Pro Ala Arg Glu Ser Asp Pro
 305 310 315 320
 Leu Val Ser Thr Cys Arg Arg Ala Ser Ser Ser Phe Cys Ser Leu
 325 330 335

<210> 163
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 163
 gtgaccatca tcaaagccgc cgcagtgcag atcagccccg tgctttacag ccgggaagcc 60
 accgtcgaaa aggtcgttcg cgagaccgcg gaactcggcc agaagggcgt gcagttcgca 120
 acgtttccgg aaaccgtggt gccgtactac ccatacttct ccgccgtcca gacgggcatc 180
 gaactgctgt ccggcaaaga gcacctgcga ctgctggagc aggccgtgac tgttccttcc 240
 cccgccactg atgcgattgc ccaggcggca cgcgaggccg gcatggtggt gtcgatcggc 300
 gtcaacgagc gtgacggcgg caccatctac aacacgcagc tgctctttga tgccgacggc 360
 acgctggtgc agcgcggccg caagatcacg ccgacgcatt tcgagcgcac ggtgtggggc 420
 cagggcgacg gttcgggcct gcgcgcagtg gataccaagg tcggccgcac tggccagctg 480
 gcctgcttcg agcacaacaa cccgctcgcg cgctacgcaa tgatggccga tggcgagcag 540
 atccattcct ccatgtaccc gggtccgcc ttccggcgac gattcgcgca gcgcattggag 600
 atcaacattc gccaacacgc cctggagtcg gggtgcttcg tggatgaatgc caccgcgtgg 660
 ctgcagcccg accagcagcg gcagatcatg aaggacacgg gctgcgccat cgggccgatc 720
 tctggcggct gcttcacgac catcgctcag ccggacggca tgctgatcgg cgaaccctc 780
 cgcgagggcg agggcgagat catcgccgac ctcgatttca ccctgatcga ccgccgcaag 840
 ctgctgatgg actcggtcgg ccactacaac cgtccggagc tgctgagcct gctgatcgac 900
 cgcacaccgg cggcgaactt ccatgagcgc agtacgcac cggccgtcga tgccgccagc 960
 ggcctcgaaa tcctctaa 978

<210> 164
 <211> 325
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 164
 Val Thr Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Glu Lys Val Val Arg Glu Thr Arg Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Thr Lys Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ser Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Asp Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ala Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Met Leu Ile
 245 250 255
 Gly Glu Pro Leu Arg Glu Gly Glu Gly Glu Ile Ile Ala Asp Leu Asp

			260						265				270				
Phe	Thr	Leu	Ile	Asp	Arg	Arg	Lys	Leu	Leu	Met	Asp	Ser	Val	Gly	His		
		275					280					285					
Tyr	Asn	Arg	Pro	Glu	Leu	Leu	Ser	Leu	Leu	Ile	Asp	Arg	Thr	Pro	Ala		
	290					295					300						
Ala	Asn	Phe	His	Glu	Arg	Ser	Thr	His	Pro	Ala	Val	Asp	Ala	Ala	Ser		
305					310					315					320		
Gly	Leu	Glu	Ile	Leu													
				325													

<210> 165
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 165

atggccaatt	tcaaattcaa	ggcggcggcg	gtgcaggccg	cgcccgtttt	cctcgatctc	60
gaggctagca	tcgccaagtc	gatcgccctg	atogaacaag	ccgccgccaa	cggcgccaag	120
ctgatcgctt	ttcccgaagt	cttcattccc	ggctaccctt	ggcacatctg	gctcgacagt	180
cccgcttggg	cgatcgggcg	cggcttcgtc	tcgogctatt	tcgagaactc	gctggactac	240
aacagccccg	aggccgagcg	cctcaggctc	gocgtcaaga	aggcgggcct	gacggcggtg	300
atcggcctct	ccgagcgcg	cggcggcagc	ctctacatcg	cgcaatggat	catcggcctt	360
gacggcgaga	ccgttgcgaa	acggcgtaag	ctcgggccga	cccattgcga	gcgcacggtc	420
tatggagaag	gcgacggcag	cgacctcgcg	gttcacgacg	tatctggcat	cggccgtctc	480
ggcgcgctct	gctgctggga	gcatatccag	ccgctgtcga	aattcgcgat	gtattcgcaa	540
aatgagcaag	tgcacgtcgc	gtcctggccg	agcttctcgc	tctacgacct	gttcgcgccg	600
gcgctgggcg	ccgaggtcaa	caacgcagcc	tcgcggtatc	atgcggtcga	aggctcatgc	660
ttcgctcattg	cgccctgcgc	gaccgtttcg	cctgcaatga	tcgaggaact	gtgcgacgcg	720
ccaaacaaac	atgcgcttct	gcacgcgggc	ggcggttctg	cgcgcatcta	tgggcgggac	780
ggcgcttcga	tcgcccagac	gctgccgcca	gacaggaag	gcttgatcta	cgccgacatc	840
gacctcaccg	cgatcggcgt	cgccaaggcc	gccgcgcatc	ccgccggcca	ttattcgcg	900
cccgcagtca	cgcgcttgc	cttcaacaag	aagcccgctc	ggcgagtcga	aacttttgct	960
ttgcccgctc	atgcgccggc	gccggagacg	cagaccgccg	cgagctga		1008

<210> 166
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 166

Met	Ala	Asn	Phe	Lys	Phe	Lys	Ala	Ala	Ala	Val	Gln	Ala	Ala	Pro	Ala
1				5				10					15		
Phe	Leu	Asp	Leu	Glu	Ala	Ser	Ile	Ala	Lys	Ser	Ile	Ala	Leu	Ile	Glu
			20					25					30		
Gln	Ala	Ala	Ala	Asn	Gly	Ala	Lys	Leu	Ile	Ala	Phe	Pro	Glu	Val	Phe
		35					40					45			
Ile	Pro	Gly	Tyr	Pro	Trp	His	Ile	Trp	Leu	Asp	Ser	Pro	Ala	Trp	Ala
	50					55				60					
Ile	Gly	Arg	Gly	Phe	Val	Ser	Arg	Tyr	Phe	Glu	Asn	Ser	Leu	Asp	Tyr
65					70					75				80	
Asn	Ser	Pro	Glu	Ala	Glu	Arg	Leu	Arg	Leu	Ala	Val	Lys	Lys	Ala	Gly
				85					90					95	
Leu	Thr	Ala	Val	Ile	Gly	Leu	Ser	Glu	Arg	Asp	Gly	Gly	Ser	Leu	Tyr
		100						105					110		
Ile	Ala	Gln	Trp	Ile	Ile	Gly	Pro	Asp	Gly	Glu	Thr	Val	Ala	Lys	Arg

$\langle 220 \rangle$

<223> Obtained from an environmental sample

<400> 168

```

Met Gly Ile Glu His Pro Lys Tyr Arg Val Ala Val Val Gln Ala Ala
 1           5           10           15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Ser Ile Ala Leu
 20           25           30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35           40           45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
 50           55           60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65           70           75
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
 85           90           95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
100           105           110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115           120           125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130           135           140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
145           150           155
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165           170           175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180           185           190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
195           200           205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210           215           220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225           230           235
Asp Arg Pro Asp Lys His Ala Leu Leu His Val Gly Gly Gly Phe Ala
245           250           255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
260           265           270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
275           280           285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
290           295           300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
305           310           315
Phe Ser Pro Pro Ser Glu Ala Val Glu Pro Thr Asp Ile Ala Ala Ala
325           330           335
Ala Ser

```

<210> 169

<211> 1077

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 169

```

atggccctca cccatccgaa attgaaagtc gccgccgtgc aggcagctcc cgcgttcctc      60
gatgtcgatg ccgcagtgga caaagcgggtg cggctaatacg acgaagcggc agcaaacggc      120
tccagtctgg tggcattccc cgagacctgg atccccggct atccgttttg gatctggctt      180
ggctcgccgg cctgggcaat catgcgcggg tttgtgtctc gctatttcga taattcgctc      240

```

```

agctatgaca gccggcaggc agagcgccctg cgcgacgccc cgaagcgcca caaactgacc 300
gtcgtcatgg gcctgtccga gcgcgcgggc ggtagccttt acatcgcgca gtggatcatt 360
gggtcccaatg gcgagaccgt cgcacagcgg cgcaagctca agcccaccca tgcggagcgc 420
accgtcttcg gcgaggggtga cggcagccac ctggcggttac acaatcttcc aatcggacgg 480
ctcgggtgcgc tgtgtgtgctg ggagcacctc cagccgctct ccaaatacgc gatgtacgcc 540
cagaacgaag agatccacgt ggcgccatgg ccgtccttct cgctctacga cccgtttgcg 600
cacgcgctcg gcgccgaagt caacaacgca gcgagccaga tctacgcggt tgaaggttcc 660
tgctttgtcg tcgcgccatg tgcggtgatc tcgcaggaaa tgatcgatct tatgtgcgat 720
acccccgaca agcatcagct tattcacgtc ggtggcggct tcaccgtgat ctatggcccc 780
gacgggtgcgc gcatcggcga caagctcgcg ccagatcagg aaggcattgt ctatgccgac 840
atcgatctcg gcatgatccc gatcgcgaaa gctgcgcggc atcctgccgg ccactatgcg 900
cgacccgacg ttacccgcct tctgttcaac aatcgtcccg ccaatcgggt ggaaaccctc 960
gtgctccccg ttgatcaggc ccgtgacatc gatgcacgtg tggaggccgc ggcacctcag 1020
gcgcgaccag caaccgggaa cgaggatccc gccgcaaagc ctatggccgc cgaatga 1077

```

<210> 170

<211> 358

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 170

```

Met Ala Leu Thr His Pro Lys Leu Lys Val Ala Ala Val Gln Ala Ala
1          5          10          15
Pro Ala Phe Leu Asp Val Asp Ala Ala Val Asp Lys Ala Val Arg Leu
20          25          30
Ile Asp Glu Ala Ala Ala Asn Gly Ser Ser Leu Val Ala Phe Pro Glu
35          40          45
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ser Pro Ala
50          55          60
Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
65          70          75          80
Ser Tyr Asp Ser Arg Gln Ala Glu Arg Leu Arg Asp Ala Ala Lys Arg
85          90          95
His Lys Leu Thr Val Val Met Gly Leu Ser Glu Arg Ala Gly Gly Ser
100          105          110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asn Gly Glu Thr Val Ala
115          120          125
Gln Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
130          135          140
Glu Gly Asp Gly Ser His Leu Ala Val His Asn Leu Pro Ile Gly Arg
145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165          170          175
Ala Met Tyr Ala Gln Asn Glu Glu Ile His Val Ala Ala Trp Pro Ser
180          185          190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
195          200          205
Asn Ala Ala Ser Gln Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Val
210          215          220
Ala Pro Cys Ala Val Ile Ser Gln Glu Met Ile Asp Leu Met Cys Asp
225          230          235          240
Thr Pro Asp Lys His Gln Leu Ile His Val Gly Gly Gly Phe Thr Val
245          250          255
Ile Tyr Gly Pro Asp Gly Ala Arg Ile Gly Asp Lys Leu Ala Pro Asp
260          265          270
Gln Glu Gly Ile Val Tyr Ala Asp Ile Asp Leu Gly Met Ile Pro Ile
275          280          285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val

```

```

      290              295              300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Ala Asn Arg Val Glu Thr Leu
305              310              315              320
Val Leu Pro Val Asp Gln Val Arg Asp Ile Asp Ala Arg Val Glu Ala
      325              330              335
Ala Ala Pro Gln Ala Arg Pro Ala Thr Gly Asn Glu Asp Pro Ala Ala
      340              345              350
Lys Pro Met Ala Ala Glu
      355

```

<210> 171
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 171
atgactaagg gaacagtga agtcgcgggc ggcaggtca cccccgtgtt catggatcgt      60
aaagccacga tcgtcaaggc ctgcgacacg atcgccgagg cgggcaagaa cggcgcgcg      120
ctgggtggtgt tcccggagac gtttgttcct ggctaccgag actgggtctg gacggcgagc      180
gctgggacgc atcgcgatat ccaaccaggc atgtacgcgg aactgctgga ccaggctgtc      240
tcgattccga gcccggcgac ggacgccctc tgccgtgctg caaagaaggc gggcgtctac      300
gtcgtcatcg gcgtcaatga gctgagtggg ccgggcgga gcctgtacaa cacgctgatc      360
tacatcgatg acgaaggcga gatcatgggc cgccaccgca agctggtccc cacgatgggc      420
gagcgccctg tctgggcacc cggcgacggc agcacgctgg aggcgtacga gacatcgatc      480
ggcaggctgg gcggactgat ctgctgggag aactacatgc cgctggcccg ctacgccatg      540
tacgcctggg gcgtgcagat ctacgtcgcg ccgacgtggg acagctcgga cgggtgggtt      600
ggcagcatgc agcacatcgc ccgcgaaggg cggacggcgg tgatcggctg ctgcatggcg      660
atccgtcgca gcgacatccc ggacaagtac gagttcaaga agctgtaccg gccgagcaag      720
agcaaagacg aagaatgggt gaacgatggc aacagcgtca tcgtcgacc cgggtggacga      780
atactcgccg ggccggctgc caaagaggag acgatcctct acgccgatct ggaccggca      840
gccgagcgcg gttcaaagtt ctcgtagat gtggcagggc actacgcgcg gccggacgtc      900
ttccagctga cgggtgaatcg cggtcgggca gaactggtga atgtggccgg tgatatcgca      960
ccggcaacca acggcaaagt caaaacaccg gcgaaattac gccgcaagta a      1011

```

<210> 172
 <211> 336
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 172
Met Thr Lys Gly Thr Val Lys Val Ala Ala Ala Gln Val Thr Pro Val
1      5      10      15
Phe Met Asp Arg Lys Ala Thr Ile Val Lys Ala Cys Asp Thr Ile Ala
20     25     30
Glu Ala Gly Lys Asn Gly Ala Arg Leu Val Val Phe Pro Glu Thr Phe
35     40     45
Val Pro Gly Tyr Pro Asp Trp Val Trp Thr Ala Thr Ala Gly Thr His
50     55     60
Arg Asp Ile His Gln Ala Met Tyr Ala Glu Leu Leu Asp Gln Ala Val
65     70     75     80
Ser Ile Pro Ser Pro Ala Thr Asp Ala Leu Cys Arg Ala Ala Lys Lys
85     90     95
Ala Gly Val Tyr Val Val Ile Gly Val Asn Glu Leu Ser Gly Pro Gly
100    105    110
Gly Ser Leu Tyr Asn Thr Leu Ile Tyr Ile Asp Asp Glu Gly Glu Ile

```

$\langle 220 \rangle$

<223> Obtained from an environmental sample

<400> 174

```

Met Lys Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Gly Thr Val Glu Arg Val Val Arg Lys Ile His Glu Leu
          20          25          30
Gly Arg Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Ile Ile Ala
 50          55          60
Gly Pro Glu His Leu Lys Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65          70          75          80
Pro Ala Thr Asp Ala Ile Ser Glu Ala Ala Arg Gln Ala Gly Val Val
          85          90          95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
          100          105          110
Gln Leu Leu Phe Asp Ala Asp Gly Ala Leu Ile Gln Arg Arg Arg Lys
          115          120          125
Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
 145          150          155          160
Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
          165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
          180          185          190
Asp Pro Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
          195          200          205
Glu Ser Ala Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
 210          215          220
Gln Gln Ala Gln Ile Cys Lys Asp Thr Gly Cys Asp Ile Gly Pro Ile
 225          230          235          240
Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Thr Leu Leu
          245          250          255
Gly Glu Pro Ile Arg Ser Gly Glu Gly Met Val Ile Val Asp Leu Asp
          260          265          270
Phe Thr Leu Ile Asp Lys Arg Lys Gln Val Met Asp Ser Arg Gly His
          275          280          285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
          290          295          300
Ala His Val His Asp Arg Ala Val Arg Pro Glu Ser Ala Ala Glu Gln
 305          310          315          320
Arg Ser Glu Glu Leu Leu Ala Thr Ala Val
          325          330

```

<210> 175

<211> 945

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 175

```

atgaccacct acgggcagtt tagacttgcc gcgatcaatg ccgcgcctgt ctacttcgac      60
agggaagcat ccaccgaaaa agcttgccgg ctcattctcg aagcgggggc atcaggggcg      120
acgctggcgg cgtttgccga gacgtggctt cccggctatc cattccacat ctggagggaa      180
gttccgactg ctctccgagt ggaatacatc gctaattgcc togagattcc cagcccaacg      240
accgaccgat tgtgcgcggc ggctcgtcag gcgaacatcg atgttgtgat cggcgttgtc      300
gaactggatg cgcagacaca cgggacggtc tactgtacgc tcttgttcat tggcagcgat      360

```

```

ggctcaattc tgggacgtca tcgaaagatt aaaccgactt tcgtggagcg aaccgcatgg 420
ggggaaggtg acggcagcag cctgatcgtc tacgagcgcc cgtatggcaa gatcagtggt 480
ctgtgttgct gggaacacaa tatggttctg ccgggctacg cgctgatggc gcaggggacg 540
cagattcata tcgccgcatg gcccggtgg gaaagcactc gccatctgct cttatcaaga 600
gcattcgctt ctcaggcagc ggcgtatgtg attgatgtag gcgctatcgt caatcgtgac 660
gaccttcggg aagattacca ggctttgatt gctggaagct actggggcgg aagttgcac 720
atcaaccag aaggcgaggt catcgctggt ccagcgaaat cggagacatc tctggttgca 780
gattgctcaa ccgagcagat ctttagctca aaagtgtct gtgatgtggg cgggcattat 840
tctcgcccg atattttca gtcctatgtc aatcgaaagc catatcaacg tatcgctcgag 900
acgaacaacc cacacccgc tccgattgag ttogattacc gttga 945

```

<210> 176

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 176

```

Met Thr Thr Tyr Gly Gln Phe Arg Leu Ala Ala Ile Asn Ala Ala Pro
 1      5      10      15
Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile
      20      25      30
Leu Glu Ala Gly Ala Ser Gly Ala Thr Leu Ala Ala Phe Gly Glu Thr
      35      40      45
Trp Leu Pro Gly Tyr Pro Phe His Ile Trp Arg Glu Val Pro Thr Ala
      50      55      60
Leu Arg Val Glu Tyr Ile Ala Asn Ala Val Glu Ile Pro Ser Pro Thr
      65      70      75      80
Thr Asp Arg Leu Cys Ala Ala Ala Arg Gln Ala Asn Ile Asp Val Val
      85      90      95
Ile Gly Val Val Glu Leu Asp Ala Gln Thr His Gly Thr Val Tyr Cys
      100      105      110
Thr Leu Leu Phe Ile Gly Ser Asp Gly Ser Ile Leu Gly Arg His Arg
      115      120      125
Lys Ile Lys Pro Thr Phe Val Glu Arg Thr Ala Trp Gly Glu Gly Asp
      130      135      140
Gly Ser Ser Leu Ile Val Tyr Glu Arg Pro Tyr Gly Lys Ile Ser Gly
      145      150      155      160
Leu Cys Cys Trp Glu His Asn Met Val Leu Pro Gly Tyr Ala Leu Met
      165      170      175
Ala Gln Gly Thr Gln Ile His Ile Ala Ala Trp Pro Gly Trp Glu Ser
      180      185      190
Thr Arg His Leu Leu Leu Ser Arg Ala Phe Ala Ser Gln Ala Ala Ala
      195      200      205
Tyr Val Ile Asp Val Gly Ala Ile Val Asn Arg Asp Asp Leu Arg Glu
      210      215      220
Asp Tyr Gln Ala Leu Ile Ala Gly Ser Tyr Trp Gly Gly Ser Cys Ile
      225      230      235      240
Ile Asn Pro Glu Gly Glu Val Ile Ala Gly Pro Ala Lys Ser Glu Thr
      245      250      255
Ile Leu Val Ala Asp Cys Ser Thr Glu Gln Ile Phe Ser Ser Lys Val
      260      265      270
Leu Cys Asp Val Gly Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu
      275      280      285
His Val Asn Arg Lys Pro Tyr Gln Arg Ile Val Glu Thr Asn Asn Pro
      290      295      300
His Pro Ala Pro Ile Glu Phe Asp Tyr Arg
      305      310

```

<210> 177
 <211> 948
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 177
 atggactcac ttaccggttg tctcgcgcaa atcgcgcccg tttggttgaa tcgggcgggg 60
 acgttgtcaa agatgttgga acaggttcga gcgcgaaaag aggcgggctg tcagcttggt 120
 gtgtttggtg aggcgttgct ccccggttat ccattttgga tcgaactgac gaacggcgca 180
 gtcttcaatt cgccgatgca aaaggaaatc cacgcgcaat acatggatca agctgtgcag 240
 atcgaagcag ggcattcttga tccattgtgc ggccgaggcaa aagcgacagg catcaccgtg 300
 gtcgcgggca tcatcgagcg tccgttggtg cgccgaggac atagtttata tgcgagtctg 360
 gtgtatatcg atttgaacgg tgtcatccaa tcggtgcatc gcaaactgat gccacacctat 420
 gaagaacgac tcacctgggt gcctggcgat ggcatggtt tacgcgtgca tacactgggc 480
 gcttttacgg ttggcaaaact caattgttg gaaaactgga tgccgctgcc gcgcgcggct 540
 ctgtatgcgc aaggcgaaga tctgcacgtt gctgtctggc ccgggtccgt gcgcaacaca 600
 caggatatta cgcgctttat cgcaatggag tcgcgcatcg ttgtcgtttc gggttcgagt 660
 ttgatgcgca agagtgcact cccacaagat acgcctcatc tctccgccat tcttgaatct 720
 gcacccgatc cactcgccaa cggaggttcg tgtctggctg gacctgacgg taaatggatc 780
 gttgaaccgg ttgcggatga agagaagttg atcgtcgcca ccattgacca tgcccgtgta 840
 cgtgaagaac gccagaactt tgatccatcc ggcatattaca gccgaccaga tgtgacacaa 900
 ttgagagtca accgccagcg acaaagcgtt atcgcttttg atgagtag 948

<210> 178
 <211> 315
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 178
 Met Asp Ser Leu Thr Val Gly Leu Ala Gln Ile Ala Pro Val Trp Leu
 1 5 10 15
 Asn Arg Ala Gly Thr Leu Ser Lys Met Leu Glu Gln Val Arg Ala Ala
 20 25 30
 Lys Glu Ala Gly Cys Gln Leu Val Val Phe Gly Glu Ala Leu Leu Pro
 35 40 45
 Gly Tyr Pro Phe Trp Ile Glu Leu Thr Asn Gly Ala Val Phe Asn Ser
 50 55 60
 Pro Met Gln Lys Glu Ile His Ala His Tyr Met Asp Gln Ala Val Gln
 65 70 75 80
 Ile Glu Ala Gly His Leu Asp Pro Leu Cys Gly Ala Ala Lys Ala His
 85 90 95
 Gly Ile Thr Val Val Ala Gly Ile Ile Glu Arg Pro Leu Asp Arg Gly
 100 105 110
 Gly His Ser Leu Tyr Ala Ser Leu Val Tyr Ile Asp Leu Asn Gly Val
 115 120 125
 Ile Gln Ser Val His Arg Lys Leu Met Pro Thr Tyr Glu Glu Arg Leu
 130 135 140
 Thr Trp Ser Pro Gly Asp Gly His Gly Leu Arg Val His Thr Leu Gly
 145 150 155 160
 Ala Phe Thr Val Gly Lys Leu Asn Cys Trp Glu Asn Trp Met Pro Leu
 165 170 175
 Pro Arg Ala Ala Leu Tyr Ala Gln Gly Glu Asp Leu His Val Ala Val
 180 185 190
 Trp Pro Gly Ser Val Arg Asn Thr Gln Asp Ile Thr Arg Phe Ile Ala
 195 200 205

```

Met Glu Ser Arg Ser Phe Val Val Ser Val Ser Ser Leu Met Arg Lys
  210                215                220
Ser Asp Phe Pro Gln Asp Thr Pro His Leu Ser Ala Ile Leu Glu Ser
225                230                235                240
Ala Pro Asp Pro Leu Ala Asn Gly Gly Ser Cys Leu Ala Gly Pro Asp
  245                250                255
Gly Lys Trp Ile Val Glu Pro Val Ala Asp Glu Glu Lys Leu Ile Val
  260                265                270
Ala Thr Ile Asp His Ala Arg Val Arg Glu Glu Arg Gln Asn Phe Asp
  275                280                285
Pro Ser Gly His Tyr Ser Arg Pro Asp Val Thr Gln Leu Arg Val Asn
  290                295                300
Arg Gln Arg Gln Ser Val Ile Ala Phe Asp Glu
305                310                315

```

<210> 179
 <211> 915
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 179
atgaccacca aagcagccat cattcaggcg cgccccatat actacgatct ggcggcgtgt      60
gtcgataaag cgcttgccct catcacccgag gcggcgccac gcggcgcgaa catcgtcacg      120
ctcggcgaga cgtggctgcc gggctatccc gcgtggctgg atgtgtgctg cgagatgggg      180
ctgtgggatc acgcgccgac caaagccgtc ttccagcggc tccatgccaa cagcgtcacc      240
atccccggcg cggagatcag ccagttctgc gacatcgccc gccgccttag catcgctgtg      300
gtgctcagcg tcaacgagcg cgtccgcaac acctgtgtca acaccctgct cagcattgac      360
gagcgcgggc acatccgcaa ccaccaccgc aagctgatgc cgacctacac tgagcgcac      420
gtctgggggc agggcgacgg cgcgggctta caggcggtcg agacggcaac cgggcgctc      480
ggcgggctga tctgctggga aactgggatg ccgctggcac ggcaggcgct gcacaacgcc      540
ggggagcaaaa ttacgctttc ggtcttcccg accgtcaacg acccgcgcca ccaagtgcgc      600
agccgccagt acgctttcga gggcgctgc ttgctgctga ccgcccgcag catccagcgc      660
gccgacgacc taccgccgga actgaccgtc aaggcgggga tcgcgccgga tgatctggtg      720
cagggcgggc gcagcgccat catcgcgccg gacatgcgct acctcgccgg accctgcttc      780
gacgaggaaa ccatcctcta cgccgacctc gacctgagcg agacgatccg cgagagcatg      840
acgctggacg tgagcgggca ttactcgcg cccgacgtgt tcaccttcga ggttaatcgg      900
cagcggaataa tttag                                     915

```

<210> 180
 <211> 304
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 180
Met Thr Thr Lys Ala Ala Ile Ile Gln Ala Arg Pro Ile Tyr Tyr Asp
  1                5                10                15
Leu Ala Ala Cys Val Asp Lys Ala Leu Ala Leu Ile Thr Glu Ala Ala
  20                25                30
Ala Arg Gly Ala Asn Ile Val Thr Leu Gly Glu Thr Trp Leu Pro Gly
  35                40                45
Tyr Pro Ala Trp Leu Asp Val Cys Val Glu Met Gly Leu Trp Asp His
  50                55                60
Ala Pro Thr Lys Ala Val Phe Gln Arg Leu His Ala Asn Ser Val Thr
  65                70                75                80
Ile Pro Gly Ala Glu Ile Ser Gln Phe Cys Asp Ile Ala Arg Arg Leu

```

$\langle 220 \rangle$

<223> Obtained from an environmental sample

<400> 182

```

Met Pro Lys Thr Val Arg Ala Ala Ala Val Gln Ile Ala Pro Asp Leu
 1          5          10          15
Thr Ser Arg Ala Gly Thr Val Glu Arg Val Leu Asn Ala Ile Ala Glu
 20          25          30
Ala Ser Asp Lys Gly Ala Glu Leu Ile Val Phe Pro Glu Thr Phe Val
 35          40          45
Pro Trp Tyr Pro Tyr Phe Ser Phe Val Leu Pro Pro Val Gln Gln Gly
 50          55          60
Pro Glu His Leu Arg Leu Tyr Glu Glu Ala Val Thr Val Pro Ser Ala
 65          70          75          80
Glu Thr Arg Ala Val Ala Asp Ala Ala Arg Lys Arg Asn Ala Val Ile
 85          90          95
Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn Thr Gln
 100         105         110
Leu Ile Phe Asp Ala Asp Gly Ser Leu Lys Leu Lys Arg Arg Lys Ile
 115         120         125
Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ala
 130         135         140
Gly Leu Lys Val Val Glu Thr Ala Ile Gly Arg Met Gly Ala Leu Ala
 145         150         155         160
Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Gln
 165         170         175
His Glu Glu Ile His Ala Ser His Phe Pro Gly Ser Leu Val Gly Pro
 180         185         190
Ile Phe Gly Glu Gln Ile Glu Val Thr Met Arg His His Ala Leu Glu
 195         200         205
Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser Glu Glu Gln
 210         215         220
Ile Ala Ser Ile His Pro Asp Pro Ser Leu Gln Lys Gly Leu Arg Asp
 225         230         235         240
Gly Cys Met Thr Cys Ile Ile Thr Pro Glu Gly Arg His Val Val Pro
 245         250         255
Pro Leu Thr Ser Gly Glu Gly Ile Leu Ile Gly Asp Leu Asp Met Arg
 260         265         270
Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ala
 275         280         285
Arg Pro Glu Leu Leu His Leu Val His Asp Thr Thr Pro Ala Arg Ala
 290         295         300
Arg Glu Gln Val Gly Leu Ser Gly Asp Phe Ser Asp Ala Gly Gln Asp
 305         310         315         320
Lys Leu Phe Glu Glu Val Gln Asp Ala
 325

```

<210> 183

<211> 1002

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 183

```

atggctgagt cacgcattat tcgtgccgcc gccgcccaga ttgcgccaga tctccatgag      60
gccagcaaaa cgctggcccg ggtgctggac gcgatcgatc aggcagccgc acagggggca      120
gagatcatcg tctttccoga gacctttgtg ccttattacc cctacttctc gtttatcacg      180
cccgcgatga ccgccggagc ggcccacatg aaattgtatg accaggcggg ggtggtgccc      240
ggcccgatca cccatgcggg gggcgaacgc gcccgctgc gcaacatcgt cgtggtgctg      300
gggggtgaatg aacgtgacca cggcacgctc tacaacaccc aactggtatt tgatgccagc      360

```

```

ggggaactgg tgctgaaacg ccgcaaaatc accccgacct atcacgaacg gatgatctgg 420
ggacaggggag acggtgccgg attaaagggtg gtggactcgg cggttgggcg catcggggct 480
ttagcctgct gggagcacta caaccactg gcgcgtaca gcctgatgac tcagcacgag 540
gagatccatt gcagccagtt ccctggttca ctggtggggc cgatttttgc cgagcagatg 600
gacgtcacca ttcgccatca tgcactggag tccggttgct ttgtcatcaa tgccaccggc 660
tggctgaccg aggagcagat caacgagctg accagcgacc cggcgttaca aaaggggctg 720
cgtggtggct gcaacaccgc catcatctcg ccggaaggcc gccatctggt gccgccactg 780
accgaagggtg aggggatttt gattgccgat ctggacatgg ccctgatcac caaacgcaaa 840
cgcatgatgg attctgtcgg ccactatgcc cgaccggaat tactcagcct gcgcctcgat 900
gcgacgcctg cccgttatgt ggtggcgcgt gataatgagt ccgaaaccgg aggaggcaac 960
gatgcagaac gtaccgtcta cgcgccagca gctgatcact ga 1002

```

<210> 184

<211> 333

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 184

```

Met Ala Glu Ser Arg Ile Ile Arg Ala Ala Ala Ala Gln Ile Ala Pro
 1          5          10          15
Asp Leu His Glu Ala Ser Lys Thr Leu Ala Arg Val Leu Asp Ala Ile
      20          25          30
Asp Gln Ala Ala Gln Gly Ala Glu Ile Ile Val Phe Pro Glu Thr
      35          40          45
Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Ala Met Thr
      50          55          60
Ala Gly Ala Ala His Leu Lys Leu Tyr Asp Gln Ala Val Val Val Pro
65          70          75          80
Gly Pro Ile Thr His Ala Val Gly Glu Arg Ala Arg Leu Arg Asn Ile
      85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
      100          105          110
Thr Gln Leu Val Phe Asp Ala Ser Gly Glu Leu Val Leu Lys Arg Arg
      115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130          135          140
Gly Ala Gly Leu Lys Val Val Asp Ser Ala Val Gly Arg Ile Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
      165          170          175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
      180          185          190
Gly Pro Ile Phe Ala Glu Gln Met Asp Val Thr Ile Arg His His Ala
      195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ala Thr Gly Trp Leu Thr Glu
      210          215          220
Glu Gln Ile Asn Glu Leu Thr Ser Asp Pro Ala Leu Gln Lys Gly Leu
225          230          235          240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Arg His Leu
      245          250          255
Val Pro Pro Leu Thr Glu Gly Glu Gly Ile Leu Ile Ala Asp Leu Asp
      260          265          270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Arg Leu Asp Ala Thr Pro Ala
      290          295          300
Arg Tyr Val Val Ala Arg Asp Asn Glu Ser Glu Thr Gly Gly Gly Asn
305          310          315          320

```

Asp Ala Glu Arg Thr Val Tyr Ala Pro Ala Ala Asp His
325 330

<210> 185
<211> 1017
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 185
atgggcattg aacatccgaa atacaaggtc gcggtgggtgc aggcggcccc cgccctggctc 60
gatctcgacg gctcgggtcga taagtcgatc gcgctgatca aggaggcggc cgagaagggg 120
gcgaagctga tcgcctttcc cgaggccttc atccccgggtt acccctggca tatctggatg 180
gactcgccgg cctggggcgat cggccgcggc ttcgtgcagc gttatttcga caattcgctg 240
tcctatgaca gtccgcaggc cgagcggctg cgcgatgcgg tgaagaaggc gaagctcacc 300
gccgtgttcg gactgtccga gcgcgacggc ggcagcctct acctcgcgca atggctgatc 360
gggcccgatg gcgagaccat cgccaagcgc cgcaagctgc ggccgaccca cgccgaacgt 420
accgtctatg gcgaaggcga cggcagcgat cttgccgtgc atgcgcgcgc cgacatcggc 480
cggatcggcg cgctctgctg ctgggagcat ctgcagccac tgtcgaaata cgcgatgtac 540
gcccagaacg aacagggtcca tgtcgcagcc tggcccagct tctcgctgta cgaccccttc 600
gcgcggcgct taggggcccga ggtcaacaac gcggcctccc gcgtctatgc ggtggaaggc 660
tcctgcttcg tgctcgcgcc gtgcgcgacg gtgtcgcagg cgatgatcga cgagctctgc 720
gaccggcccg acaagaacgc gctgctgcac gtcggcgggc gctttgccgc gatctatggc 780
cccgcggca gccagatcgg cgacaagctg gcgcgggacc aggaggggct gctgatcgcc 840
gagatcgacc ttggcgccat cgggtgtcgcc aagaacgccg ccgatcccgc cgggcactat 900
tcgcgtcccg acgtgacgcg gttgctgctc aacaagaagc gataccagcg cgtcgagcag 960
ttcgcgctgc cgtcgcacac cgtcgcagccg gcggatatcg gcgcagcggc gagctga 1017

<210> 186
<211> 338
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 186
Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Ala Trp Leu Asp Leu Asp Gly Ser Val Asp Lys Ser Ile Ala Leu
20 25 30
Ile Lys Glu Ala Ala Glu Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35 40 45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
50 55 60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Asp Ala Val Lys Lys
85 90 95
Ala Lys Leu Thr Ala Val Phe Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130 135 140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Ala Arg Ala Asp Ile Gly
145 150 155 160
Arg Ile Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165 170 175

Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Pro Asp Lys Asn Ala Leu Leu His Val Gly Gly Gly Phe Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
 260 265 270
 Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Arg Tyr Gln Arg Val Glu Gln
 305 310 315 320
 Phe Ala Leu Pro Val Asp Thr Val Glu Pro Ala Asp Ile Gly Ala Ala
 325 330 335
 Ala Ser

<210> 187
 <211> 1059
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 187
 atgggcatca atcatcccaa gtacaaagtg gccgtcgtgc aagcggcacc tgtctggctc 60
 gacctggatg gaacagtcga caagtgcatt cggctgatag gcgaggccgc tgagaagggg 120
 tgcaagctca ttgcatttcc cgagacgttc atcccggggg acccctggca catctggatg 180
 ggagctccgg cctggacgat cgggcgcgga ttctgtcagc gatacttoga caattcgctt 240
 gcgtacgaca gtccgcaggc aaacaagctt cgcgcgcggy tgaagcgcgc cggagtgcgc 300
 gcagttctcg gcttgtcgga gcgcgcgga ggctccctgt acatcgccca gtggctcatc 360
 ggacctgatg gcgagaccat cgctcaacgg cgaaagctgc gccccacca tgcggagcgc 420
 accgtcttcg gcgagggcga tggcagcgat ttggcgggtg acagccgccc cgacatcggc 480
 cgactgggtg ccctttgctg ctgggaacat ctccagcctt tgaccaagta cgcgatgtac 540
 gcgcaagacg agcaagtgcg cgctcgctgca tggccgagct tctcgatgta cgagccttcc 600
 gcgcacgccc tggggtggga gacgaacaac gcggtgagca aggtgtacgc ggctgaaggt 660
 tcgtgctacg tcctggcccc ctgcgccatc atctctcagg cgatggtgga cgaactcgtc 720
 gacagcgagg acaagaagcc gctggttcat gccggcgggg ggcatgcggt gatctatggt 780
 cccgatggca ccctgcttac tcccaagctt gcagaagacg aggagggcct actgatcgcg 840
 gagatcgatc tgggggcaat cgggggtcgcc aagaacgcgg cagaccccg cggccactac 900
 tcgcggcccc atgtcaccgc cctgctcttc aacaaccggc cggccaagcg cgtggagacg 960
 atgctgctcc cggtcgacgc ggcagaagtc gtggagccgg cggacggagc gctcaatgcg 1020
 tccgaggggac gccagcgaca gttcaagctg cccgcctag 1059

<210> 188
 <211> 352
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 188
 Met Gly Ile Asn His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala

1	5	10	15
Pro Val Trp	Leu Asp Leu Asp Gly Thr Val Asp Lys Cys Ile Arg Leu		
	20	25	30
Ile Gly Glu	Ala Ala Glu Lys Gly Cys Lys Leu Ile Ala Phe Pro Glu		
	35	40	45
Thr Phe Ile	Pro Gly Tyr Pro Trp His Ile Trp Met Gly Ala Pro Ala		
	50	55	60
Trp Thr Ile	Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu		
	65	70	75
Ala Tyr Asp	Ser Pro Gln Ala Asn Lys Leu Arg Ala Ala Val Lys Arg		
	85	90	95
Ala Gly Val	Thr Ala Val Leu Gly Leu Ser Glu Arg Arg Gly Gly Ser		
	100	105	110
Leu Tyr Ile	Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala		
	115	120	125
Gln Arg Arg	Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly		
	130	135	140
Glu Gly Asp	Gly Ser Asp Leu Ala Val His Ser Arg Pro Asp Ile Gly		
	145	150	155
Arg Leu Gly	Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Thr Lys		
	165	170	175
Tyr Ala Met	Tyr Ala Gln Asp Glu Gln Val His Val Ala Ala Trp Pro		
	180	185	190
Ser Phe Ser	Met Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Thr		
	195	200	205
Asn Asn Ala	Val Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Tyr Val		
	210	215	220
Leu Ala Pro	Cys Ala Ile Ser Gln Ala Met Val Asp Glu Leu Val		
	225	230	235
Asp Ser Glu	Asp Lys Lys Pro Leu Val His Ala Gly Gly Gly His Ala		
	245	250	255
Val Ile Tyr	Gly Pro Asp Gly Thr Leu Leu Thr Pro Lys Leu Ala Glu		
	260	265	270
Asp Glu Glu	Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly		
	275	280	285
Val Ala Lys	Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp		
	290	295	300
Val Thr Arg	Leu Leu Phe Asn Asn Arg Pro Ala Lys Arg Val Glu Thr		
	305	310	315
Met Leu Leu	Pro Val Asp Ala Ala Glu Val Val Glu Pro Ala Asp Gly		
	325	330	335
Ala Leu Asn	Ala Ser Glu Gly Arg Gln Arg Gln Phe Lys Leu Pro Ala		
	340	345	350

<210> 189

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 189

atgcaagaca	cgaaattcaa	agttgcagtc	gtccaggccg	cgccggtatt	catggatgcg	60
ccagcctccg	tggccaaggc	gatcggtttc	atccaggagg	cgggcgagc	cggggcgaag	120
ctgctggcgt	tcccgagggt	ctggattccg	ggctaccctt	ggtggctttg	gctcgggacg	180
ccggcgtggg	gaatgcagtt	tgtgcccgcg	tatcacgcca	attcgctgcg	tgctgatgga	240
cccgaaatcc	tcgctctttg	tgcggcgcgc	gccgaagcga	agatcaacgt	cgtgatgggc	300
ttctccgaaa	tcgacggagg	aacgctctac	ctaagtcagg	ttttcatcag	cgatgcgggc	360
aagatcatct	tcaagcgccg	aaagctcaag	ccgacccacg	tcgaacgtac	gctatttggt	420
gaaggagatg	ggtctgattt	ccgagtcgtc	gacagcagcg	tcgggcgcct	cggagccctg	480

```

tgctgtgccg aacacattca gccgtttgtcg aaatacgcca tgtacgcgat gaacgagcaa 540
attcatgtgg cgtcgtggcc atctttcacg ctctatcgcg gcaaagccta cgctttgggt 600
catgaggtga atcttgccgc cagccaaatc tacgcgctcg aaggagggtg cttcgtcttg 660
catgccacgg caattaccgg tcaggatatg ttcgacatgc ttgcgacac tccggaaagg 720
gcggatttgc tgaatgcgga gggagcaaag ccgggtggag gctattcgat gatttttggt 780
cccgatggtc agccgatgtg cgagcatctg ccgcaggaca aggaaggcat cctctatgcc 840
ggcgtagacc tgtcgatgat tgcgatcgcc aaagcggcct acgatcctac ggggcactac 900
gcccgcggtg atgtcgtccg tctcatggtc aaccgcagcc cccgtcgcac gagcgtcagc 960
ttcagcgaag acgagaacgc ggcggtcact ttcaccgaga cctga 1005

```

<210> 190

<211> 334

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 190

```

Met Gln Asp Thr Lys Phe Lys Val Ala Val Val Gln Ala Ala Pro Val
1      5      10      15
Phe Met Asp Ala Pro Ala Ser Val Ala Lys Ala Ile Gly Phe Ile Gln
20      25      30
Glu Ala Gly Ala Ala Gly Ala Lys Leu Leu Ala Phe Pro Glu Val Trp
35      40      45
Ile Pro Gly Tyr Pro Trp Trp Leu Trp Leu Gly Thr Pro Ala Trp Gly
50      55      60
Met Gln Phe Val Pro Arg Tyr His Ala Asn Ser Leu Arg Ala Asp Gly
65      70      75      80
Pro Glu Ile Leu Ala Leu Cys Ala Ala Ala Glu Ala Lys Ile Asn
85      90      95
Val Val Met Gly Phe Ser Glu Ile Asp Gly Gly Thr Leu Tyr Leu Ser
100     105     110
Gln Val Phe Ile Ser Asp Ala Gly Lys Ile Ile Phe Lys Arg Arg Lys
115     120     125
Leu Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly
130     135     140
Ser Asp Phe Arg Val Val Asp Ser Ser Val Gly Arg Leu Gly Ala Leu
145     150     155     160
Cys Cys Ala Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ala
165     170     175
Met Asn Glu Gln Ile His Val Ala Ser Trp Pro Ser Phe Thr Leu Tyr
180     185     190
Arg Gly Lys Ala Tyr Ala Leu Gly His Glu Val Asn Leu Ala Ala Ser
195     200     205
Gln Ile Tyr Ala Leu Glu Gly Cys Phe Val Leu His Ala Thr Ala
210     215     220
Ile Thr Gly Gln Asp Met Phe Asp Met Leu Cys Asp Thr Pro Glu Arg
225     230     235     240
Ala Asp Leu Leu Asn Ala Glu Gly Ala Lys Pro Gly Gly Tyr Ser
245     250     255
Met Ile Phe Gly Pro Asp Gly Gln Pro Met Cys Glu His Leu Pro Gln
260     265     270
Asp Lys Glu Gly Ile Leu Tyr Ala Gly Val Asp Leu Ser Met Ile Ala
275     280     285
Ile Ala Lys Ala Ala Tyr Asp Pro Thr Gly His Tyr Ala Arg Gly Asp
290     295     300
Val Val Arg Leu Met Val Asn Arg Ser Pro Arg Arg Thr Ser Val Ser
305     310     315     320
Phe Ser Glu Asp Glu Asn Ala Ala Val Thr Phe Thr Glu Thr
325     330

```

<210> 191
 <211> 945
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 191
 atgaaaaagt tagctgtggt tcaacgtgcg tcaggatttt tagataagca gcagagcatc 60
 gcgttggcgg tggaaagtat tcagtctgct gcgaataatg gcgcagagct tgttgttttt 120
 acggaagcct ttattcctgg ttatcctgtc tggttatggc gtctgcgccc tggcaaagac 180
 tggggggacaa cagacagtcct ttatcaacgc ttaataagca acgcggttga ttttaagctca 240
 tcggatttgg atccgattta tgaagcggca aaacgtcatc acgtcacggg tgtatgcggc 300
 attaatgaac gcgactccag cgtcagccga acaacgctat acaacactta catcacgggt 360
 tgtcatgagg gcaatctcat caatgttcat cgaaaactga tgccgaccaa cccagagaga 420
 atggtgtggg gcttttggtga tgcgactgga ttaagggtag tagacactcc tgtcgggaagg 480
 attggctcac tcgtttgctg ggagaactac atgccgttgg caccgtatgc actttatgct 540
 caggcgctcg aaattttacat tggcgctact tatgacagtg gctcggactg gactgaaagc 600
 ttgcgccata tcgccagaga gggcagatgc tacgttgcgc gcagcggtaa cttgttgaga 660
 gccagcgacc tgcttgatga ttttccagaa aaagaaaccc tctatcctga taaagacgag 720
 tggattaacg gcggagactc taccgttacc gctcccggcg gtgaaacatt agttgctccg 780
 ctgcatgcag aggaaggcat actgtattgc gatattgata ctgataaagt ggcggcggtc 840
 cggcgcttctt tcgacgttgc aggccattac tctcgcccag acatattttac actcaacgta 900
 aatcgagcgc cgcaaacatc tctgcgtatc agggaagccg agtaa 945

<210> 192
 <211> 314
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 192
 Met Lys Lys Leu Ala Val Val Gln Arg Ala Ser Gly Phe Leu Asp Lys
 1 5 10 15
 Gln Gln Ser Ile Ala Leu Ala Val Glu Ser Ile Gln Ser Ala Ala Asn
 20 25 30
 Asn Gly Ala Glu Leu Val Val Phe Thr Glu Ala Phe Ile Pro Gly Tyr
 35 40 45
 Pro Val Trp Leu Trp Arg Leu Arg Pro Gly Lys Asp Trp Gly Thr Thr
 50 55 60
 Asp Ser Leu Tyr Gln Arg Leu Ile Ser Asn Ala Val Asp Leu Ser Ser
 65 70 75 80
 Ser Asp Leu Asp Pro Ile Tyr Glu Ala Ala Lys Arg His His Val Thr
 85 90 95
 Val Val Cys Gly Ile Asn Glu Arg Asp Ser Ser Val Ser Arg Thr Thr
 100 105 110
 Leu Tyr Asn Thr Tyr Ile Thr Val Cys His Glu Gly Asn Leu Ile Asn
 115 120 125
 Val His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
 130 135 140
 Phe Gly Asp Ala Thr Gly Leu Arg Val Val Asp Thr Pro Val Gly Arg
 145 150 155 160
 Ile Gly Ser Leu Val Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
 165 170 175
 Ala Leu Tyr Ala Gln Gly Val Glu Ile Tyr Ile Ala Pro Thr Tyr Asp
 180 185 190
 Ser Gly Ser Asp Trp Thr Glu Ser Leu Arg His Ile Ala Arg Glu Gly

```

      195              200              205
Arg Cys Tyr Val Val Gly Ser Gly Asn Leu Leu Arg Ala Ser Asp Leu
      210              215              220
Pro Asp Asp Phe Pro Glu Lys Glu Thr Leu Tyr Pro Asp Lys Asp Glu
225              230              235              240
Trp Ile Asn Gly Gly Asp Ser Thr Val Ile Ala Pro Gly Gly Glu Thr
      245              250              255
Leu Val Ala Pro Leu His Ala Glu Glu Gly Ile Leu Tyr Cys Asp Ile
      260              265              270
Asp Thr Asp Lys Val Ala Ala Ala Arg Arg Ser Phe Asp Val Ala Gly
      275              280              285
His Tyr Ser Arg Pro Asp Ile Phe Thr Leu Asn Val Asn Arg Ala Pro
      290              295              300
Gln Thr Ser Leu Arg Ile Arg Glu Ala Glu
305              310

```

<210> 193
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 193
atgtcaaacg agaaccacaa ccaaacattc aaagttgccg cgggtgcaggc cacacctgta      60
ttcctcgatc gtgaagcgac catcgacaaa gcttgtgagt tgattgctgc agcoggcaat      120
gaaggagcgc ggctgggttg cttcccgag gcattcatcc catcctaccc agattgggta      180
tgggcaatcc caccgggcga agaaggcgtg ctcaatgagt tgtacgcgga actgctctcc      240
aattcgggtca cgattcccag tgatgtgacg gatagactgt gccgagccgc gagacttgcc      300
aatgcctacg tagtgatggg gatgagcgaa cgcaatgccg aggccagtgg cgcaagcctg      360
tataacacgc tgttgtagat cgatgcgcag ggcgagattc tgggcaaaca tcgaaagctg      420
gtgcccacag gcggcgaaac gctgggtgtg gcgcagggcg atggcagcac gctgcaggtc      480
tacgatactc cactgggtaa actcggcggt ttgatttgct gggagaatta tatgccgctg      540
gcccgtctaca ccatgtacgc atggggcaca caaatctatg ttgcggcgac atgggatcgc      600
gggcaaccct ggctctccac tttacggcat atcgccaaag aaggcagggt gtacgtgatc      660
ggctgctgta tcgtgatgcg caaagacgat atcccagatc gttaccgat gaagcagaag      720
ttttacgcgg aggccgatga gtggatcaac ataggggaca gcgcaatcgt caatcctgaa      780
gggcagttta gcgccgggcc ggtacgcaaa caggaagaga ttctctacgc ggaaattgat      840
ccgcgcatgg tgcaaggccc gaagtggatg ctcgacgtag cagggcacta cgcgaggccg      900
gacgtattcc agttgacggt gcatacggat gcgaggcaga tgatcaggtt ggaacacgat      960
gtttaa

```

<210> 194
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 194
Met Ser Asn Glu Asn His Asn Gln Thr Phe Lys Val Ala Ala Val Gln
1              5              10              15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
      20              25              30
Glu Leu Ile Ala Ala Ala Gly Asn Glu Gly Ala Arg Leu Val Val Phe
      35              40              45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
      50              55              60
Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser

```

65					70					75					80
Asn	Ser	Val	Thr	Ile	Pro	Ser	Asp	Val	Thr	Asp	Arg	Leu	Cys	Arg	Ala
				85					90					95	
Ala	Arg	Leu	Ala	Asn	Ala	Tyr	Val	Val	Met	Gly	Met	Ser	Glu	Arg	Asn
			100					105					110		
Ala	Glu	Ala	Ser	Gly	Ala	Ser	Leu	Tyr	Asn	Thr	Leu	Leu	Tyr	Ile	Asp
		115					120					125			
Ala	Gln	Gly	Glu	Ile	Leu	Gly	Lys	His	Arg	Lys	Leu	Val	Pro	Thr	Gly
	130					135					140				
Gly	Glu	Arg	Leu	Val	Trp	Ala	Gln	Gly	Asp	Gly	Ser	Thr	Leu	Gln	Val
145					150				155					160	
Tyr	Asp	Thr	Pro	Leu	Gly	Lys	Leu	Gly	Gly	Leu	Ile	Cys	Trp	Glu	Asn
			165						170					175	
Tyr	Met	Pro	Leu	Ala	Arg	Tyr	Thr	Met	Tyr	Ala	Trp	Gly	Thr	Gln	Ile
		180					185						190		
Tyr	Val	Ala	Ala	Thr	Trp	Asp	Arg	Gly	Gln	Pro	Trp	Leu	Ser	Thr	Leu
	195					200					205				
Arg	His	Ile	Ala	Lys	Glu	Gly	Arg	Val	Tyr	Val	Ile	Gly	Cys	Cys	Ile
	210					215					220				
Val	Met	Arg	Lys	Asp	Asp	Ile	Pro	Asp	Arg	Tyr	Pro	Met	Lys	Gln	Lys
225				230					235					240	
Phe	Tyr	Ala	Glu	Ala	Asp	Glu	Trp	Ile	Asn	Ile	Gly	Asp	Ser	Ala	Ile
			245					250					255		
Val	Asn	Pro	Glu	Gly	Gln	Phe	Ser	Ala	Gly	Pro	Val	Arg	Lys	Gln	Glu
		260					265					270			
Glu	Ile	Leu	Tyr	Ala	Glu	Ile	Asp	Pro	Arg	Met	Val	Gln	Gly	Pro	Lys
	275					280					285				
Trp	Met	Leu	Asp	Val	Ala	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Phe	Gln
	290				295					300					
Leu	Thr	Val	His	Thr	Asp	Ala	Arg	Gln	Met	Ile	Arg	Leu	Glu	His	Asp
305					310				315					320	
Val															

<210> 195

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 195

atgaaagtcg	tcaaagccgc	cgcggtacag	ttcagcccgg	tgctctatag	ccgtgaggca	60
accgctcgcca	aggctcgtgca	gaagatccac	gaactcggcc	agaaaggcgt	gcagttcgcc	120
accttccccc	aaacggtcgt	gccttattac	ccttactttg	cggccgtcca	gacgggcatc	180
gagcttctct	cgggcaccga	acatctgcgc	ctgctcgaac	aggctgtgac	tgtcccgtcc	240
gctgctaccg	acgcgatcgg	cgaagccgcg	cgaaaggccg	gcatggtcgt	gtccattggc	300
gtcaatgagc	gcgatggcgg	cacgctgtac	aacgcacaac	tgctcttcga	tgccgacggt	360
acgctgatcc	agcgccgccc	caagatcacg	ccgacgcatt	tcgaacgcat	gatctggggc	420
cagggagatg	gctcgggctt	gcgtgcagtc	gacagcgccg	tcggccgcgt	cggccagctc	480
gcatgtttcg	agcacaacaa	cccgtcgcgc	cgctacgcaa	tgatcgccga	cggcgagcag	540
atccattcgg	cgatgtaccc	tggtctcgcc	tttggcgagg	gcttcgcccc	gcgtatggaa	600
atcaacatcc	gccagcatgc	gctcagatcc	gccgctttcg	tcgtcaacgc	aacagcgtgg	660
ctggacgccc	accagcaggc	gcaaatcatg	aaggacaccg	gttggtggaat	cgggtccgatc	720
acgggcggct	gcttcaccac	gatcgtctct	cctgacggca	tgctgatggc	cgagccgctt	780
cgctcgggtg	aaggcgaagt	gatcgtcgat	ctcgacttca	cgcagatcga	ccgccgcaag	840
atgctgatgg	actcggccgg	ccactacaac	cgcctgaac	tgctgagtct	gatgatcgac	900
cgtacgccga	ccgcgcgatg	tcacgaacgc	gcttcgcacc	cgatgatcgt	caacgaccag	960
ggttcggacg	atctgcgcac	ccaggctgca	tga			993

<210> 196
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 196
 Met Lys Val Val Lys Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Ala Lys Val Val Gln Lys Ile His Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Ala
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Val Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Thr Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Gln Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ser His Pro Met Ile Val Asn Asp Gln
 305 310 315 320
 Gly Ser Asp Asp Leu Arg Thr Gln Ala Ala
 325 330

<210> 197
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 197

```

atgggcatcg aacatccaaa ataccgcgtt gccgccgtgc aggctgcgcc ggccctggctc    60
gacctcgatc gctcgatcga caaggctatt gcactgatcg aggaggccgc cgcgaacggc    120
gccagattga tcgcattccc ggaggtcttc atccccggct acccctggca tatctggctc    180
gactcgccgc cctgggggat cggccgcggc ttctgtgcagc gttatttcga caattcgctc    240
gcttatgata gtccgcaggc cgagcggctc cgcgccagcg tccgcaaggc gcgcctgacc    300
gccgtgatcg gcctttcgga gccgagcggc ggcagcctct acatcgcgca atggctcggt    360
ggccccgacg gcgagaccat cgcgaagcgc cgcaagctcc gtccgacgca tgccgagcgc    420
acggtctatg gcgagggcga cggcagcgat ctggcggtcc atgaccggcc cgatatcgga    480
cggctcggcg cgctgtgctg ctgggaacat ctgcaaccgt tgtcgaaata tgogatgtat    540
gccagaacg agcaggtcca tgtggcgta tggccgagtt ttctgctcta cgatcccttt    600
gccccggcgc tcggcgcgga ggtgaacaat gcggcctccc gggctctatg ggtcgaaggc    660
tctgtcttcg tgctggcgcc gtgcgcgacc gtctcgcagg ccatgatcga tgagctgtgc    720
gaccggcccc acaagcacgc gctgctccat gccggcgggt gctttgccgc gatctacggg    780
cccgcgggca gttcgtggtc cgaaggctc gcgcgggacc aggagggcct gctttacgcc    840
gacatcgatc tcggcgcgat cggcgctcgc aagaacgccg ccgaccggc agggcattat    900
tcgcggcccc atgtcacgcg gctgctgctg aacaacaagc cctacaagcg cgtggagcat    960
tttgctttgc ccggcgatac cgtggcgccct gccgatgtgg atgcggcggc gagctga    1017

```

<210> 198

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 198

```

Met Gly Ile Glu His Pro Lys Tyr Arg Val Ala Ala Val Gln Ala Ala
  1          5          10          15
Pro Ala Trp Leu Asp Leu Asp Arg Ser Ile Asp Lys Ala Ile Ala Leu
  20          25          30
Ile Glu Glu Ala Ala Ala Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu
  35          40          45
Val Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Leu Asp Ser Pro Ala
  50          55          60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
  65          70          75          80
Ala Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Ala Ala Val Arg Lys
  85          90          95
Ala Arg Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Ser Gly Gly Ser
  100         105         110
Leu Tyr Ile Ala Gln Trp Leu Val Gly Pro Asp Gly Glu Thr Ile Ala
  115         120         125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
  130         135         140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Asp Ile Gly
  145         150         155         160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
  165         170         175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ser Trp Pro
  180         185         190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
  195         200         205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
  210         215         220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
  225         230         235         240
Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala
  245         250         255
Ala Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Glu Lys Leu Ala Pro
  260         265         270

```

```

Asp Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
      275                      280                      285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
      290                      295                      300
Val Thr Arg Leu Leu Leu Asn Asn Lys Pro Tyr Lys Arg Val Glu His
305                      310                      315                      320
Phe Ala Leu Pro Gly Asp Thr Val Ala Pro Ala Asp Val Asp Ala Ala
      325                      330                      335
Ala Ser

```

<210> 199
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 199
atgtcaaacg cactgaagcc gttcaaaatc gccgccgttc aggcgacgcc ggtttttctg      60
aaccgggaag ccacggcgga gaaggccgcg gctttgatcc gcgaagcggg aagcgccgga      120
gccaaagctca tcgttttccc ggaatcgttt attccggcct atccggactg ggtctgggtg      180
gtccccctcg ggagggatcg ccttctcagc ggcctctacg gggagatgct cgaaaacgcc      240
gtggaatccc ccggcccggc cacggggcat atcgcccggg cggcgaagga atcgggcgct      300
tatgtcgtca tgggctgac cgagcgggac acggaggcga gcggagccag tttgttcaac      360
accttgattt atttcggtcc gaccggggaa attttgggca aacaccggaa gctggttccc      420
accggggggcg aacggatcgt ctgggcccag ggggacggaa gcaccctgga ggtctacgat      480
acgcccctgg gaaaactggg cgggctgatc tgctgggaaa actacatgcc cctggcccgg      540
tacgccatgt acgctgggg aacccagctt tacgtggccg ccacctggga ccgagcgaa      600
ccctggcttt cgacgcttcg gcatatcgcc aaggaagggc ggggtgtatg catcggtg      660
tgcacgcca tgcggaaagg ggatatcccg gatcggttcg aacacaaggg gctctacgcc      720
cccgaccggg actggatcaa cccggcgac agcgcgatcg tcaaccccca gggggagatg      780
atcgccgggc ccgcttccaa taaggaaagag atcctttatg cggaagtcca cccgcagatg      840
atgcgcgggc ccaaattgat gctcgatgtg gccggccatt acgcgcggcc cgatgtcttc      900
gagctcaccg tccgcgggga accgcggccg atgatccgcg tggcgggagg cgcgggcggg      960
accgaaccca aagagaagaa gaccgccggc tga      993

```

<210> 200
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 200
Met Ser Asn Ala Leu Lys Pro Phe Lys Ile Ala Ala Val Gln Ala Thr
 1      5      10      15
Pro Val Phe Leu Asn Arg Glu Ala Thr Ala Glu Lys Ala Ala Ala Leu
      20      25      30
Ile Arg Glu Ala Gly Ser Ala Gly Ala Lys Leu Ile Val Phe Pro Glu
      35      40      45
Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Val Val Pro Ser Gly
      50      55      60
Arg Asp Arg Leu Leu Ser Gly Leu Tyr Gly Glu Met Leu Glu Asn Ala
      65      70      75      80
Val Glu Ile Pro Gly Pro Ala Thr Gly His Ile Gly Arg Ala Ala Lys
      85      90      95
Glu Ser Gly Ala Tyr Val Val Met Gly Val Thr Glu Arg Asp Thr Glu
      100      105      110

```

Ala Ser Gly Ala Ser Leu Phe Asn Thr Leu Ile Tyr Phe Gly Pro Thr
 115 120 125
 Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130 135 140
 Arg Ile Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145 150 155 160
 Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Leu Tyr Val
 180 185 190
 Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
 195 200 205
 Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Met
 210 215 220
 Arg Lys Gly Asp Ile Pro Asp Arg Phe Glu His Lys Gly Leu Tyr Ala
 225 230 235 240
 Pro Asp Arg Asp Trp Ile Asn Pro Gly Asp Ser Ala Ile Val Asn Pro
 245 250 255
 Gln Gly Glu Met Ile Ala Gly Pro Ala Ser Asn Lys Glu Glu Ile Leu
 260 265 270
 Tyr Ala Glu Val Asp Pro Gln Met Met Arg Gly Pro Lys Trp Met Leu
 275 280 285
 Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Thr Val
 290 295 300
 Arg Arg Glu Pro Arg Pro Met Ile Arg Val Ala Gly Gly Ala Gly Gly
 305 310 315 320
 Thr Glu Pro Lys Glu Lys Lys Thr Ala Gly
 325 330

<210> 201

<211> 930

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 201

atgaccacga	agagcatccg	catcgcgggc	gtacaggcgg	ctcccgcgtt	tctcgacctg	60
gctggtacgc	tggaccggct	cgaggcctgg	gcccgcaagg	ccgccgccac	cggtgcccgc	120
gtcatcgcg	tccccgagac	ctggctgccc	ggctaccggg	cgtggatcga	ctcgtcgccg	180
gaggccgcga	tctggggcca	tcccggctcg	cgcgacctgc	accagcgcc	gatggagaat	240
gccgtcgagg	tcccggggcc	cgcgaccg	cgcatcgcca	agctcgccg	cgagctcgcc	300
gtgacgatcg	tggtcgggc	gcacgagcgg	gcggggaaca	ccctctacaa	cacggcgctg	360
acgttcgggc	ccgagggcag	gctgctcaat	caccaccgga	agctggtgcc	gacctacagc	420
gaacggctgc	tgtggggcta	cggcgacggc	gctggactgg	tggcgcggc	ggtggacggt	480
gtgaaggtcg	gggcgctgg	gtgctgggag	cactggatgc	cgctcaccg	ccaggcgatg	540
cacgacgtcg	gcgagcacgt	gcacgtcgcc	ctgtggccc	gcgtccacga	gatgcaccag	600
gtggcctcgc	ggcactatgc	gttcgagggc	cgctgtttcg	tgatcgcggt	cgggagcatc	660
ctgcgcgtgg	accagatgcc	gaagcagctg	ccgccgctgg	agaagtacgc	gaagagcgcc	720
aaggggctga	tgatcgcggg	cggcagcgcc	atcatcgcg	cgaacggccg	ctacgtcgcg	780
gcgcccgtgt	acgacgagga	gacgatcgtc	accgccgact	gcgacctcgg	cgagatccc	840
cgcgaggcgc	agacgctcga	tgtctcgggc	cactacagcc	ggccggacgt	gttcagcttc	900
gggggtggtca	gacaccggcc	gcgtgcgtaa				930

<210> 202

<211> 309

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 202

```

Met Thr Thr Lys Ser Ile Arg Ile Ala Ala Val Gln Ala Ala Pro Ala
 1          5          10          15
Phe Leu Asp Leu Ala Gly Thr Leu Asp Arg Leu Glu Ala Trp Ala Arg
 20          25          30
Lys Ala Ala Ala Thr Gly Ala Arg Val Ile Ala Phe Pro Glu Thr Trp
 35          40          45
Leu Pro Gly Tyr Pro Ala Trp Ile Asp Ser Ser Pro Glu Ala Ala Ile
 50          55          60
Trp Gly His Pro Gly Ser Arg Asp Leu His Gln Arg Leu Met Glu Asn
 65          70          75          80
Ala Val Glu Val Pro Gly Pro Ala Thr Ala Arg Ile Ala Lys Leu Ala
 85          90          95
Gly Glu Leu Gly Val Thr Ile Val Val Gly Ala His Glu Arg Ala Gly
100          105          110
Asn Thr Leu Tyr Asn Thr Ala Leu Thr Phe Gly Pro Glu Gly Arg Leu
115          120          125
Leu Asn His His Arg Lys Leu Val Pro Thr Tyr Ser Glu Arg Leu Leu
130          135          140
Trp Gly Tyr Gly Asp Gly Ala Gly Leu Val Ala Pro Ala Val Asp Gly
145          150          155          160
Val Lys Val Gly Ala Leu Val Cys Trp Glu His Trp Met Pro Leu Thr
165          170          175
Arg Gln Ala Met His Asp Val Gly Glu His Val His Val Ala Leu Trp
180          185          190
Pro Gly Val His Glu Met His Gln Val Ala Ser Arg His Tyr Ala Phe
195          200          205
Glu Gly Arg Cys Phe Val Ile Ala Val Gly Ser Ile Leu Arg Val Asp
210          215          220
Gln Met Pro Lys Gln Leu Pro Pro Leu Glu Lys Tyr Ala Lys Ser Ala
225          230          235          240
Lys Gly Leu Met Ile Ala Gly Gly Ser Ala Ile Ile Ala Pro Asn Gly
245          250          255
Arg Tyr Val Ala Pro Val Tyr Asp Glu Glu Thr Ile Val Thr Ala
260          265          270
Asp Cys Asp Leu Gly Glu Ile Pro Arg Glu Ala Gln Thr Leu Asp Val
275          280          285
Ser Gly His Tyr Ser Arg Pro Asp Val Phe Ser Phe Gly Val Val Arg
290          295          300
His Arg Pro Arg Ala
305

```

<210> 203

<211> 966

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 203

```

atgtcaagct tacccacatc cgcgttcacc gtgcgcgcgc cgcaagcgtc gccagtgttc      60
ctcgaccgcg acgcgacgct gcagaaggct tgcgggctga tcgccgacgc cgggcgcgcg      120
ggcgcgcgcc tgatcgtctt ccccgaagcc ttcattcccg cctaccccgga ttgggtgtgg      180
gcgggtccag ctggcggaaga ggggatgctg agcgagctct acgccgagct ggtcgcgaat      240
tcgctggcta ttccgagcga cgcgaccgat cggctatgtc gcgcggcgca ggccgcgcac      300
atcaatgtgg tcgtgggggt gagcgagcgc aatgtcgagg ccagcggcgc cagcctctac      360
aacacgctgc tgtatatcga cgcggcgga acgatcctgg gtaaacaccg caagcttgtg      420
ccgaccggcg gggagcgccct ggtctgggcg cagggcgacg gcagcacgct cgatgtgtac      480

```

```

gacaccgctc tcggcaagct cggcggcctg atctgttggg aaaactacat gccgctggca 540
cgctacgcgc tgtacgcctg ggggtgtgcaa atctatgtcg cggccacctg ggatcgcggc 600
gagccctggc tttctactct gcgacatatc gccaaaggaag gccgtgtcta cgtgatcggc 660
tgtggcatgg cgctgcgcag agatgatatt cccgatcgct tcgctttcaa gcagcgcttc 720
tatgcccagg ccggcgaatg gatcaacgtc ggcgacagcg cgatcggtcaa cccgagcggc 780
gagtttattg ccggacctgt gcgcgaacgc gaggagattc tgtacgcgga ggtcgacctg 840
gagcagatga gcggggccaaa gtggatgctc gacgtggccg ggcactacgg gcggccggat 900
gtcttcgggc tcagcggtcaa ccgggcgccc caccagatga tccagacgga gaaccgggag 960
acctga

```

<210> 204
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 204
Met Ser Ser Leu Pro Thr Ser Ala Phe Thr Val Ala Ala Ala Gln Ala
 1      5      10
Ser Pro Val Phe Leu Asp Arg Asp Ala Thr Leu Gln Lys Ala Cys Gly
      20      25      30
Leu Ile Ala Asp Ala Gly Arg Ala Gly Ala Arg Leu Ile Val Phe Pro
      35      40      45
Glu Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala
 50      55      60
Gly Glu Glu Gly Met Leu Ser Glu Leu Tyr Ala Glu Leu Val Ala Asn
65      70      75      80
Ser Leu Ala Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Arg Ala Ala
      85      90      95
Gln Ala Ala His Ile Asn Val Val Val Gly Leu Ser Glu Arg Asn Val
      100     105     110
Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala
      115     120     125
Ala Gly Thr Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly
      130     135     140
Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Asp Val Tyr
145     150     155     160
Asp Thr Ala Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr
      165     170     175
Met Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Val Gln Ile Tyr
      180     185     190
Val Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg
      195     200     205
His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Gly Met Ala
      210     215     220
Leu Arg Arg Asp Asp Ile Pro Asp Arg Phe Ala Phe Lys Gln Arg Phe
225     230     235     240
Tyr Ala Gln Ala Gly Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val
      245     250     255
Asn Pro Ser Gly Glu Phe Ile Ala Gly Pro Val Arg Glu Arg Glu Glu
      260     265     270
Ile Leu Tyr Ala Glu Val Asp Pro Glu Gln Met Ser Gly Pro Lys Trp
      275     280     285
Met Leu Asp Val Ala Gly His Tyr Gly Arg Pro Asp Val Phe Arg Leu
290     295     300
Ser Val Asn Arg Ala Pro His Gln Met Ile Gln Thr Glu Asn Arg Glu
305     310     315     320
Thr

```

<210> 205
 <211> 969
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 205
 atgaccaccg taaaagccgc cgcagtacag atcagccccg tgctctatag ccgggaggcc 60
 accgtagaca aggtcgttcg caagatccgc gagotcggcc aaaagggagt gcagttcgcc 120
 accttcccg aaaccgtagt gccgtactac cctactttcg ctgcagtcca gacaggcatc 180
 gaactgttgt ccggcaagga acacatgcgc ctgctggagc aggccgttac cgtcccctcg 240
 cccgccacgg atgcgattgc tcaggcggcg cgcgaagcca atatggtggt gtccatcggc 300
 gtcaacgagc gcgacggcgg caccatctac aacacgcagc tgctcttcga tgccgacggc 360
 acgctcgtgc agcgccgccc caagataacg ccaacgcact tcgagcgcat ggtctggggc 420
 caggggcgatg gttcgggatt gcgcgccggc gacaccaagg ttggccgcac cggccagttg 480
 gcctgcttcg agcacaacaa cccgctcgcc cgttacgcca tgatggccga tggcgagcag 540
 atccactccg ccatgtaccc gggctcggcc ttccggcgagg gcttcgcgca gcgcatggag 600
 atcaacatcc gccagcatgc cctggagtct ggctgcttcg tggatgaatgc gaccgcctgg 660
 ctccgatgccg accaacaggc gcagatcatg aaggacaccg gttgctcgat cggcccgatc 720
 tccggcggtc gcttcacgac catcgtcacg cctgagggca tgctgattgg cgagccgctc 780
 cgcgagggcg aaggcgaaat catcgccgac ctccgatttct cgatgatcga tcgccgcaag 840
 ctgctgatgg actcggtcgg tcaactaac cgtccggagc ttctgagcct cctgatcgat 900
 cgcacgcctg ccgcgaactt ccatgaacgt accgcgagcc aggcgaacgc cggcgctcgaa 960
 atcctctga 969

<210> 206
 <211> 322
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 206
 Met Thr Thr Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Asp Lys Val Val Arg Lys Ile Arg Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Lys Glu His Met Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Asn Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Ala Asp Thr Lys Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190

Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Glu Gly Met Leu Ile
 245 250 255
 Gly Glu Pro Leu Arg Glu Gly Glu Gly Glu Ile Ile Ala Asp Leu Asp
 260 265 270
 Phe Ser Met Ile Asp Arg Arg Lys Leu Leu Met Asp Ser Val Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Ala
 290 295 300
 Ala Asn Phe His Glu Arg Thr Ala Ser Gln Ala Asn Ala Gly Val Glu
 305 310 315 320
 Ile Leu

<210> 207
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 207
 atgtcaaacg agaacaacaa cgctacattc aaagttgccg cagtacaggc tacacctggt 60
 tttctcgatc gtgaagcgac tctcgacaag gcttgcgatt tgatcgccgc cgccggagggt 120
 gaaggggacac gattggttgt ctttccagaa gccttcatac cggcctatcc ggattgggta 180
 tgggcaatcc caccgggtga agagggcgta cttaatgagt tgtacgcaga gctgctctcc 240
 aactcgggtca cgattcccag tgacgcgcag gacagactgt gccgggcccgc gaggcttgct 300
 aatgcttacg tggatgatgg gataagcgaa cgcaatgtcg aggcgagtg agcaagcctg 360
 tataacacgc tgttgatcat cgatgcgcag ggtgagattc taggcaaaca tcgaaagcta 420
 gtgccaacgg gcggcgagcg gctggtgtgg gcgcagggcg atggcagcac actgcaggtc 480
 tacgatactc cactgggaaa actcggcggt ttaatttgct gggagaatta tatgccgctg 540
 gcccgctata ccatgtatgc ctggggcaca caaatctatg tcgccgctac gtggggtcgc 600
 gggcaaccct ggctctccac tttgcggcat atcgccaaag aaggcagggt gtacgtgatt 660
 ggttggttga tcgcgatgcg caaagacgat atccctgatc gttacgcaat gaagcagaag 720
 ttttacgcgg aggcagatga gtggatcaat ataggtgaca gcgcgattgt caatcctgaa 780
 gggcaattta tcgcagggcc agtacgcaag caggaagaga ttctctacgc agagattgat 840
 ccgcgcgatg tacaagggcc gaagtggatg ctgcacgtgg cggggcacta tgccaggccg 900
 gatgtgttcc agttgacggt gcatacggat gtgcgcacaga tgattcggat ggaacacgat 960
 tcttaa 966

<210> 208
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 208
 Met Ser Asn Glu Asn Asn Asn Ala Thr Phe Lys Val Ala Ala Val Gln
 1 5 10 15
 Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Leu Asp Lys Ala Cys
 20 25 30
 Asp Leu Ile Ala Ala Ala Gly Gly Glu Gly Ala Arg Leu Val Val Phe
 35 40 45

Pro Glu Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Ile Pro
 50 55 60
 Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser
 65 70 75 80
 Asn Ser Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Arg Ala
 85 90 95
 Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Ile Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
 115 120 125
 Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ala Met Lys Gln Lys
 225 230 235 240
 Phe Tyr Ala Glu Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Met Glu His Asp
 305 310 315 320
 Ser

<210> 209

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 209

atgaaagtcg	tcaaagccgc	cgctgtccag	atcagtcocg	ttctotacag	ccgtgaggca	60
acogtcgaaa	aggtcgtgaa	gaaaattcac	gagcttggcc	aactgggcgt	gcagttcgcc	120
acctttcccg	agaccgtagt	gccttactac	ccgtactttt	ccgcogtcca	gacaggcatt	180
gagcttctgt	ccggaactga	gcatctgcgg	ctgctcgatc	aggcogtgac	ggtaccgtct	240
cccgctacog	atgcgatcgg	agaggcggcc	cgcaaggcgg	gcatgggtgg	gtccatcggc	300
gtgaatgaac	gcgacggcgg	caccttgtac	aacacacagt	tgctcttcga	tgccgatggc	360
accttgatcc	agcgccgcgg	caagatcacg	cccacccact	tcgaacggat	gatctggggc	420
caggggggacg	gctcggggcct	gcgcgccgtc	gacagcaagg	ttggtcgcat	tggtcagctt	480
gcctgcttcg	agcacaacaa	cccgttgccc	cgctacgcgc	tgattgccga	cggcgagcag	540
atccattccg	ccatgtatcc	gggttctgct	ttcggcgaa	gctttgccca	aaggatggaa	600
atcaatatcc	gccagcatgc	gctggagtct	ggtgcctttg	tcgtcaacgc	aacggcctgg	660
ctggatgctg	accagcaggc	gcaaatcatc	aaggacaccg	gctgtgggat	tgcccgcgac	720
tcggggcggt	gcttcaccac	gatcgtggca	cccgaacggc	tgctgatggc	cgaacctctg	780
cgttcggggcg	aggggtgaggt	catcgtggat	ctcgacttca	cgctgatcga	ccgacgcaag	840
atgttgatgg	actcggcggg	ccactataac	cgtccagaac	tgctcagttc	catgattgac	900

cgtaccgcga cggcgcatgt tcacgaacgc gctgcgcata cgggtgtcggg cgcggagcag
 ggtccggagg atctgcgcac tccggccgcg tga

960
 993

<210> 210
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 210
 Met Lys Val Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Glu Lys Val Val Lys Lys Ile His Glu Leu
 20 25 30
 Gly Gln Leu Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Ile Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Ala Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ala His Pro Val Ser Gly Ala Glu Gln
 305 310 315 320
 Gly Pro Glu Asp Leu Arg Thr Pro Ala Ala
 325 330

<210> 211
 <211> 1062
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 211

```

atgggcgtcg cacatccgaa atacaaagtg gccgccgtgc aggcagcgcc cgcttttctc      60
gacctggacg cctcgggtcga aaaggccgtc cgtttcacatcg acgaagccgg cgccgccggc      120
gcccgccctca tcgccttttc ggagacctgg ataccgcgtt acccctgggtg gatctggcta      180
ggcgcgccgg cctgggctat catgcgcggc ttcgtctcgc gctatttcga caactcgctc      240
agctacgaca gccgcgaggc cgagaagctc cgcgccggccg ccaagcgcaa caagatggtg      300
gtggtgctcg gcctctccga gcgcgacggc ggcagccttt acatcgcgca atggatcatc      360
ggcccgacg gcgaaaccat cgccaagcgc cgcaagctca agccgaccca cgcgagcgcg      420
accgtgttcg gcgaaggcga cggctcgcac cttgcggtgc acgagcttga tgttgcccg      480
ctcgcgcgcg tgtgtctgtg ggaacacctg cagccgctgt ccaaatacgc catgtatgcg      540
cagaacgaac aggtgcatgt cgcggcctgg ccgagctttt cgctttacga tccgttcgcg      600
cacgcgctcg gcgcggaagt gaacaatgcg gcgagcaaaa tctatgcggg cgagggctcg      660
tgtttcgtca tcgcgcgctg cgcgaccgtt tcgcaggcga tgatcgacga actctgcgat      720
acgcccggaga agcatcagtt cctgcatgcc ggcggcggtt ttgccgtgat ttacggcccc      780
gacgcgcccc cgctcgcggc gccgctgccc cccgacaagg aaggcttgct ctacgccgac      840
atcgatctcg ggatgatctt ggttgccaaa gcggcagccg atccggccgg gcattatgca      900
cgccccgacg tcacccgggt tctgtttcaac aatcggcctg ggtatcgggg cgagaccatg      960
gcgttgccga tcgatgcgga gaccaaggcg gaagcaccgg ctaagccgga acccaaggca     1020
ccgaacgtgg cgccgttcgc gccggtgcaa gcggccgagt ga                               1062

```

<210> 212

<211> 353

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 212

```

Met Gly Val Ala His Pro Lys Tyr Lys Val Ala Ala Val Gln Ala Ala
 1              5              10              15
Pro Ala Phe Leu Asp Leu Asp Ala Ser Val Glu Lys Ala Val Arg Phe
 20              25              30
Ile Asp Glu Ala Gly Ala Ala Gly Ala Arg Leu Ile Ala Phe Pro Glu
 35              40              45
Thr Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50              55              60
Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65              70              75              80
Ser Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Ala Lys Arg
 85              90              95
Asn Lys Met Val Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100              105              110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Glu Thr Ile Ala
115              120              125
Lys Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
130              135              140
Glu Gly Asp Gly Ser His Leu Ala Val His Glu Leu Asp Val Gly Arg
145              150              155              160
Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165              170              175
Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro Ser
180              185              190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
195              200              205
Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile
210              215              220
Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys Asp
225              230              235              240

```

```

Thr Pro Glu Lys His Gln Phe Leu His Ala Gly Gly Gly Phe Ala Val
      245      250      255
Ile Tyr Gly Pro Asp Gly Ala Pro Leu Ala Ala Pro Leu Pro Pro Asp
      260      265      270
Lys Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Val
      275      280      285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val
      290      295      300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Gly Tyr Arg Val Glu Thr Met
      305      310      315
Ala Leu Pro Ile Asp Ala Glu Thr Lys Ala Glu Ala Pro Ala Lys Pro
      325      330      335
Glu Pro Lys Ala Pro Asn Val Ala Pro Phe Ala Pro Val Gln Ala Ala
      340      345      350
Glu

```

<210> 213
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 213
atgagagttg ttaaagccgc tgctgtccaa ctgagtcccg tcctctatag tgcgcagggga      60
acggtcgaaa aggtcgtgcg gaagatccat gaacttgccg aagagggagt cgagttcgcc      120
acctttcctg agaccgtggt gccttactac ccgtactttt ccttcggtca gacgcccttg      180
gagcaaatct tcggaacaga gtatctgagg ctgctcgacc aggcagtcac cgtgccatcc      240
cctgccaccg acgcgatcgg cgaggcagcc aggttcgctg gattgttgt ctcgatcggc      300
gtcaacgagc gagacggggg aactctatac aacactcagc ttctcttcga tgccgacggc      360
aggataattc agcggcgccg caagatcacg cccacccatt acgagcgcat gatctggggc      420
cagggcgacg gctcaggtct gcgggccggt gatagcaagg ccggccggtat tggtcagctg      480
gcatgctggg agcacaacaa tccactggcg cgctacgcgc tgatggccga cggcgagcag      540
atccattccg ccatgtatcc gggctccatg ttccggcgact cgtttgccca gaagaccgaa      600
atcaatatcc ggcagcatgc cctagagtct ggggtgcttcg tcgtgaacgc aacggcctgg      660
ctggacggcg atcagcaggc gcatatcatg aaggacaccg gctgcagcat cggcccgatc      720
tccggcggtt gcttcactgc gatcgctgca cccgatggta gcctgctggg cgaacccatc      780
cgttccggtg agggcgtggt catcgccgac ctgcacttca cgttgatcga caggcgtaag      840
caggtgatgg actcgcgagg ccattacagc cggccggagt tgctcagcct cttaatagac      900
cgaccccta cgcgcactt tcacgaacgc gcttcgcccc ccacgacaga agctgagcaa      960
ggctccgagg atgtgttcga ggctcgcatt taa                               993

```

<210> 214
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 214
Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
  1      5      10      15
Ser Arg Glu Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
      20      25      30
Ala Glu Glu Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
      35      40      45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Glu Gln Ile Phe
      50      55      60

```

Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Phe Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Arg Ile Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
 180 185 190
 Asp Ser Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Gly Asp
 210 215 220
 Gln Gln Ala His Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Ser Leu Leu
 245 250 255
 Gly Glu Pro Ile Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
 275 280 285
 Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Phe His Glu Arg Ala Ser Pro Pro Thr Thr Glu Ala Glu Gln
 305 310 315 320
 Gly Ser Glu Asp Val Phe Glu Ala Arg Ile
 325 330

<210> 215
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 215
 atgagtatta cccaccccaa atttaaagct gctgttgttc aagctgcccc agtattttcta 60
 gacctagatg ggtctgttaa taaggcgatt aatctcattg atgaagctgc cgctgccgga 120
 gccaaagctca ttgccttccc tgaaaccttc attccaggct atccatggtg gatttggctg 180
 ggatcgccgg cgtgggctct gggccggggg ttcgttcagc gttacttcga caattccctg 240
 cagtacgaca gccgcagggc ggatcgctta cgcgaggcgg cagcagcga cagcattacg 300
 gtcgtgctgg gcttgtccga gcgatgatggc ggttctctct atatcgca gtggctgatc 360
 ggcccggatg gcgaaccat cgcgcagcgg cgcaagcttc gtcctactca tggggagcgc 420
 acggatattcg gtgaagggga tggcagcgat ctggtgggtc atcaaaccga actggggcgt 480
 cttggcgccgc ttaactgctg ggagaacatc ctgtctctga acaaatatgt gatgtactcc 540
 cagcatgaac aggtccatgt agcatcctgg cccagtttct cgacgtatga accgttcgcg 600
 catgcgctcg gctatgaggt aaacaacgca attagccagg tctatgcggt ggaaggcggg 660
 tgcttcgtgt tggccccgtg ctctaccatc tctgaagaaa tgattgccga actgtgcgat 720
 acacccgata aattcgagct gacgcagctg ggtggcggcc acgcaatcat ctatggtccg 780
 gacggctcgt cctctgtcga aaagctgccc gagaaccagg agggcctgct gtacgcggaa 840
 atcgatctgg ggtgatcttc tatggcaaaa agtgccatgg atcctgtcgg ccattactct 900
 cgccccgatg tctaccgtgt gctgttcaat aagatcccgg caaagcgtat cgagcacttc 960
 aatttgccgt tggatgagca agcaggggaa gagccaccag ctgattaa 1008

<210> 216
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 216
 Met Ser Ile Thr His Pro Lys Phe Lys Ala Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Asp Leu Asp Gly Ser Val Asn Lys Ala Ile Asn Leu
 20 25 30
 Ile Asp Glu Ala Ala Ala Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ser Pro Ala
 50 55 60
 Trp Ala Leu Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Gln Tyr Asp Ser Pro Gln Ala Asp Arg Leu Arg Glu Ala Ala Arg Arg
 85 90 95
 Asn Ser Ile Thr Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Gln Arg Arg Lys Leu Arg Pro Thr His Gly Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Val Val His Gln Thr Glu Leu Gly Arg
 145 150 155 160
 Leu Gly Ala Leu Asn Cys Trp Glu Asn Ile Leu Ser Leu Asn Lys Tyr
 165 170 175
 Val Met Tyr Ser Gln His Glu Gln Val His Val Ala Ser Trp Pro Ser
 180 185 190
 Phe Ser Thr Tyr Glu Pro Phe Ala His Ala Leu Gly Tyr Glu Val Asn
 195 200 205
 Asn Ala Ile Ser Gln Val Tyr Ala Val Glu Gly Gly Cys Phe Val Leu
 210 215 220
 Ala Pro Cys Ser Thr Ile Ser Glu Glu Met Ile Ala Glu Leu Cys Asp
 225 230 235 240
 Thr Pro Asp Lys Phe Glu Leu Thr His Ala Gly Gly Gly His Ala Ile
 245 250 255
 Ile Tyr Gly Pro Asp Gly Arg Ala Leu Cys Glu Lys Leu Pro Glu Asn
 260 265 270
 Gln Glu Gly Leu Leu Tyr Ala Glu Ile Asp Leu Gly Val Ile Ser Met
 275 280 285
 Ala Lys Ser Ala Met Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 Tyr Arg Val Leu Phe Asn Lys Ile Pro Ala Lys Arg Ile Glu His Phe
 305 310 315 320
 Asn Leu Pro Leu Asp Glu Gln Ala Gly Glu Glu Pro Pro Ala Asp
 325 330 335

<210> 217
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 217

```

gtgggtatca gccatccgaa attcaaggct gcggtcgtac aggccggggcc tgccttccctc      60
gacctcgacg gcggcgctga acgagccgtg tcgctcatcg gccaaagcagc ggccgaaggg      120
gcacagctga ttgcctttcc tgaaacgtgg attcccgtgt acccgtggca cacctggctt      180
ggcagcccg   cgtgggcaat ggaaaaaggc tttgtccaac gatatttcga caacgcgttg      240
cggcatggtt ctccgcaagc cgagcgaatc tccggggctg cggcggagca caagattatg      300
gtgtcgcttg ggtttgcgga acgcgatgga ggcacgcctt atatcgcgca gtggctcatc      360
ggacccgacg gccaaactat ctcaogacgg cggaagctta agccgactca cgtcgagcgc      420
actgtatttg gcgagggaga cggaagcgat ctctccgtgc atgatacggc gcttggaagt      480
atcggctcac tttgttgctg ggagcatttg caaccgttgt cgaaatacgc aatgtacgcc      540
cagaatgaac agattcacat tggcgcatgg cccagctttt cgctatacca gccatttgcg      600
aatgcgctga gtcccgaagt caatatcgca gtaagccgcg tgtacgccgt ggaaggccag      660
tgtttcttcc tcgcgccgtg cgcgacgggt tcggacgcca tgatcgaaac actgtgcgat      720
acgcccgaaaa agcagggact gattcggggc ggtggcgggc acgccgcgat cttcggccca      780
gatggaagtc tgctgacgcc tacggtagcg gatacttacg agggcctgct gtatgcagaa      840
ctcgacctcg gcgtcatttc gatcgccaag agtgcagcgg accccgccgg ccactattcg      900
cggccagatg tcacacgcct tctattgaat cagacgcctt cgaagcgcgt tcagaatatg      960
gtgttaccac tggagacggt cacggagccc gaaggcccgg ttcagcccta g      1011

```

<210> 218

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 218

```

Val Gly Ile Ser His Pro Lys Phe Lys Ala Ala Val Val Gln Ala Gly
 1          5          10          15
Pro Ala Phe Leu Asp Leu Asp Gly Gly Val Glu Arg Ala Val Ser Leu
 20          25          30
Ile Gly Gln Ala Ala Ala Glu Gly Ala Gln Leu Ile Ala Phe Pro Glu
 35          40          45
Thr Trp Ile Pro Gly Tyr Pro Trp His Thr Trp Leu Gly Ser Pro Ala
 50          55          60
Trp Ala Met Glu Lys Gly Phe Val Gln Arg Tyr Phe Asp Asn Ala Leu
 65          70          75          80
Arg His Gly Ser Pro Gln Ala Glu Arg Ile Ser Gly Ala Ala Ala Glu
 85          90          95
His Lys Ile Met Val Ser Leu Gly Phe Ala Glu Arg Asp Gly Gly Thr
100          105          110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Gln Thr Ile Ser
115          120          125
Arg Arg Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly
130          135          140
Glu Gly Asp Gly Ser Asp Leu Ser Val His Asp Thr Ala Leu Gly Arg
145          150          155          160
Ile Gly Ser Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165          170          175
Ala Met Tyr Ala Gln Asn Glu Gln Ile His Ile Gly Ala Trp Pro Ser
180          185          190
Phe Ser Leu Tyr Gln Pro Phe Ala Asn Ala Leu Ser Pro Glu Val Asn
195          200          205
Ile Ala Val Ser Arg Val Tyr Ala Val Glu Gly Gln Cys Phe Phe Leu
210          215          220
Ala Pro Cys Ala Thr Val Ser Asp Ala Met Ile Glu Thr Leu Cys Asp
225          230          235          240
Thr Pro Glu Lys Gln Gly Leu Ile Arg Ala Gly Gly Gly His Ala Ala
245          250          255
Ile Phe Gly Pro Asp Gly Ser Leu Leu Thr Pro Thr Val Ala Asp Thr

```

<400>	220																
Met	Lys	Ile	Val	Lys	Ala	Ala	Ala	Val	Gln	Ile	Ser	Pro	Val	Leu	Tyr		
1				5					10					15			
Ser	Arg	Asp	Gly	Thr	Val	Glu	Lys	Val	Val	Arg	Lys	Ile	His	Glu	Leu		
			20					25					30				
Gly	Gln	Gln	Gly	Val	Gln	Phe	Ala	Thr	Phe	Pro	Glu	Thr	Val	Ile	Pro		
			35				40						45				
Tyr	Tyr	Pro	Tyr	Phe	Ser	Phe	Leu	Gln	Pro	Ala	Tyr	Gln	Ile	Ala	Ala		
	50					55					60						
Gly	Gln	Glu	His	Leu	Lys	Leu	Leu	Asp	Gln	Ala	Val	Thr	Val	Pro	Ser		
65					70					75					80		
Ala	Ala	Thr	His	Ala	Ile	Gly	Gln	Ala	Cys	Lys	Gln	Ala	Gly	Val	Val		
				85					90					95			
Val	Ser	Ile	Gly	Ile	Asn	Glu	Arg	Asp	Asn	Gly	Thr	Ile	Tyr	Asn	Thr		
			100					105					110				
Gln	Leu	Leu	Phe	Asp	Ser	Asp	Gly	Thr	Leu	Leu	Gln	Arg	Arg	Arg	Lys		

```
<210> 222
<211> 381
<212> PRT
```

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 222

```

Met Leu Thr Tyr Lys Gly Val Phe Lys Ala Ala Thr Val Gln Ala Glu
 1          5          10          15
Pro Val Trp Met Asp Ala Asp Ala Thr Ile Thr Lys Ala Ile Arg Ile
      20          25          30
Ile Glu Glu Ala Ala Asp Asn Gly Ala Lys Phe Val Ala Phe Pro Glu
      35          40          45
Val Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Thr Ala Met
      50          55          60
Trp Gly Ala Lys Phe Val Val Pro Phe His Glu Asn Cys Leu Glu Leu
      65          70          75          80
Gly Asp Lys Arg Met Gln Arg Ile Gln Ala Ala Ala Lys Gln Asn Gly
      85          90          95
Ile Ala Leu Val Met Gly Tyr Gly Glu Arg Asp Gly Gly Ser Arg Tyr
      100          105          110
Met Ser Gln Val Phe Ile Asp Asp Ser Gly Lys Ile Val Ala Asn Arg
      115          120          125
Arg Lys Leu Lys Pro Thr His Glu Glu Arg Thr Ile Phe Gly Glu Gly
      130          135          140
Asn Gly Ser Asp Phe Ile Thr His Asp Phe Pro Phe Ala Arg Val Gly
      145          150          155          160
Gly Phe Asn Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Met Met
      165          170          175          180
Tyr Ser Leu Gln Glu Gln Val His Val Ala Ser Trp Pro Ala Met Cys
      180          185          190
Thr Tyr Gln Pro Asp Val Pro Gln Leu Gly Ala Gly Ala Asn Glu Ala
      195          200          205
Val Thr Arg Ser Tyr Ala Ile Glu Gly Ala Cys Tyr Val Leu Gly Ala
      210          215          220
Thr Leu Val Ile Gly Lys Ala Ala His Asp Ala Phe Cys Asp Thr Glu
      225          230          235          240
Glu His His Lys Leu Leu Gly Met Gly Gly Gly Trp Ala Arg Ile Phe
      245          250          255
Gly Pro Asp Gly Glu Tyr Leu Ala Glu Ser Leu Ala His Asp Ala Glu
      260          265          270
Gly Ile Leu Tyr Ala Asp Ile Asp Leu Ser Lys Ile Leu Leu Ala Lys
      275          280          285
Ala Asn Thr Asp Thr Val Gly His Tyr Ala Arg Pro Asp Val Leu Ser
      290          295          300
Leu Leu Val Asn Thr His Asn Pro Gly Pro Val Arg Tyr Leu Asp Glu
      305          310          315          320
Glu Gly Arg Gln Val Ser Thr Ser Ile Arg Arg His Glu Lys Leu Glu
      325          330          335
Gly Gln Ser Leu Asp Leu Glu Val Thr Pro Ala Thr Pro Ala Thr Leu
      340          345          350
Asp Ile Ala Ser Leu Val Gln Gln Ala Lys Pro Ser Thr Val Lys Ser
      355          360          365
Glu Ser Asn Ala Ser Thr Lys Gln Pro Asp Leu Ala Val
      370          375          380

```

<210> 223

<211> 996

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 223

atgagagttg	ttaaagccag	cgcagttcaa	ctgaagcctg	tactttatag	ccgcgagggg	60
acggtcgaaa	aggtcgtagc	gaagattcat	gagctagggc	agcaggggtg	gcagttcgcc	120
gcggttcctg	agaccgtggg	gccttattac	ccgtactttt	cgatcgtgca	gtccggctat	180
caaatacctt	gcgggcggta	gttcgtcaag	ctcctcgatc	agtccgtgac	ggtgccatct	240
tatagcactg	aagccatcgg	cgaagcctgc	aggcaggagg	agatggttgt	ctccataggc	300
gtcaacgagc	gtgatggcgg	aacgatctac	aacgcgcagt	tactctttga	ttccgacggc	360
acgttgatcc	aaagacgacg	caagatcacc	cccacccatt	acgaacgcat	gatctggggc	420
cagggcgatg	gctcaggtct	gcgcgctgtt	gacagcaatg	tcgcacgcat	tggtcaactg	480
gcatgctttg	agcaactaaa	ccctcttgcg	cggtagcgga	tgatggccga	tggcgagcag	540
atccattccg	ccatgttccc	cggttccatg	ttcggcgatg	gttttgcgga	gaggacggaa	600
attgccgtaa	ggcaacatgc	gatggagtcc	gggtgctttg	tcgtttgcgc	tacggcctgg	660
ctcgatcccg	gccagcaggc	tcagatcgcc	aacgacaccg	gtatcaccga	catcggcccc	720
atctccgggg	gttgcttcac	tgcgatcatc	gcacccgatg	ggagcctgct	gggccaacct	780
atccgctcgg	gtgaaggcga	agtcatcgtc	gacctcgatt	tcacgttaat	tgacaagcgg	840
aaacatattg	tcgactcgag	aggacattac	agccggccag	aattgctgag	cctgctgac	900
gatcgcactc	ccaccgcgca	ccttcacgac	cgcgctgtgc	agcacaatgc	cggatcgga	960
ggagcgtcgg	aacatcttcg	cgaagacgcc	gcctga			996

<210> 224

<211> 331

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 224

Met	Arg	Val	Val	Lys	Ala	Ser	Ala	Val	Gln	Leu	Lys	Pro	Val	Leu	Tyr	
1				5					10					15		
Ser	Arg	Glu	Gly	Thr	Val	Glu	Lys	Val	Val	Ala	Lys	Ile	His	Glu	Leu	
			20					25					30			
Gly	Gln	Gln	Gly	Val	Gln	Phe	Ala	Ala	Phe	Pro	Glu	Thr	Val	Val	Pro	
		35					40					45				
Tyr	Tyr	Pro	Tyr	Phe	Ser	Ile	Val	Gln	Ser	Gly	Tyr	Gln	Ile	Leu	Arg	
	50					55					60					
Gly	Gly	Glu	Phe	Val	Lys	Leu	Leu	Asp	Gln	Ser	Val	Thr	Val	Pro	Ser	
	65				70				75					80		
Tyr	Ser	Thr	Glu	Ala	Ile	Gly	Glu	Ala	Cys	Arg	Gln	Glu	Glu	Met	Val	
				85					90					95		
Val	Ser	Ile	Gly	Val	Asn	Glu	Arg	Asp	Gly	Gly	Thr	Ile	Tyr	Asn	Ala	
			100					105					110			
Gln	Leu	Leu	Phe	Asp	Ser	Asp	Gly	Thr	Leu	Ile	Gln	Arg	Arg	Arg	Lys	
			115				120					125				
Ile	Thr	Pro	Thr	His	Tyr	Glu	Arg	Met	Ile	Trp	Gly	Gln	Gly	Asp	Gly	
	130					135					140					
Ser	Gly	Leu	Arg	Ala	Val	Asp	Ser	Asn	Val	Ala	Arg	Ile	Gly	Gln	Leu	
	145				150					155				160		
Ala	Cys	Phe	Glu	His	Tyr	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Met	Met	Ala	
				165					170					175		
Asp	Gly	Glu	Gln	Ile	His	Ser	Ala	Met	Phe	Pro	Gly	Ser	Met	Phe	Gly	
			180					185					190			
Asp	Gly	Phe	Ala	Glu	Arg	Thr	Glu	Ile	Ala	Val	Arg	Gln	His	Ala	Met	
	195						200					205				
Glu	Ser	Gly	Cys	Phe	Val	Val	Cys	Ala	Thr	Ala	Trp	Leu	Asp	Pro	Gly	
	210					215					220					
Gln	Gln	Ala	Gln	Ile	Ala	Asn	Asp	Thr	Gly	Ile	Thr	Asp	Ile	Gly	Pro	
	225				230					235				240		
Ile	Ser	Gly	Gly	Cys	Phe	Thr	Ala	Ile	Ile	Ala	Pro	Asp	Gly	Ser	Leu	

```

                245                250                255
Leu Gly Gln Pro Ile Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu
                260                265                270
Asp Phe Thr Leu Ile Asp Lys Arg Lys His Ile Val Asp Ser Arg Gly
                275                280                285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
                290                295                300
Thr Ala His Leu His Asp Arg Ala Val Gln His Asn Ala Gly Ser Glu
305                310                315                320
Gly Ala Ser Glu His Leu Arg Glu Asp Ala Ala
                325                330

```

<210> 225
 <211> 951
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 225
atgaccaccg tcaaagccgc cgctgtccag atgagtcccc tgctttacag tcgcgacgat      60
accatcgaga aaatttgtcg acagatcatc gagcttggcc gacaggagat gcagttcgcc      120
acgtttccag agacagttat tccgtattat ccatatttcg ccttcgtgca gcggccttac      180
gaaatgtcgg cccaatatca tcagttgctt gatcaagcgg tgaccgtgcc ttccggttca      240
acgcacgcca ttggggccgc ctgtaaaca gcccgaattg ttgtctcaat cggcgctcaac      300
gagcgggagg gcggcacgct ctatggcaca cagttgctgt ttgatgcaga cggcctcttg      360
atccagcgtc gccgcaagat cactccgacc taccacgagc ggatgatttg gggacagggt      420
gacggttccg ggctgcgagc cgtagatagc gcggtcggtc gaatcggaca gttggcggtg      480
tggaacacc acaatccgct ggctcgttat gctttagcgg ccgatggcga acaaattcac      540
gcggcgatgt accctggctc gatcttgggt gaactatttg ccgagcagat tcagggtcaac      600
atccggcagc acgccatgga atctggttgc ttcgctcgta acgccacggc ctgggctaagc      660
gaggaacagc aagcccgaat catgaaggac accggatcat tcgatagccc aatcaccggt      720
ggttgcttta ccgccattgt cgcgcccac gggcagataa tcggtgaacc gctgcgcac      780
ggcgaaggcg tcgtgattgc cgatttggac ttcgctttga ttgatgagag gaagcggctg      840
atggactcac gcggcctcta tagccgcct gagttgctaa gcttgttaat cgacagaatg      900
cctacatccc atgtgcatga acgggttgag cgtagcatgg cgatggcatg a          951

```

<210> 226
 <211> 316
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 226
Met Thr Thr Val Lys Ala Ala Ala Val Gln Met Ser Pro Val Leu Tyr
 1                5                10                15
Ser Arg Asp Asp Thr Ile Glu Lys Ile Cys Arg Gln Ile Ile Glu Leu
                20                25                30
Gly Arg Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Ile Pro
                35                40                45
Tyr Tyr Pro Tyr Phe Ala Phe Val Gln Arg Pro Tyr Glu Met Ser Ala
 50                55                60
Gln Tyr His Gln Leu Leu Asp Gln Ala Val Thr Val Pro Ser Gly Ser
 65                70                75                80
Thr His Ala Ile Gly Ala Ala Cys Lys Gln Ala Gly Ile Val Val Ser
                85                90                95
Ile Gly Val Asn Glu Arg Glu Gly Gly Thr Leu Tyr Gly Thr Gln Leu
                100                105                110

```

Leu Phe Asp Ala Asp Gly Leu Leu Ile Gln Arg Arg Arg Lys Ile Thr
 115 120 125
 Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ser Gly
 130 135 140
 Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu Ala Cys
 145 150 155 160
 Trp Glu His His Asn Pro Leu Ala Arg Tyr Ala Leu Ala Ala Asp Gly
 165 170 175
 Glu Gln Ile His Ala Ala Met Tyr Pro Gly Ser Ile Leu Gly Glu Leu
 180 185 190
 Phe Ala Glu Gln Ile Gln Val Asn Ile Arg Gln His Ala Met Glu Ser
 195 200 205
 Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Ser Glu Glu Gln Gln
 210 215 220
 Ala Arg Ile Met Lys Asp Thr Gly Ser Phe Asp Ser Pro Ile Thr Gly
 225 230 235 240
 Gly Cys Phe Thr Ala Ile Val Ala Pro Asn Gly Gln Ile Ile Gly Glu
 245 250 255
 Pro Leu Arg Ile Gly Glu Gly Val Val Ile Ala Asp Leu Asp Phe Ala
 260 265 270
 Leu Ile Asp Glu Arg Lys Arg Leu Met Asp Ser Arg Gly Leu Tyr Ser
 275 280 285
 Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Met Pro Thr Ser His
 290 295 300
 Val His Glu Arg Val Glu Arg Ser Met Ala Met Ala
 305 310 315

<210> 227

<211> 1035

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 227

atgtccgatac	gacgcatcgt	tgcgcgggca	gccattcaga	tgcggccgga	tctcgagcgc	60
tgcagtgtaa	cgctcgagaa	ggtttgctog	gcgatcgacg	aagccgcggg	caaagcgct	120
caactgagcg	tctttcccga	gaccttcgtc	ccgtactacc	cctatttctc	gtttgtccgc	180
cctccggtcg	catcgggggc	cgatcacatg	cggctatacg	aggaagcggg	ggtggtgccg	240
ggtcccgtga	cgcaggctgt	ttccgaacgt	gcgcgcatgc	atgggatggg	ggtggtgctc	300
ggcgtcaacg	agcgcgacca	cgggagcctc	tacaacaccc	aactgatttt	cgattgcgat	360
ggtcggctcg	ctctgaaacg	ccgcaagatc	acgccgacgt	ttcacgagcg	catgatctgg	420
ggccagggcg	acgccagtgg	actgaaagtc	gcgcgcacgg	gtatcggggc	ggtcggcgcg	480
ctcgcgtgct	gggagcatta	caaccgcgtc	gcgcgctacg	cgctgatgac	ccagcacgaa	540
gagatccatt	gcagtcaatt	tccaggctcg	ctcgtcgggtc	cgatcttctc	cgagcagatg	600
gacgtgacga	tccgccatca	cgccctcgaa	tccgggtgct	tcgtcgtgaa	cgcaaccggt	660
tggctcacgg	acgcgcagat	cgcctcgatc	accgatgacc	cgaagcttca	acgggcgctg	720
cgcggtggct	gcaacacggc	gatcgtttca	ccggaaggcc	agcatctggc	ggagccgttg	780
cgcgaaggcg	aggggatggg	ggtcgcggac	ctcgacatgt	cgctcatcac	caagcgcaag	840
cgaatgatgg	attcggtcgg	ccactatgcg	cggccggaac	tggtgagcct	cgcgatcaac	900
gatcgtcccg	cagccccctt	cggccggatg	tgcgctgccg	aagcaatgcg	gggagccgac	960
gacgtcgtca	cagtaggagc	atttcatgag	cgccagcgag	aacgtgtcgg	cgaagagccg	1020
gcaattgatg	actga					1035

<210> 228

<211> 344

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 228

```

Met Ser Asp Arg Arg Ile Val Arg Ala Ala Ala Ile Gln Ile Ala Pro
 1      5      10      15
Asp Leu Glu Arg Cys Ser Val Thr Leu Glu Lys Val Cys Ser Ala Ile
 20      25      30
Asp Glu Ala Ala Gly Lys Gly Ala Gln Leu Ser Val Phe Pro Glu Thr
 35      40      45
Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Pro Pro Val Ala
 50      55      60
Ser Gly Ala Asp His Met Arg Leu Tyr Glu Glu Ala Val Val Val Pro
 65      70      75      80
Gly Pro Val Thr Gln Ala Val Ser Glu Arg Ala Arg Met His Gly Met
 85      90      95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
100      105      110
Thr Gln Leu Ile Phe Asp Cys Asp Gly Arg Leu Ala Leu Lys Arg Arg
115      120      125
Lys Ile Thr Pro Thr Phe His Glu Arg Met Ile Trp Gly Gln Gly Asp
130      135      140
Ala Ser Gly Leu Lys Val Ala Arg Thr Gly Ile Gly Arg Val Gly Ala
145      150      155      160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
165      170      175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
180      185      190
Gly Pro Ile Phe Ser Glu Gln Met Asp Val Thr Ile Arg His His Ala
195      200      205
Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Asp
210      215      220
Ala Gln Ile Ala Ser Ile Thr Asp Asp Pro Lys Leu Gln Arg Ala Leu
225      230      235      240
Arg Gly Gly Cys Asn Thr Ala Ile Val Ser Pro Glu Gly Gln His Leu
245      250      255
Ala Glu Pro Leu Arg Glu Gly Glu Gly Met Val Val Ala Asp Leu Asp
260      265      270
Met Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
275      280      285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Arg Pro Ala
290      295      300
Ala Pro Phe Gly Arg Met Cys Ala Ala Glu Ala Met Arg Gly Ala Asp
305      310      315      320
Asp Val Val Thr Val Gly Ala Phe His Glu Arg Gln Arg Glu Arg Val
325      330      335
Gly Glu Glu Pro Ala Ile Asp Asp
340

```

<210> 229

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 229

```

atgcctgaaa acaaagtcaa agttgccctc gttcagcatc cgcctgtttt tctgaatttg      60
ccgaaaacgt tggaaaaagt agaaggtttg gcgcgagagt gcgccgccaa tgaagcgaaa      120
atcgttgtct ttcctgaaac ctggctgacc ggctatccgg tctggcttga tgaagcgccg      180
agagccgcgc tgtgggatta tccgcccgcc aagcgtttgt atcaatacct cacggaaaat      240

```

```

tcattgcaga ttccgagcgc tgagtttgaa tctttgcgcg aaatcgctaa gaaaaattcc 300
ctttatttag tcgttggagt tcacgaacga agcggcgga cgctctacaa tacgataatt 360
tatctcacgc ccgacggcag ttataaaact caccgcaa atggttccaac ttacacggaa 420
agacttgtct ggggcgcagg cgacggaagc ggtctaaatg ttgtggaaac gccttacggg 480
attctcggag gtttgatttg ctgggaacat tggatgcctc tggctagggc ggcaatgcat 540
tcaaaaaatg aagcgattca cgtttgccaa tttcccacgg ttcacgagcg acatcaaatac 600
gccagccgtc attacgcctt cgaagggcag tgttttgtct tgacttccgg ttgcgcgatg 660
acgaaaacgg atgttttgga aggttttgaa tcgctcgaaa caaacgacca cgaagttttc 720
gggcttttgg attcgataga aaaggaagaa ctgatgcgtg gcggaagcgc gattattgcg 780
cccgatttga gctattcggc cgagccggtt tttgacgaaa aaacgattgt ttacggcgaa 840
ttaaattctc atttaaccaa gcaggacat ctgtttttgg ataccgacgg acattattcg 900
cgtcccgatg ttttcgagtt gcgcgtcaac gataaagcga accgaaacgt ccgtttttgca 960
tccgaaacag tatag 975

```

<210> 230

<211> 324

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 230

```

Met Pro Glu Asn Lys Val Lys Val Ala Leu Val Gln His Pro Pro Val
1      5      10      15
Phe Leu Asn Leu Pro Lys Thr Leu Glu Lys Val Glu Gly Leu Ala Arg
20      25      30
Glu Cys Ala Ala Asn Glu Ala Lys Ile Val Val Phe Pro Glu Thr Trp
35      40      45
Leu Thr Gly Tyr Pro Val Trp Leu Asp Glu Ala Pro Arg Ala Ala Leu
50      55      60
Trp Asp Tyr Pro Pro Ala Lys Arg Leu Tyr Gln Tyr Leu Thr Glu Asn
65      70      75      80
Ser Leu Gln Ile Pro Ser Ala Glu Phe Glu Ser Leu Arg Glu Ile Ala
85      90      95
Lys Lys Asn Ser Leu Tyr Leu Val Val Gly Val His Glu Arg Ser Gly
100     105     110
Gly Thr Leu Tyr Asn Thr Ile Ile Tyr Leu Thr Pro Asp Gly Ser Tyr
115     120     125
Lys Thr His Arg Lys Leu Val Pro Thr Tyr Thr Glu Arg Leu Val Trp
130     135     140
Gly Ala Gly Asp Gly Ser Gly Leu Asn Val Val Glu Thr Pro Tyr Gly
145     150     155     160
Ile Leu Gly Gly Leu Ile Cys Trp Glu His Trp Met Pro Leu Ala Arg
165     170     175
Ala Ala Met His Ser Lys Asn Glu Ala Ile His Val Cys Gln Phe Pro
180     185     190
Thr Val His Glu Arg His Gln Ile Ala Ser Arg His Tyr Ala Phe Glu
195     200     205
Gly Gln Cys Phe Val Leu Thr Ser Gly Cys Ala Met Thr Lys Thr Asp
210     215     220
Val Leu Glu Gly Phe Glu Ser Leu Glu Thr Asn Asp His Glu Val Phe
225     230     235     240
Gly Leu Leu Asp Ser Ile Glu Lys Glu Glu Leu Met Arg Gly Gly Ser
245     250     255
Ala Ile Ile Ala Pro Asp Leu Ser Tyr Ser Val Glu Pro Val Phe Asp
260     265     270
Glu Lys Thr Ile Val Tyr Gly Glu Leu Asn Leu Asp Leu Thr Lys Gln
275     280     285
Gly His Leu Phe Leu Asp Thr Asp Gly His Tyr Ser Arg Pro Asp Val
290     295     300

```

Phe Glu Leu Arg Val Asn Asp Lys Ala Asn Arg Asn Val Arg Phe Ala
 305 310 315 320
 Ser Glu Thr Val

<210> 231
 <211> 1062
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 231
 atgagtcaga tccatccaaa acttaaggct gcggccgtgc aggctgcccc cgcctttctc 60
 gatctcgatg catcgatcga aaagacaata cgctatgtcg acgaagcggc tgcggccggg 120
 gcgaagttga ttgogtttcc ggaaacctgg attcccggct acccatgggtg gatctggctc 180
 ggcgctccgg cctgggcat catgcgtggc ttctgtctgc gctatttcga caactcgctg 240
 caatatggca gtccggaagc tgaacggctg cgggacgccg ccaggcgcaa caagatatac 300
 atcgccctcg gcctgtccga gcgcgacggg ggagctcttt atatcgcgca atggatcatc 360
 gggcctggcg gcgaaacggg tgcacaacgc cgcaagctca agcccacgca cgccgagcgc 420
 actgtattcg gcgaaggcga tggttcacat ctggccgtgc atgatctcga tattggaaga 480
 ttgggcgcgc tttgttgctg ggaacatctg caaccgttgt cgaaatatgc aatgtacgcc 540
 cagaacgagc aaattcacgt cgcgccttg cggagcttct cgctatacga tccctttgca 600
 cagcactcg gcgcggaggt caataacgct gcgagcaaga tctatgcggt cgagggatcg 660
 tgcttcgtca ttgcgccgtg cgcaacgggt tcgcaggtga tgatcgatga gctctgcgat 720
 acccccgaag agcatcaatt ccttcacgtc ggccggcggt tcgccgtcat ttacggtccc 780
 gacggctcgc cactggccaa acctcttcgg ccagaccagg agggacttct ctatgccgac 840
 atcgatctcg gcatgatctc ggtcgccaag gccgcagccg atcccggcgg acattatgca 900
 cgtcccgatg taactcgctt gctgttcaac aatcgcccgg caaacgcgct cgagaagctg 960
 gcgttgccgg tcgatcagga ggccgaagtg gatagtccgc tgaaggctcc cgacgcattc 1020
 cccaaagtga cggcgctcaa gccgtcgcag gctgcggagt ag 1062

<210> 232
 <211> 353
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 232
 Met Ser Gln Ile His Pro Lys Leu Lys Val Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Ala Phe Leu Asp Leu Asp Ala Ser Ile Glu Lys Thr Ile Arg Tyr
 20 25 30
 Val Asp Glu Ala Ala Ala Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Gln Tyr Gly Ser Pro Glu Ala Glu Arg Leu Arg Asp Ala Ala Arg Arg
 85 90 95
 Asn Lys Ile Tyr Ile Ala Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Gly Gly Glu Thr Val Ala
 115 120 125
 Gln Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser His Leu Ala Val His Asp Leu Asp Ile Gly Arg

```

145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
          165          170          175
Ala Met Tyr Ala Gln Asn Glu Gln Ile His Val Ala Ala Trp Pro Ser
          180          185          190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
          195          200          205
Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile
          210          215          220
Ala Pro Cys Ala Thr Val Ser Gln Val Met Ile Asp Glu Leu Cys Asp
225          230          235          240
Thr Pro Glu Lys His Gln Phe Leu His Val Gly Gly Gly Phe Ala Val
          245          250          255
Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Lys Pro Leu Pro Pro Asp
          260          265          270
Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Val
          275          280          285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val
          290          295          300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Ala Asn Arg Val Glu Lys Leu
305          310          315          320
Ala Leu Pro Val Asp Gln Glu Ala Glu Val Asp Ser Pro Leu Lys Ala
          325          330          335
Pro Asp Ala Ser Pro Lys Val Thr Ala Leu Lys Pro Ser Gln Ala Ala
          340          345          350
Glu

```

<210> 233
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 233
gtgagcacca tcgtcaaagc cgcggccgtg cagatcagcc ccgtgctgta cagccgcgag      60
ggcaccgtcg agcgggtcgt gaagaagatc cgggagctgg gcgaaaaggg cgtccagttc      120
gccaccttcc ccgagaccgt catcccttac taccogtact ttcccttcgt tcagacgccc      180
ttgcagatcc tcgccggccc cgagcatctg aagctgctcg accagtcggt gaccgtgccg      240
tcccccgcca cggacgcgat cggccaggcc gcccggcagg caggaatggg ggtgtccatc      300
ggcgtcaacg agcgtgacgg cggcaccctg tacaacacgc agctgctctt cgacgcggac      360
ggcgcgctga tccagcgtcg ccgcaagatc aagccccacc actacgagcg catgatctgg      420
ggcgagggcg acggctccgg cctgcgcgcc gtcgacagcc aggtcgggtcg tatcgccag      480
ctggcctgct gggagcacaa caacccctg gcgcgctacg ccgatgatggc cgacggcgag      540
cagatccatt cggccatgta tccgggctcg atgttcggcg acccgttcgc ccagaagacg      600
gaaatcaaca tccggcagca tgcgctggaa tccgatgct tgcgtctctg ctcgacggcc      660
tggttggacg ccgatcagca ggcgcaaatc atgcaggaca cgggctgcgc catcgcccgc      720
atctcggggc gctgcctcac ggcgatcgtg gcgcccgcgc gcacgttcct gggcgaaccg      780
ctcacgtcgg gcgagggcga ggtcatcgcc gacctcgatt tcaagctgat cgacaagcgc      840
aagcagacga tggactcgcg cggccactac aaccgccccg aactgctcag cctgctgatc      900
gatcgaacgc cgacgtcgaa cgtccatgag cgcgcgcgcg acccgaaggt cgaggcgtca      960
caaacggctg gcgacacgga gcggaccgcg gaggtcctgt aa      1002

```

<210> 234
 <211> 333
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 234

```

Val Ser Thr Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu
1      5      10      15
Tyr Ser Arg Glu Gly Thr Val Glu Arg Val Val Lys Lys Ile Arg Glu
20     25     30
Leu Gly Glu Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Ile
35     40     45
Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Ile Leu
50     55     60
Ala Gly Pro Glu His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro
65     70     75     80
Ser Pro Ala Thr Asp Ala Ile Gly Gln Ala Ala Arg Gln Ala Gly Met
85     90     95
Val Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn
100    105    110
Thr Gln Leu Leu Phe Asp Ala Asp Gly Ala Leu Ile Gln Arg Arg Arg
115    120    125
Lys Ile Lys Pro Thr His Tyr Glu Arg Met Ile Trp Gly Glu Gly Asp
130    135    140
Gly Ser Gly Leu Arg Ala Val Asp Ser Gln Val Gly Arg Ile Gly Gln
145    150    155    160
Leu Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met
165    170    175
Ala Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe
180    185    190
Gly Asp Pro Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala
195    200    205
Leu Glu Ser Gly Cys Phe Val Val Cys Ser Thr Ala Trp Leu Asp Ala
210    215    220
Asp Gln Gln Ala Gln Ile Met Gln Asp Thr Gly Cys Ala Ile Gly Pro
225    230    235    240
Ile Ser Gly Gly Cys Leu Thr Ala Ile Val Ala Pro Asp Gly Thr Phe
245    250    255
Leu Gly Glu Pro Leu Thr Ser Gly Glu Gly Glu Val Ile Ala Asp Leu
260    265    270
Asp Phe Lys Leu Ile Asp Lys Arg Lys Gln Thr Met Asp Ser Arg Gly
275    280    285
His Tyr Asn Arg Pro Glu Leu Ser Leu Leu Ile Asp Arg Thr Pro
290    295    300
Thr Ser Asn Val His Glu Arg Ala Ala His Pro Lys Val Glu Ala Ser
305    310    315    320
Gln Thr Ala Gly Asp Thr Glu Arg Thr Arg Glu Val Leu
325    330

```

<210> 235

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 235

```

atgaaaattg ttaaagcggc agcagttcag ctgagccccg tcctctatag ccgcgagggg 60
acggtcgaaa gagtagtgcg gaagattcat caacttggtc aacagggagt gcagtttgcc 120
accttcccgg aaacagtggg gccttactac ccgtattttt cgatcgtgca gtccgggtat 180
caaatccttc gcggcgggtga gttcgtgaag ctgctcgatc agtcagtgac ggtgccatct 240
cttgccaccg aagcgatcgc cgaggcctgc aggcaggcgg gcgtcgttgt ctccatcggc 300
gtcaatgagc gtgacggcgg aactatatac aatgcgcagc ttctgtttga ttcggacggc 360

```

```

acattgattc agaggcgacg caagatcacg cccaccact acgagcgcat gatctggggc 420
cagggcgatg gctcgggtct gcgggctgtg gacagcaagg tggcacgtat tggtaactg 480
gcgtgctttg agcattacaa cccctcgca cgatacgca tgatcgccga tggcgagcag 540
atccactctg caatgtttcc cggttccatg ttcggcgatg gtttcgcgga gaggaccgag 600
atcgcggtca ggcagcatgc gcaggagtcc ggatgctttg tagtttgtgc tacggcggtg 660
ctggatgccg accagcaggc tcaaattgcc gcggacacag gcatcaccga cctgggaccg 720
atctccggcg gttgcttcac tgcgatcatt gcacctgatg ggagcctgct gggtaacca 780
atccgctcgg gcgaagggtga cgtcattgtc gatctcgatt tcaactctgat cgacaggcgg 840
aagcatgttg tggactcgag aggtcactac agccggccgg aattgctaag cctgctgatc 900
gaccgtactc ccacagcgca cgttcacgaa cgggcccgcg actctcactt ggccgccgag 960
caatgcttgg aggatcttaa cgcgcttgct taa 993

```

<210> 236

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 236

```

Met Lys Ile Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
1      5      10
Ser Arg Glu Gly Thr Val Glu Arg Val Arg Lys Ile His Gln Leu
20     25     30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Arg
50     55     60
Gly Gly Glu Phe Val Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
65     70     75     80
Leu Ala Thr Glu Ala Ile Ala Glu Ala Cys Arg Gln Ala Gly Val Val
85     90     95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala
100    105    110
Gln Leu Leu Phe Asp Ser Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
115    120    125
Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
130    135    140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Ala Arg Ile Gly Gln Leu
145    150    155    160
Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
165    170    175
Asp Gly Glu Gln Ile His Ser Ala Met Phe Pro Gly Ser Met Phe Gly
180    185    190
Asp Gly Phe Ala Glu Arg Thr Glu Ile Ala Val Arg Gln His Ala Gln
195    200    205
Glu Ser Gly Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
210    215    220
Gln Gln Ala Gln Ile Ala Ala Asp Thr Gly Ile Thr Asp Leu Gly Pro
225    230    235    240
Ile Ser Gly Gly Cys Phe Thr Ala Ile Ile Ala Pro Asp Gly Ser Leu
245    250    255
Leu Gly Gln Pro Ile Arg Ser Gly Glu Gly Asp Val Ile Val Asp Leu
260    265    270
Asp Phe Thr Leu Ile Asp Arg Arg Lys His Val Val Asp Ser Arg Gly
275    280    285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
290    295    300
Thr Ala His Val His Glu Arg Ala Ala His Ser His Leu Ala Ala Glu
305    310    315    320

```

Gln Cys Leu Glu Asp Leu Asn Ala Leu Ala
 325 330

<210> 237

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 237

atgaaagtgcg	tcaaagccgc	cgcagtgcag	atcagtcctg	ttctctacag	ccgagaggca	60
accgtcgcca	aggctcgtgca	gaagatccac	gaactcggcc	agaaaggcgt	gcagttcgcc	120
acctttccag	agaccgtagt	gccttactac	ccgtactttt	ccgccgtcca	gacaggcatc	180
gagctttctgt	ccggcacgga	gcattctccg	ctgctcgatc	aggccgtgac	ggtgccgtct	240
gccgctaccg	accgatcg	agaggcagcc	cggaaaggcag	gcatgggtgg	gtcgatcggc	300
gtcaatgaac	gcgatggcgg	caccttgtag	aacacacagt	tgctcttcga	tgccgatggc	360
accttgatcc	agcgccgccc	caagatcacg	ccgaccact	tcgaacgcat	gatctggggc	420
cagggggacg	gttcggggcct	gcgcgctgtc	gacagcaagg	tcgggtcgcat	tggccagttg	480
gcctgcttcg	agcacaacaa	cccgtgggcc	cgctacgcgt	tgattgccga	cggcgagcag	540
atccattccg	ccatgtatcc	gggttctgtc	tttggcgaag	gatttgccca	aaggatggaa	600
atcaatatcc	gccagcatgc	gctggagtcg	ggtgcgttcg	tcgtcaacgc	aacggcctgg	660
ctggatgctg	accagcaggc	gcagatcatg	aaggacaccg	gctgcgggat	tggcccgatc	720
tcgggcggtt	gcttcaccac	gatcgtgtca	cccgcaggca	tgctgatggc	cgaacccctg	780
cgctcggg	aggggtgagg	catcgtcgat	ctcgacttca	cgctgatcga	ccgtcgcaag	840
atgttgatgg	actcggcggg	ccactataac	cgcccggaa	tgctcagttc	catgatcgac	900
cgcaccccg	ccgcgcacgt	tcatgaacgc	gctgcgcgtc	cgggtgctggg	cgttgagcag	960
aacccgagg	aacttcgcat	cccggccgcg	tga			993

<210> 238

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 238

Met	Lys	Val	Val	Lys	Ala	Ala	Ala	Val	Gln	Ile	Ser	Pro	Val	Leu	Tyr
1				5					10					15	
Ser	Arg	Glu	Ala	Thr	Val	Ala	Lys	Val	Val	Gln	Lys	Ile	His	Glu	Leu
			20					25					30		
Gly	Gln	Lys	Gly	Val	Gln	Phe	Ala	Thr	Phe	Pro	Glu	Thr	Val	Val	Pro
		35					40					45			
Tyr	Tyr	Pro	Tyr	Phe	Ser	Ala	Val	Gln	Thr	Gly	Ile	Glu	Leu	Leu	Ser
	50					55					60				
Gly	Thr	Glu	His	Leu	Arg	Leu	Leu	Asp	Gln	Ala	Val	Thr	Val	Pro	Ser
65					70				75					80	
Ala	Ala	Thr	Asp	Ala	Ile	Gly	Glu	Ala	Ala	Arg	Lys	Ala	Gly	Met	Val
				85				90						95	
Val	Ser	Ile	Gly	Val	Asn	Glu	Arg	Asp	Gly	Gly	Thr	Leu	Tyr	Asn	Thr
			100					105					110		
Gln	Leu	Leu	Phe	Asp	Ala	Asp	Gly	Thr	Leu	Ile	Gln	Arg	Arg	Arg	Lys
			115				120				125				
Ile	Thr	Pro	Thr	His	Phe	Glu	Arg	Met	Ile	Trp	Gly	Gln	Gly	Asp	Gly
	130					135				140					
Ser	Gly	Leu	Arg	Ala	Val	Asp	Ser	Lys	Val	Gly	Arg	Ile	Gly	Gln	Leu
145					150				155					160	
Ala	Cys	Phe	Glu	His	Asn	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Leu	Ile	Ala
				165				170						175	

Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ala Arg Pro Val Ser Gly Val Glu Gln
 305 310 315 320
 Asn Pro Glu Glu Leu Arg Ile Pro Ala Ala
 325 330

<210> 239
 <211> 969
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 239
 atgtccaatg agaataagta tgacacattt aaagttgctg cagtccaggc cacacctgtg 60
 tttcttgatc gtgaagcaac catcgacaaa gcttgcgagt tgattgctac tgcagggtcgt 120
 gaaggtgctc gcctgattgt ctttccagaa gcgttcatcc catcctatcc cgagtgggta 180
 tggggatttc cctctggtga gcaagggtta ctcaacgaac tttattcaga gttgctcacc 240
 aatgcgggta ccatacccag cgacgcgact gacagattgt gcgaggcggc aaagcttgcg 300
 aatgcctatg tagtgatggg aatgagcgaa cggaatgtcg aagcgagtgg tgcaagcctg 360
 tataacacga tgttgatata agatgcacag ggggagattt tagggaaaca tcggaagctg 420
 gtgccaacgg gtggtgaacg cctggtatgg gcgcaagggt atggcagcac gctgcaggtc 480
 tacgatactc cattgggaaa acttgggtggg ttaatttgct gggaaaatta tatgccgctg 540
 gcacgctata cgatgtatgc ctggggaaca caaatctatg ttgcagcaac gtgggattgc 600
 ggccaaccct ggctctcaac gatacggcat attgctaaag aaggcagggt atactgtggt 660
 ggttgctgta tcgcgatgcg taaagatgat attccagatc gttactctat gaagcagaaa 720
 tattatgctg aaatggatga atggataaat gttggggata gcgcgattgt caatcccga 780
 ggacatttta ttgcagggcc tgtgcgcaag caagaagaaa ttctctatgc ggagattgat 840
 ccacgtatga tgcaaggccc gaagtggatg cttgacgtgg cgggacatta tgcaagacca 900
 gatgtgttcc agttgacggg gcatacggat gtgaggcaga tgatacgggt ggaagatgat 960
 tctcaatga 969

<210> 240
 <211> 322
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 240
 Met Ser Asn Glu Asn Lys Tyr Asp Thr Phe Lys Val Ala Ala Val Gln
 1 5 10 15
 Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
 20 25 30

Glu Leu Ile Ala Thr Ala Gly Arg Glu Gly Ala Arg Leu Ile Val Phe
 35 40 45
 Pro Glu Ala Phe Ile Pro Ser Tyr Pro Glu Trp Val Trp Gly Ile Pro
 50 55 60
 Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ser Glu Leu Leu Thr
 65 70 75 80
 Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
 85 90 95
 Ala Lys Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Met Leu Tyr Ile Asp
 115 120 125
 Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Thr Trp Asp Cys Gly Gln Pro Trp Leu Ser Thr Ile
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Val Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ser Met Lys Gln Lys
 225 230 235 240
 Tyr Tyr Ala Glu Met Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Met Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Val Glu Asp Asp
 305 310 315 320
 Ser Gln

<210> 241

<211> 972

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 241

atgatatcca	acgagcataa	caataactcca	ttcaaggttg	ctgctgtgca	ggctacacct	60
gtgtttcttg	atcgcgaaagc	aacgatcgat	aaagcgtgtg	aactgatcgc	tactgccggt	120
catgaaggcg	ctcgtttgat	tgtttttcca	gaagcgttca	tcccatccta	tcccagagtgg	180
gtatggggaa	ttccctctgg	cgagcaaggt	ttgctcaacg	atctgtatgc	agagttactc	240
accaattcag	ttacgataacc	cagcaacgca	actgacaggc	tttgtagagc	cgcgaagctt	300
gctaattgcct	acgtggtgat	ggggatgagc	gaacggaata	tcgaagcgag	cggcgcaagc	360
ctgtacaata	cgatgttata	tatagatgca	cagggtgaga	ttttgggcaa	acatcgaaag	420
ctgggtgcaa	cgggcggaga	acgcctggta	tgggcacaag	gagatggaag	cacgctgcag	480
gtttacgata	cacctctagg	aaagcttggt	ggtttaattt	gctgggaaaa	ttatatgccg	540
ctggcacgct	acgctatgta	tgccctggga	actcaaactc	acgtcgcggc	aacgtgggat	600
cgcggccaac	cctggctctc	aacgatacgg	catatcgcta	aagagggcag	ggtatacgta	660
atcggttgct	gtatcgcgat	gcgtaaagac	gatattccag	ataggtactc	catgaagcag	720
aagtattatg	cggagatgga	tgaatggatc	aacgtagggtg	acagcgcgat	tgtcaatcct	780

```

gagggggact tcattgcggg gcctgtgagc aagcaggagg aaattctcta tgcggagatt      840
gatccgcgga tgggtcaagg tccgaagtgg atgctggatg tggcggggca ttacgcgagg      900
cctgatgtgt tcgagttgac ggtgcatacg gatgtgaggg agatgatgcg ggtggagcat      960
gattatcaat ga                                                              972

```

<210> 242
 <211> 323
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 242

Met	Ile	Ser	Asn	Glu	His	Asn	Asn	Thr	Pro	Phe	Lys	Val	Ala	Ala	Val
1				5					10					15	
Gln	Ala	Thr	Pro	Val	Phe	Leu	Asp	Arg	Glu	Ala	Thr	Ile	Asp	Lys	Ala
			20					25					30		
Cys	Glu	Leu	Ile	Ala	Thr	Ala	Gly	His	Glu	Gly	Ala	Arg	Leu	Ile	Val
		35					40					45			
Phe	Pro	Glu	Ala	Phe	Ile	Pro	Ser	Tyr	Pro	Glu	Trp	Val	Trp	Gly	Ile
	50					55					60				
Pro	Ser	Gly	Glu	Gln	Gly	Leu	Leu	Asn	Asp	Leu	Tyr	Ala	Glu	Leu	Leu
65				70					75					80	
Thr	Asn	Ser	Val	Thr	Ile	Pro	Ser	Asn	Ala	Thr	Asp	Arg	Leu	Cys	Arg
			85					90					95		
Ala	Ala	Lys	Leu	Ala	Asn	Ala	Tyr	Val	Val	Met	Gly	Met	Ser	Glu	Arg
		100					105					110			
Asn	Ile	Glu	Ala	Ser	Gly	Ala	Ser	Leu	Tyr	Asn	Thr	Met	Leu	Tyr	Ile
	115					120						125			
Asp	Ala	Gln	Gly	Glu	Ile	Leu	Gly	Lys	His	Arg	Lys	Leu	Val	Pro	Thr
	130					135					140				
Gly	Gly	Glu	Arg	Leu	Val	Trp	Ala	Gln	Gly	Asp	Gly	Ser	Thr	Leu	Gln
145					150					155					160
Val	Tyr	Asp	Thr	Pro	Leu	Gly	Lys	Leu	Gly	Gly	Leu	Ile	Cys	Trp	Glu
			165						170				175		
Asn	Tyr	Met	Pro	Leu	Ala	Arg	Tyr	Ala	Met	Tyr	Ala	Trp	Gly	Thr	Gln
		180					185						190		
Ile	Tyr	Val	Ala	Ala	Thr	Trp	Asp	Arg	Gly	Gln	Pro	Trp	Leu	Ser	Thr
	195					200						205			
Ile	Arg	His	Ile	Ala	Lys	Glu	Gly	Arg	Val	Tyr	Val	Ile	Gly	Cys	Cys
	210				215						220				
Ile	Ala	Met	Arg	Lys	Asp	Asp	Ile	Pro	Asp	Arg	Tyr	Ser	Met	Lys	Gln
225				230						235					240
Lys	Tyr	Tyr	Ala	Glu	Met	Asp	Glu	Trp	Ile	Asn	Val	Gly	Asp	Ser	Ala
			245						250				255		
Ile	Val	Asn	Pro	Glu	Gly	Asp	Phe	Ile	Ala	Gly	Pro	Val	Ser	Lys	Gln
		260					265						270		
Glu	Glu	Ile	Leu	Tyr	Ala	Glu	Ile	Asp	Pro	Arg	Met	Val	Gln	Gly	Pro
		275					280					285			
Lys	Trp	Met	Leu	Asp	Val	Ala	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Phe
	290					295					300				
Glu	Leu	Thr	Val	His	Thr	Asp	Val	Arg	Glu	Met	Met	Arg	Val	Glu	His
305					310					315					320
Asp	Tyr	Gln													

<210> 243
 <211> 999
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 243

```

atgaagcaaa ctcgagtagc gatcattcag gcggaacctg tataatctcaa tttgcaagcg      60
agtgttgcca gggctatcga tcttgccgga cgcgccgcga agcaaggagc gcgtctgata      120
gtgttttgag agacctggtt gccgggttat cccgcgtggc tggattactg tcccggcatg      180
gcgttctggg atcaccggcc gacaaaagaa gtgtttgccc ggaccgcga gaacagtgtt      240
gtaattccgg gaaaggaaat cgaacagctc tgtaaaactg cggcggagct gggagttgta      300
atttcgatcg gtgtaaacga aaaaattctg gaaggccccg gaaacggcac gctctacaat      360
tctcttttgc tgattgatga atcaggaaaa ctggccggcc atcaccgcaa actggttccg      420
acttatacgg aacggatggt gtggggaatg ggtgatggag gtggaatgga agccatatcg      480
actgcagccg gcagggttgg cggattgatt tgctgggagc actggatgcc attgagccgg      540
cagggtgctgc acatgtcggg tgaggaaatt catgtggcag tgtggcccac ggttcatgag      600
gtgcaccagc ttgcatcacg ccattatgca tttgaagggc gttgttttgt gctcgagcc      660
ggattgttga tgaagggtcc ggatattcct cggagctgg aattgccttc tcagatgtcg      720
cgtgaatccg aagactggct tctgcgcggc gggagcgcgc tcattgggtcc ggatggaaaag      780
tacattgtgg agccgttgtt tgatcgagag gcgattctca cagccgatct tgaattagcc      840
gcatgcgata gtgaaaaaat gacgtgggac gtaacgggac attattccc ccccgatctt      900
tttcacctgg aattcaggaa acagcaatcc ggccatattg cgggagcagg aacgatcagc      960
cggcaaaaat cagcgcgcga ccgcgcggac gatcactaa      999

```

<210> 244

<211> 332

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 244

```

Met Lys Gln Thr Arg Val Ala Ile Ile Gln Ala Glu Pro Val Tyr Leu
 1          5          10          15
Asn Leu Gln Ala Ser Val Ala Arg Ala Ile Asp Leu Ala Gly Arg Ala
 20          25          30
Ala Lys Gln Gly Ala Arg Leu Ile Val Phe Gly Glu Thr Trp Leu Pro
 35          40          45
Gly Tyr Pro Ala Trp Leu Asp Tyr Cys Pro Gly Met Ala Phe Trp Asp
 50          55          60
His Arg Pro Thr Lys Glu Val Phe Ala Arg Thr Arg Glu Asn Ser Val
 65          70          75          80
Val Ile Pro Gly Lys Glu Ile Glu Gln Leu Cys Lys Thr Ala Ala Glu
 85          90          95
Leu Gly Val Val Ile Ser Ile Gly Val Asn Glu Lys Ile Leu Glu Gly
100          105          110
Pro Gly Asn Gly Thr Leu Tyr Asn Ser Leu Leu Leu Ile Asp Glu Ser
115          120          125
Gly Lys Leu Ala Gly His His Arg Lys Leu Val Pro Thr Tyr Thr Glu
130          135          140
Arg Met Val Trp Gly Met Gly Asp Gly Gly Gly Met Glu Ala Ile Ser
145          150          155          160
Thr Ala Ala Gly Arg Val Gly Gly Leu Ile Cys Trp Glu His Trp Met
165          170          175
Pro Leu Ser Arg Gln Val Leu His Met Ser Gly Glu Glu Ile His Val
180          185          190
Ala Val Trp Pro Thr Val His Glu Val His Gln Leu Ala Ser Arg His
195          200          205
Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Leu Leu Met
210          215          220
Lys Val Arg Asp Ile Pro Pro Glu Leu Glu Leu Pro Ser Gln Met Ser

```

```

225          230          235          240
Arg Glu Ser Glu Asp Trp Leu Leu Arg Gly Gly Ser Ala Val Ile Gly
          245          250          255
Pro Asp Gly Lys Tyr Ile Val Glu Pro Leu Phe Asp Arg Glu Ala Ile
          260          265          270
Leu Thr Ala Asp Leu Glu Leu Ala Ala Cys Asp Arg Glu Lys Met Thr
          275          280          285
Leu Asp Val Thr Gly His Tyr Ser Arg Pro Asp Leu Phe His Leu Glu
          290          295          300
Phe Arg Lys Gln Gln Ser Gly His Ile Ala Gly Ala Gly Thr Ile Ser
305          310          315          320
Arg Gln Lys Ser Ala Pro Asp Arg Ala Asp Asp His
          325          330

```

<210> 245
 <211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 245
atgggtgaga atgccaactt cacogtcgca gctgtccagg caacgccggt cttcttagac      60
cgggatgcga cggtcgagaa ggcttgcgag ctcatcgctg aagccgggcg aaacggagcg      120
cgccctggcgg tttttcccgga ggcgtttgtg ccggcttacc cggactgggt ctgggctggt      180
ccgccgggagc attcaaggct gctgcacgag ctctacggtg agctgatcca gaactctgtc      240
acgattccca gcgagtcgac ggagaaactc tgccggggccg cccgcggggc caaagtctgc      300
gtggcgatcg gcatcaacga gaggaatgag gaggcaagcg ggggtagcct ctacaacagc      360
ctcctgtaca tcagcccga cggccaggtc ctcggaagc accgcaagct cgttcccacc      420
ggagcggagc ggcttgtctg ggcgcagggc gacggcagca ctatcgacgt gtttgagttg      480
cctttctgtc gtttgggtgg cctcatctgt tgggagaact acatgccgct ggcccgttat      540
gcgatgtacg cctggggcac gcaggctctac gtgcgggcaa cgtgggacca cggcgaacct      600
tggctctcaa ccttgaggca tatcgccagg gagggcggtg catatgtcat tggcgtttgc      660
atgccgatgc gcatgagcga catcccggac cgatacgagt tcaagcgcaa gtactatggc      720
gggcgcgact ggatcaatac tgggtgacagc gccatcggtg gtccggacgg aaacttcac      780
gccggccccc tgagcgagcg cgaagagatc ctgtacgccg atatagacct gaatcggtt      840
gcgaactcga agtggatgct ggacgtcgcc gggcactatg cacggccgga cgtcttccag      900
ttgaccgtta accgcgagcc gaaccgatg atctctgagg atgggcacaa gacggttccc      960
acgctaccga aacgtgcggg gaagagtagg acgagatga

```

<210> 246
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 246
Met Gly Glu Asn Ala Asn Phe Thr Val Ala Ala Val Gln Ala Thr Pro
1          5          10          15
Val Phe Leu Asp Arg Asp Ala Thr Val Glu Lys Ala Cys Glu Leu Ile
          20          25          30
Ala Glu Ala Gly Arg Asn Gly Ala Arg Leu Ala Val Phe Pro Glu Ala
          35          40          45
Phe Val Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly Asp
50          55          60
Ser Arg Leu Leu His Glu Leu Tyr Gly Glu Leu Ile Gln Asn Ser Val
65          70          75          80
Thr Ile Pro Ser Glu Ser Thr Glu Lys Leu Cys Arg Ala Ala Arg Gly

```

$\langle 210 \rangle$	248
$\langle 211 \rangle$	329

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 248
Met Pro Thr Pro Lys Glu Lys Phe Arg Ile Ala Ala Val Gln Ala Cys
1 5 10 15
Pro Val Phe Leu Asp Arg Gly Glu Thr Val Lys Lys Ala Cys Arg Leu
20 25 30
Ala Ala Glu Ala Gly Gly Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
35 40 45
Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
50 55 60
Arg Glu Lys Leu Leu Asn Glu Met Tyr Ala Glu Phe Leu Ala Gly Ala
65 70 75 80
Val Glu Val Pro Gly Pro Val Thr Glu Glu Leu Gly Arg Ala Ala Glu
85 90 95
Arg Ala Gly Ala Tyr Leu Val Met Gly Val Thr Glu Arg Asp Thr Glu
100 105 110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Gly Pro Gln
115 120 125
Gly Ser Leu Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130 135 140
Arg Thr Val Trp Ala Arg Gly Asp Gly Ser Thr Leu Gln Val Tyr Asp
145 150 155 160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
165 170 175
Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile Tyr Leu
180 185 190
Ala Pro Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
195 200 205
Ile Ala Lys Glu Gly Arg Val Tyr Val Val Gly Cys Cys Met Ala Met
210 215 220
Gln Lys Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gln Lys Tyr Tyr
225 230 235 240
Pro Ala Ala Arg Glu Trp Ile Asn Thr Gly Asp Ser Ala Ile Leu Asn
245 250 255
Pro Glu Gly Glu Phe Ile Ala Gly Pro Ala Gly Lys Lys Glu Glu Ile
260 265 270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Gly Gly Pro Lys Trp Met
275 280 285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
290 295 300
Val His Arg Glu Ala Arg Pro Met Ile Arg Val Thr Glu Ala Pro Ser
305 310 315 320
Pro Gly Glu Lys Glu Thr Gly Glu Gly
325

<210> 249
<211> 1017
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 249
atgggcattc aacatccgaa atatcgcgtc gcggtgggtgc aggcggcacc ggcctggctc
gacctcgagg cgctcggtcag caagagcatc gcgctgatag aggaggccgc cgccaagggc

60
120

```

gccaagctga tcgcgttccc cgaggccttc atccccggt atccctggta catctggctg 180
gactcgccgg cctgggcat cggccgcggc ttcgtgcagc gctatttcga caattcgctc 240
agctatgaca gccgcaggc ggagcgccgt aggtcgcag tgaagaaggc cggcatgacc 300
gcagtgtctcg ccctgtccga gcgcgacggc ggcagcctct atctcgcgca atgggtgatc 360
ggacccgacg gcgagacccat cgcaaagcgg cgcaagctgc ggccgaccca tgccgagcgc 420
accgtctacg gcgagggcga cggcagcgac cttgcggtgc atgaccgccc cggcatcggc 480
cgctcgggtg cgctgtgctg ctgggagcat ctgcagccgc tgtcgaaata cgcgatgtac 540
gccagaacg agcaggtgca tgtcgcgcc tggccgagct tctcgctgta cgatccgttc 600
gcgcccggcg tcggctggga ggtaacaat gcggcctcgc gcgtctatgc cgtcgagggc 660
tcctgcttcg tgctggcgcc ctgcgccacc gtctcgagg cgatgatcga cgagctctgc 720
gaccgcgacg acaagcatgc gctgctgcat gttggcggcg gccatgccgc gatcttcggc 780
cccgacggca gcgcgatcgc ggacaagctt ccgtccgacc aggagggcct cctgttcggc 840
gacatcgatc tcggcgcgat cgggatcgcg aagaatgccg ctgatccggc cgggcactat 900
tcgcgccggg acgtgacgcg gctgctgctc aacaagaagc cctcgaagcg cgtcgagcac 960
ttcgcgctgc cgctcgacac gctcgcgggc gaggagatcg acgcggccgc aagctaa 1017

```

<210> 250

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 250

```

Met Gly Ile Gln His Pro Lys Tyr Arg Val Ala Val Val Gln Ala Ala
1          5          10          15
Pro Ala Trp Leu Asp Leu Glu Ala Ser Val Ser Lys Ser Ile Ala Leu
20          25          30
Ile Glu Glu Ala Ala Ala Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35          40          45
Ala Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Leu Asp Ser Pro Ala
50          55          60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65          70          75          80
Ser Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Leu Ala Val Lys Lys
85          90          95
Ala Gly Met Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100          105          110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115          120          125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130          135          140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Gly Ile Gly
145          150          155          160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165          170          175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180          185          190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Trp Glu Val
195          200          205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210          215          220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225          230          235          240
Asp Arg Asp Asp Lys His Ala Leu Leu His Val Gly Gly Gly His Ala
245          250          255
Ala Ile Phe Gly Pro Asp Gly Ser Ala Ile Ala Asp Lys Leu Pro Ser
260          265          270
Asp Gln Glu Gly Leu Leu Phe Ala Asp Ile Asp Leu Gly Ala Ile Gly
275          280          285

```

Ile Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Ser Lys Arg Val Glu His
 305 310 315 320
 Phe Ala Leu Pro Leu Asp Thr Leu Ala Gly Glu Glu Ile Asp Ala Ala
 325 330 335
 Ala Ser

<210> 251
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 251
 gtgaccatcg tgagagctgc cgccgtgcag atcagtcccg tgctctacag ccgggaagcc 60
 accgtagaaa aagtcgttcg caagatccgc gaactgggaa gaaacggcgt gcagttcgcc 120
 accttcccgg aaaccctggg gccctactac ccgtacttcg cggccgtgca gacgggcatc 180
 gaactgctgt ccggcaagga gcacctgcga ctgctggaac aatccgtaac ggttccctcg 240
 cccgccaccg atgccattgc ccaggcggca cgcgaagccg gcatgggtgg gtccatcggt 300
 gtcaacgagc gcgacggagg caccatctac aacacgcagc tgctgtttga cgcgcagcggc 360
 acgtgggtac agcgccgccc caagatcacg ccgacgcatt tcgagcgcgt ggtctggggc 420
 cagggcgacg gctcgggcct gcgagccgtg gacaccaagg ccggccgcat cggtcagctc 480
 gcctgcttcg agcacaacaa cccgctggcg cgctacgcca tgatcgccga cgggtgagcag 540
 atccattcgg ccatgtaccc gggctctgcc ttccggcgagg gcttcgcgca gcgcattggaa 600
 atcaacatac gccagcacgc cctggagtct ggctgcttcg tggatgaatgc gaccgcgtgg 660
 ctggatgccg accagcaggc gcagatcatg aaggatacgg gctgcggcat cggcccgcgtc 720
 tccggcggtc gcttcacgac catcgctcag ccggacggca tgctgatcgg tgaacccctc 780
 cgcaaggcgc aaggcgaagt catcgccgac ctcgatttca ccctgatcga ccggcgcaag 840
 ctgctggtgg actcgggtgg ccactacaac cgtccggagc tgctgagcct gctgatcgat 900
 cgcacccctg cggcgaaact ccatgagcgc aatgcgcttc cgtccgtcaa caccgccagc 960
 agcctcgaaa tcgtctga 978

<210> 252
 <211> 325
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 252
 Val Thr Ile Val Arg Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Glu Lys Val Val Arg Lys Ile Arg Glu Leu
 20 25 30
 Gly Arg Asn Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Leu Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ser Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Arg Lys
 115 120 125

```

Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130      135      140
Ser Gly Leu Arg Ala Val Asp Thr Lys Ala Gly Arg Ile Gly Gln Leu
145      150      155      160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
      165      170      175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
      180      185      190
Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
      195      200      205
Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
      210      215      220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
225      230      235      240
Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Met Leu Ile
      245      250      255
Gly Glu Pro Leu Arg Glu Gly Glu Gly Glu Val Ile Ala Asp Leu Asp
      260      265      270
Phe Thr Leu Ile Asp Arg Arg Lys Leu Leu Val Asp Ser Val Gly His
      275      280      285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Ala
      290      295      300
Ala Asn Phe His Glu Arg Asn Ala Leu Pro Ser Val Asn Thr Ala Ser
305      310      315      320
Ser Leu Glu Ile Val
      325

```

<210> 253
 <211> 924
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 253
atgtcaaacy agaaccacaa ccaaacattc aaagttgccg cgggtgcaggc cacacctgta      60
ttcctcgatc gtgaagcgac catcgacaaa gcttgcgagt tgattgctgc agcgggcaat      120
gaaggggcga ggctggttgt cttcccgag gcattcatcc cgtcctatcc agattgggta      180
tgggcaatcc caccgggcga agaaggcgtg ctcaatgagt tgtacgcgga actgctctcc      240
aattcgggtca cgattcccag tgacgtgacg gatagactgt gccgggccgc gaggcttgcc      300
aatgcctacg tagtgatggg gatgagcgaa tgcaatgccg aggccagtgg cgcaagcctg      360
tataacacgc tattgtacat cgatgcgaag ggtgaaatcc tgggtaaaca tcgaaagttg      420
gtgccaaactg gcggcgagcg actggtgtgg gcacaggcg atggcagcac gctgcaggtc      480
tacgatactc cactgggtaa actoggcggt ttaatttgct gggagaatta tatgccgtg      540
gcccgttaca ccatgtacgc ctggggcaca caaatctata tcgcagcgac atgggatcgc      600
gggcaaccct ggctctccac cttgcggcat atcgccaaag aaggcagggt gtacgtgatc      660
ggctgttgta tcgcgatgcg caaagatgat atcccagagc gttaccatgaat gaagcagaag      720
ttttacgcgg aggccgatga gtggatcaat ataggcgaca gcgcgatcgt caatcctgaa      780
gggcagttta tcgcggggcc ggtacgcaaa cagggaagaga ttctctacgc ggagattaat      840
ccgcgcatgg tgcaaggccc gaagtggatg ctgcagctgg cagggcacta cgccaggccg      900
gacgtattcc agttgacagt gtaa

```

<210> 254
 <211> 307
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 254

```

Met Ser Asn Glu Asn His Asn Gln Thr Phe Lys Val Ala Ala Val Gln
1      5      10      15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
20      25      30
Glu Leu Ile Ala Ala Ala Gly Asn Glu Gly Ala Arg Leu Val Val Phe
35      40      45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
50      55      60
Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser
65      70      75      80
Asn Ser Val Thr Ile Pro Ser Asp Val Thr Asp Arg Leu Cys Arg Ala
85      90      95
Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Cys Asn
100     105     110
Ala Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
115     120     125
Ala Lys Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
130     135     140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145     150     155     160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
165     170     175
Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
180     185     190
Tyr Ile Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
195     200     205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
210     215     220
Ala Met Arg Lys Asp Asp Ile Pro Glu Arg Tyr Pro Met Lys Gln Lys
225     230     235     240
Phe Tyr Ala Glu Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
245     250     255
Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
260     265     270
Glu Ile Leu Tyr Ala Glu Ile Asn Pro Arg Met Val Gln Gly Pro Lys
275     280     285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
290     295     300
Leu Thr Val
305

```

<210> 255

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 255

```

atgacaatgt ctaagaccaa atttagggtt gcagctgtgc aggcggcgcc gggttttcctt      60
gatcggaag cgacgttgga taaagcttgt ggattgattg aggaggcggg ccgcaacggc      120
gccagcctcg tcgtcttccc tgagtcattc attccggcct accccgattg gggtttgggct      180
gtgccggcgg gcgaagaagc tttactcaat gaactgtacg cacaactgtt ggccaacgcc      240
gttgaaattc ccggcccggc cactcaacgt ttgagccagg cggctaataaa ggctaagggtt      300
cacctggcta tgggcctgac cgaacgcaac agcgaggcca gcggcggcag cctttacaac      360
accttgctct atcttgaccc gcagggccac attctgggca agcatcgtaa gctggtgccc      420
accggcggtg agcggctggt ttgggcccag ggcgacggca gcactttgca agtttacgat      480
acgcctctgg gtaaactcag cggcctgatt tgctgggaaa attatatgcc gctggcgcgcc      540
tacgcgctgt atgcctgggg tacgcaaat tatlattgcgg ccacctggga tcgggggtgag      600

```

```

ccgtggcctt  cgacgttgcg  gcatattgcc  aaagagggcc  ggggtgttggt  catcggttgc  660
ggtatggcct  tgcgcaaggc  tgatattcct  gatcattttg  aattcaagca  gcgcttttat  720
caaaacgccg  ccgagtggat  caacgggggc  gacagcgcca  ttgtcaaccc  tgatggtgaa  780
tttattgctg  gcccttaag  cgagcaggaa  ggcattttgt  acgccgagat  tgatccggcc  840
cagatgggcg  ggccaaagtg  gatgctcgac  gtggccgggc  attacgctcg  cccggatgtg  900
tttgaactga  cgggccatac  cgccgcccga  cccatgatca  cctcgaaaaa  ggatggccta  960
acaccgcgcg  aggccgttac  gcaagtaacg  aaagcattat  tgtaa  1005

```

<210> 256
 <211> 334
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 256

Met	Thr	Met	Ser	Lys	Thr	Lys	Phe	Arg	Val	Ala	Ala	Val	Gln	Ala	Ala		
1				5					10					15			
Pro	Val	Phe	Leu	Asp	Arg	Glu	Ala	Thr	Leu	Asp	Lys	Ala	Cys	Gly	Leu		
			20					25					30				
Ile	Glu	Glu	Ala	Gly	Arg	Asn	Gly	Ala	Ser	Leu	Val	Val	Phe	Pro	Glu		
			35				40						45				
Ser	Phe	Ile	Pro	Ala	Tyr	Pro	Asp	Trp	Val	Trp	Ala	Val	Pro	Ala	Gly		
	50					55					60						
Glu	Glu	Ala	Leu	Leu	Asn	Glu	Leu	Tyr	Ala	Gln	Leu	Leu	Ala	Asn	Ala		
65					70					75				80			
Val	Glu	Ile	Pro	Gly	Pro	Ala	Thr	Gln	Arg	Leu	Ser	Gln	Ala	Ala	Lys		
				85				90						95			
Lys	Ala	Lys	Val	His	Leu	Ala	Met	Gly	Leu	Thr	Glu	Arg	Asn	Ser	Glu		
			100					105					110				
Ala	Ser	Gly	Gly	Ser	Leu	Tyr	Asn	Thr	Leu	Leu	Tyr	Leu	Asp	Pro	Gln		
			115				120					125					
Gly	His	Ile	Leu	Gly	Lys	His	Arg	Lys	Leu	Val	Pro	Thr	Gly	Gly	Glu		
	130					135					140						
Arg	Leu	Val	Trp	Ala	Gln	Gly	Asp	Gly	Ser	Thr	Leu	Gln	Val	Tyr	Asp		
145					150					155				160			
Thr	Pro	Leu	Gly	Lys	Leu	Ser	Gly	Leu	Ile	Cys	Trp	Glu	Asn	Tyr	Met		
				165				170						175			
Pro	Leu	Ala	Arg	Tyr	Ala	Leu	Tyr	Ala	Trp	Gly	Thr	Gln	Ile	Tyr	Ile		
			180					185					190				
Ala	Ala	Thr	Trp	Asp	Arg	Gly	Glu	Pro	Trp	Leu	Ser	Thr	Leu	Arg	His		
			195				200					205					
Ile	Ala	Lys	Glu	Gly	Arg	Val	Leu	Val	Ile	Gly	Cys	Gly	Met	Ala	Leu		
	210					215				220							
Arg	Lys	Ala	Asp	Ile	Pro	Asp	His	Phe	Glu	Phe	Lys	Gln	Arg	Phe	Tyr		
225					230				235					240			
Gln	Asn	Ala	Ala	Glu	Trp	Ile	Asn	Gly	Gly	Asp	Ser	Ala	Ile	Val	Asn		
				245				250						255			
Pro	Asp	Gly	Glu	Phe	Ile	Ala	Gly	Pro	Leu	Ser	Glu	Gln	Glu	Gly	Ile		
			260					265					270				
Leu	Tyr	Ala	Glu	Ile	Asp	Pro	Ala	Gln	Met	Gly	Gly	Pro	Lys	Trp	Met		
			275				280					285					
Leu	Asp	Val	Ala	Gly	His	Tyr	Ala	Arg	Pro	Asp	Val	Phe	Glu	Leu	Thr		
	290					295					300						
Val	His	Thr	Ala	Ala	Arg	Pro	Met	Ile	Thr	Ser	Lys	Lys	Asp	Gly	Leu		
305					310				315						320		
Thr	Pro	Ala	Glu	Ala	Val	Thr	Gln	Val	Thr	Lys	Ala	Leu	Leu				
				325				330									

<210> 257

<211> 942
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 257
 atgaacaaga tcgcgatcat tcagcgccca cccgtgctac tcgaccgcat cgccacgctg 60
 gcggttgccg tggagtcgat cgacgaagct gccgcagccg gtgcctcact gatcggttctt 120
 ccagaaacct tcatcccccg ctacccgccc tggatctggc gtctcgcgcc ggggagggat 180
 ggtgcgctca ttgccagtt gcatgcccga ctgctcgcca acgcggtcga tcttgccggt 240
 ggagatctgg atgccctgtg tgaagttgcg cacggccacc ggtgaccgt ggtgtgcccg 300
 ctcaacgaat gcgagcgag tcgcggcggg ggcactctct acaacacggt cgtcgtgatc 360
 gaccccgacg gcaagctgtg caatcgccac cgcaagctga tgccgaccaa cccggaacgc 420
 atggtgcacg gtctgggtga tgcacgggc ctgcgcgccg tcgacacccc ggtgggtcga 480
 gtgggcgcac tcatctgctg ggaaaactat atgocgctgg cagctacgc actttacgcc 540
 gagggggtgg aagtctacgt ggcgcccacc tatgacagcg gcgatggctg gatcagtacg 600
 atgcgctcata ttgcgcttga gggacgctgc tgggtgctgg gtacgggaac cgtactgcgt 660
 ggcagcgacg tcccagaaga ctttcgctca caoctggacc tgtttcccga cgcggaggaa 720
 tggatcaatc cgggcgactc ggtggtcgtc gatcctcagg gcaagatcgt cgcaggcccg 780
 atgcgacgtg agacaggcat tctctacgca gaaatcgacg ccgaacgggt cgcgccttcg 840
 cgccgcacgc tcgatgtcgc cggacactac gcccgcccg atattttcga gctccatgtc 900
 cgacgtacgc cggcgatgcc ggtccacgcc gttgatgcat ga 942

<210> 258
 <211> 313
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 258
 Met Asn Lys Ile Ala Ile Ile Gln Arg Pro Pro Val Leu Leu Asp Arg
 1 5 10 15
 Ile Ala Thr Leu Ala Val Ala Val Glu Ser Ile Asp Glu Ala Ala Ala
 20 25 30
 Ala Gly Ala Ser Leu Ile Val Leu Pro Glu Thr Phe Ile Pro Gly Tyr
 35 40 45
 Pro Ser Trp Ile Trp Arg Leu Ala Pro Gly Arg Asp Gly Ala Leu Ile
 50 55 60
 Ala Gln Leu His Ala Arg Leu Leu Ala Asn Ala Val Asp Leu Ala Ala
 65 70 75 80
 Gly Asp Leu Asp Ala Leu Cys Glu Val Ala His Gly His Arg Val Thr
 85 90 95
 Val Val Cys Gly Leu Asn Glu Cys Glu Arg Ser Arg Gly Gly Gly Thr
 100 105 110
 Leu Tyr Asn Thr Val Val Val Ile Asp Pro Asp Gly Lys Leu Cys Asn
 115 120 125
 Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val His Gly
 130 135 140
 Leu Gly Asp Ala Ser Gly Leu Arg Ala Val Asp Thr Pro Val Gly Arg
 145 150 155 160
 Val Gly Ala Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
 165 170 175
 Ala Leu Tyr Ala Glu Gly Val Glu Val Tyr Val Ala Pro Thr Tyr Asp
 180 185 190
 Ser Gly Asp Gly Trp Ile Ser Thr Met Arg His Ile Ala Leu Glu Gly
 195 200 205
 Arg Cys Trp Val Leu Gly Ser Gly Thr Val Leu Arg Gly Ser Asp Val

```

      210      215      220
Pro Glu Asp Phe Pro Ser His Leu Asp Leu Phe Pro Asp Ala Glu Glu
225      230      235      240
Trp Ile Asn Pro Gly Asp Ser Val Val Val Asp Pro Gln Gly Lys Ile
      245      250      255
Val Ala Gly Pro Met Arg Arg Glu Thr Gly Ile Leu Tyr Ala Glu Ile
      260      265      270
Asp Ala Glu Arg Val Ala Pro Ser Arg Arg Thr Leu Asp Val Ala Gly
      275      280      285
His Tyr Ala Arg Pro Asp Ile Phe Glu Leu His Val Arg Arg Thr Pro
      290      295      300
Ala Met Pro Val His Ala Val Asp Ala
305      310

```

<210> 259
 <211> 981
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 259
atggccatca tcaaagccgc cgccgtccag atcagtcagg tgctgtatag ccgcgagggg 60
accgtggaca aggtctgcca gcagatcatc gccctcgggc agcaaggcgt gcaatttgcg 120
gtctttccgg aaacgggtgg gccgtactac ccctatttct ccttcgtcca gccgcggttc 180
gccatgggca aggaacacct gaaactgttg gaacaatcgg tgattgtgcc gtcggctgcc 240
accttggcga tcggcgaagc gtgcaaacaa gcgggaatgg tgggtgtctat cggcgctcaat 300
gagcgcgatg gcggcacgat ctacaacgcc cagttgctgt ttgacgctga tggcagcttg 360
attcagcacc gtgcgaaaaa aaccccgcgc taccacgagc ggatgatctg gggcaaggc 420
gacggctccg ggttgccgcgc catcgacagc gcggtcgggc gtattggctc gctggcctgc 480
tggaacatt acaaccctt ggcccgctac gccctgatgg ccgacggcga gcagattcac 540
gcgctatgt ttcccggtc tctgggtggg gacatttttg ccgatcagat agaggctact 600
attcgctatc acgccttgga gtccggctgc ttctgggtca actccaccgc gtggcttgat 660
gctgatcagc aaggccaaat catgcaggac accggttgca gcattggccc aatctcgggt 720
ggctgcttca cggccatcgt ttcccgga ggcaaattac tcggcgaacc gctgcgttca 780
ggtgagggcg cagtcacgc cgacctggac atggcattga tcgacaagcg caaacggatg 840
atggattccg tcggccatta cagccgcccc gaactgctca gtttattgat cgaccgcacg 900
cccaccgctc atgtgcatga gcgcggcgcc catcaccttg ccgtagcctc tatcggggag 960
cttgaccatg caaaccaatg a

```

<210> 260
 <211> 326
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 260
Met Ala Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Ala Leu
      20      25      30
Gly Gln Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
      35      40      45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Ala Met Gly Lys
      50      55      60
Glu His Leu Lys Leu Leu Glu Gln Ser Val Ile Val Pro Ser Ala Ala
      65      70      75      80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val Val Ser

```

<210>	261
<211>	1014
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

$\langle 210 \rangle$	262
$\langle 211 \rangle$	337

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 262
Met Gly Leu Val His Gln Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Val Phe Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Ile Ala Leu
20 25 30
Ile Glu Glu Ala Ser Ala Gln Gly Ala Lys Leu Val Ala Phe Pro Glu
35 40 45
Thr Phe Ile Pro Gly Tyr Pro Trp Gln Ile Trp Leu Gly Ala Pro Ala
50 55 60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Gly Phe Asp Ser Pro Gln Ala Glu Lys Ile Arg Gln Ala Val Lys Arg
85 90 95
Ala Lys Leu Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly
130 135 140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Ala Asp Val Gly
145 150 155 160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165 170 175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Gly Ala Trp Pro
180 185 190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly His Glu Val
195 200 205
Asn Asn Ala Ala Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Phe
210 215 220
Leu Gly Pro Cys Ala Val Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225 230 235 240
Asp Ser Pro Glu Lys His Ala Phe Leu His Val Gly Gly Gly His Ala
245 250 255
Val Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Glu Lys Leu Pro Pro
260 265 270
Asp Gln Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Gly
275 280 285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
290 295 300
Val Thr Arg Leu Leu Leu Asn Thr Thr Arg Ala Asn Arg Val Glu His
305 310 315 320
Phe Ser Leu Pro Val Asp Ala Glu Val Met Ser Glu Ile Arg Leu Gln
325 330 335
Ala

<210> 263
<211> 1014
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 263

```

atgaaagtcg tcaaagcggc agcggttcag ttgagccctg tcctctacag ccgcgaggca      60
accgtcgcga aggtcgtgcg gaagatccac gagcttgggc agcagggcgt gcagttcgcc      120
accttcccgg aaaccgttgt gccgtactac cgtatttct ccgcggtcca gacgccgatg      180
cagcttctgg ctggaaccga gcatctgaaa ttgctcgacc aggccgtgac ggtgccgtct      240
cccgcgaccg acgcgatcgg cgaggcagcc cggaaggcgg gcatgggtgg gtccatcggc      300
gtcaacgagc gtgatggtag aaccctgtac aacacccaat tgctcttcga cgccgatggc      360
accctgatcc agcgccgccg caagatcacg cccacccatt tcgagcgcat gatctggggc      420
cagggtagac ggtcggggcct gcgtgccgtc gacagcaagg tcggccgcat tggccagctg      480
gcatgcttcg agcacaacaa tcctctggcg cgctacgcga tgatggccga cggcgagcag      540
atccattcgg ccatgtatcc gggttctgcc ttccggcgagg gctttgccca gaggatggaa      600
atcaatatcc gccagcacgc actggagtcc ggggtgcttcg tcgtgaacgc gacggcctgg      660
ctggatgcgg accagcaggc gcaaatcatg aaagacacgg gctgcgggat cggtcggatc      720
tcgggcggtt gcttcaccac gatcgtggca cccgacggca cgctgctggg ggaacctctg      780
cgctcggggc agggcgagggt catcgccgat ctcgatttca cggagatcga ccggcgcaag      840
atgctgatgg actcggcagg ccactacaac cgtccggaac tgctcagtct gctgatcgac      900
cgcacgccga ccgcaaacgt gcacgaacgg atggcgcatc cccaagcgag cacgaagcag      960
ccgcgctccg gcgatctgcc cgctgcgctg gctggcgcgc aggagatcct gtga      1014

```

<210> 264

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 264

```

Met Lys Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Ala Thr Val Ala Lys Val Val Arg Lys Ile His Glu Leu
      20          25          30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
      35          40          45
Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Met Gln Leu Leu Ala
      50          55          60
Gly Thr Glu His Leu Lys Leu Leu Asp Gln Ala Val Thr Val Pro Ser
      65          70          75          80
Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
      85          90          95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
      100          105          110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
      115          120          125
Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
      130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
      145          150          155          160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
      165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
      180          185          190
Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
      195          200          205
Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
      210          215          220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
      225          230          235          240
Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Thr Leu Leu
      245          250          255
Gly Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp
      260          265          270

```

Phe Thr Glu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala Asn Val His Glu Arg Met Ala His Pro Gln Ala Ser Thr Lys Gln
 305 310 315 320
 Pro Arg Ser Gly Asp Leu Pro Ala Ala Leu Ala Gly Ala Gln Glu Ile
 325 330 335
 Leu

<210> 265
 <211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 265
 atgcttaatc taggcatagt ccagatgaac gcagagccgc tcaacgtgga aggcaacctg 60
 ctcaaggcgg agcgctatgt cgcggaagtgc gccgcggacg gcgcccact cgtgggtgctg 120
 ccggagatgt tcaacgtcgg cttccacctc ggcgagtcgc tgatgatggt cgccgagccc 180
 ctggacggca agaccgtgca gtggctgcaa cggcaggcgt ccaccataa catatatatc 240
 accgggagct tatacgagcg ttacgacgag catttctaca acaccatggt catgggtggga 300
 tacgacggca gcgtgcagta ctaccgcaag cgcaatccta cctgggtccga gtcggcggtg 360
 tggcgccgca gcgaggtgcc aggccccggt atattcgata ccccgttcgg gcgcatcggg 420
 ggcgtcatct gcttcgattc cttcgcgcg gagacccacg agggcttcaa gcagagcggg 480
 gtcgaggcgg tggtaatcat cgccctgtgg gccgcgaacc gtgcgcgggc attcttctg 540
 cgcccgacc tcctgctaag ccgggaagggt ctgggtccgtt ggtcccggct ggcctcggag 600
 gacgtcccc gaaatcacgc gaaagagctc ggggtcccgg tcgccttcgt caaccagagt 660
 ggcaccatcc gcatgaccag ccccatccct ttcccgcact ggccgggtgca gagctccttc 720
 tacgacttca tcggcaagtc ccacgtccgg gacgcatccg gagaggtgat cgcgagggtg 780
 gacgaggggg agatcgactc ctgcctggtg gtcccggtag aggtcgagca ggcgagagc 840
 aggcoggaga tcaggaagtc aaatatatcg cccggctacc tcggcaagga ttactatttc 900
 gtggagccgc cgcttatctg caagctcttc caggtctggt tcctcagcgg cctgggtgcc 960
 accgaatacg aggcgcggcg tctgcccac ctgttctga 999

<210> 266
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 266
 Met Leu Asn Leu Gly Ile Val Gln Met Asn Ala Glu Pro Leu Asn Val
 1 5 10 15
 Glu Gly Asn Leu Leu Lys Ala Glu Arg Tyr Val Ala Lys Cys Ala Ala
 20 25 30
 Asp Gly Ala Gln Leu Val Val Leu Pro Glu Met Phe Asn Val Gly Phe
 35 40 45
 His Leu Gly Glu Ser Leu Met Met Val Ala Glu Pro Leu Asp Gly Lys
 50 55 60
 Thr Val Gln Trp Leu Gln Arg Gln Ala Ser Thr His Asn Ile Tyr Ile
 65 70 75 80
 Thr Gly Ser Leu Tyr Glu Arg Tyr Asp Glu His Phe Tyr Asn Thr Met
 85 90 95
 Val Met Val Gly Tyr Asp Gly Ser Val Gln Tyr Tyr Arg Lys Arg Asn
 100 105 110

```

Pro Thr Trp Ser Glu Ser Ala Val Trp Arg Arg Ser Glu Val Pro Gly
      115      120      125
Pro Gly Ile Phe Asp Thr Pro Phe Gly Arg Ile Gly Gly Val Ile Cys
      130      135      140
Phe Asp Ser Phe Ala Arg Glu Thr His Glu Gly Phe Lys Gln Ser Gly
145      150      155      160
Val Glu Ala Val Val Ile Ile Ala Leu Trp Gly Ala Asn Arg Ala Arg
      165      170      175
Ala Phe Phe Trp Arg Pro Asp Leu Leu Leu Ser Arg Glu Gly Leu Val
      180      185      190
Arg Trp Ser Arg Leu Ala Ser Glu Asp Val Pro Arg Asn His Ala Lys
      195      200      205
Glu Leu Gly Val Pro Val Ala Phe Val Asn Gln Ser Gly Thr Ile Arg
      210      215      220
Met Thr Ser Pro Ile Pro Phe Pro Asp Trp Pro Val Gln Ser Ser Phe
225      230      235      240
Tyr Asp Phe Ile Gly Lys Ser His Val Arg Asp Ala Ser Gly Glu Val
      245      250      255
Ile Ala Arg Val Asp Glu Gly Glu Ile Asp Ser Cys Leu Val Val Pro
      260      265      270
Val Glu Val Glu Gln Ala Gln Ser Arg Pro Glu Ile Arg Lys Ser Asn
      275      280      285
Ile Ser Pro Gly Tyr Leu Gly Lys Asp Tyr Tyr Phe Val Glu Pro Pro
      290      295      300
Leu Ile Cys Lys Leu Phe Gln Val Trp Phe Leu Ser Gly Leu Val Pro
305      310      315      320
Thr Glu Tyr Glu Ala Arg Arg Leu Arg His Leu Phe
      325      330

```

<210> 267
 <211> 1038
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 267
atgggcatcga gttcaaggcc gcggcggtac aggcggcgcc gggctttctc 60
gacagcgagg ccaccgtoga caagacgatc cgcctgatgc aggaagcggc ggaccacggc 120
gcctcgctga tcgtctttcc ggaagcctgg ctgcccgggt atccgtggtg gatctggctc 180
ggtccgccc cctggggcat gcagttcgtg cagcgctact tcgacaattc gccgagcgtc 240
ggcgatgatc tttccgccc gatogagcgc gcggccgcca aggcgaagat cgaagtggtc 300
ctcggtctca gcgagcgcg tgccgggtcg ctgtacctcg cgcaggcggt catctoctca 360
acgggcgaga cgcgcgcagt gcgcgcgaag ttgcgaccaa cgcacgtcga gcgaaccggt 420
ttcggcgagg gcgatggcag cgacttcaag gtgttcgaca ctccgctggg ccgcgtcggt 480
ggtctcttgt gctgggaaca cctgcaaccg ctgtcgcgct acgcgatggt ctcgatgaac 540
gagcagggtc acgccgccgc ctggccgacg ttcagcctct acacggatgt tgcccatgcc 600
ctcggccacg aactgaatct cgcagccagc gctacttacg cggctgaagg gcagtgtctac 660
gtgattgccg cctgtggcgt ggtcacgcag gagatgctgg atctgatgaa ggcgccgtgc 720
cccccggaat atctgcgggt cggcggcgga tacgccatga tctttgcgcc cgacggacgg 780
cgcatctgcg cggcgctgcc gccggaacaa gaagggtgta ttacgccga catcgatctt 840
tcgatgatct ctctcgccaa ggcggctgcc gatcccaccg gtcactactc gcggccggat 900
gtcgtgcggc ttatgctgaa taccgaaccg atgcagcggg tcgaaaagct gcagccgccc 960
ctggactcag ccgcgcgcg tgagaatgaa ccggcacgcg agaccgcagc ggcgaccgag 1020
agccgccagc cccagtaa

```

<210> 268
 <211> 344
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 268

```

Met Gly Ile Thr His Pro Lys Phe Lys Ala Ala Ala Val Gln Ala Ala
 1           5           10           15
Pro Gly Phe Leu Asp Ser Glu Ala Thr Val Asp Lys Thr Ile Arg Leu
          20           25           30
Met Gln Glu Ala Ala Asp His Gly Ala Ser Leu Ile Val Phe Pro Glu
          35           40           45
Ala Trp Leu Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Pro Pro Ala
          50           55           60
Trp Gly Met Gln Phe Val Gln Arg Tyr Phe Asp Asn Ser Pro Ser Val
          65           70           75           80
Gly Asp Asp Leu Phe Arg Arg Ile Glu Arg Ala Ala Ala Lys Ala Lys
          85           90           95
Ile Glu Val Val Leu Gly Leu Ser Glu Arg Ala Ala Gly Ser Leu Tyr
          100          105          110
Leu Ala Gln Ala Phe Ile Ser Ser Thr Gly Glu Thr Arg Ala Val Arg
          115          120          125
Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly
          130          135          140
Asp Gly Ser Asp Phe Lys Val Phe Asp Thr Pro Leu Gly Arg Val Gly
          145          150          155          160
Gly Leu Leu Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met
          165          170          175
Phe Ser Met Asn Glu Gln Val His Ala Ala Ala Trp Pro Thr Phe Ser
          180          185          190
Leu Tyr Thr Asp Phe Ala His Ala Leu Gly His Glu Leu Asn Leu Ala
          195          200          205
Ala Ser Ala Thr Tyr Ala Ala Glu Gly Gln Cys Tyr Val Ile Ala Ala
          210          215          220
Cys Gly Val Val Thr Gln Glu Met Leu Asp Leu Met Lys Ala Pro Cys
          225          230          235          240
Pro Pro Glu Tyr Leu Arg Val Gly Gly Gly Tyr Ala Met Ile Phe Ala
          245          250          255
Pro Asp Gly Arg Arg Ile Ala Ala Ala Leu Pro Pro Glu Gln Glu Gly
          260          265          270
Leu Ile Tyr Ala Asp Ile Asp Leu Ser Met Ile Ser Leu Ala Lys Ala
          275          280          285
Ala Ala Asp Pro Thr Gly His Tyr Ser Arg Pro Asp Val Val Arg Leu
          290          295          300
Met Leu Asn Thr Glu Pro Met Gln Arg Val Glu Lys Leu Gln Pro Pro
          305          310          315          320
Leu Asp Ser Ala Ala Arg Arg Glu Asn Glu Pro Ala Arg Glu Thr Ala
          325          330          335
Ala Ala Thr Glu Ser Arg Gln Pro
          340

```

<210> 269

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 269

```

atgtctgaaa cagccttcaa gatcgcggtc gtacaggcgg ctccggtttt tctcgacgca    60
aaggcgacgg tggacaaggc gatcggtctg atggccgaag ccggcgccaa gggcgccaag    120

```

```

ctgctcgcat tcccgggaagt attcatcccc ggctaccctt ggtgggtgtg gctgggcaca 180
ccggcatggg gcatgcagtt tgttgccaag tatcacgcga actcgcttcg tgcagacggg 240
cctgaattgg cagccctcgc ggccggcgcg gcgaagtccg atatcaatgc cgtcatcggc 300
ttctcggaga tgaacggcgg ttccctctac atcagccagg cgctcatcag cgacaagggc 360
gagataatgt tcaaacggcg caagctgaag ccgacgcacg tcgaacgcac gttgttcggc 420
gaaggggacg ggtccgactt ccaggtcgtg gacacgagcg tcggcaggct cgggtgcctt 480
tggtgcgccc aacacataca gccgctgtcg aagtacgcga tgtactccat gcacgaacag 540
gtgcacgtcg cctcctggcc gtcatttact ttgtaccgcg gcacggcata tgccttgggc 600
cacgaggtca atctggccgc gagccagatt tatgcgctcg agggaggctg tttcgtcctt 660
catgcgagcg ccatcaccgg ccaggacatg tttgacgtgc tgtgcgacac tccggagagg 720
acgcaactgc tgaactccga cggcggaag gtcggcgcg gctactcgat gatcttcgg 780
cccgatggcc agcccttgt tgggcatctg cctcaagaca ccgagggaat actctacgca 840
gatattgacc tggcgaacat ttocgttgcc aaagcgccct acgaccgctc cggacactat 900
gcgcgcggag acgtggtgcg cttgatggtc aatcgcaacc cgcgccatac gagtgttgog 960
ttcggcgggg gcgcggcgga ggcagcaacc tggacggaag caaaagcgga gtga 1014

```

<210> 270

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 270

```

Met Ser Glu Thr Ala Phe Lys Ile Ala Val Val Gln Ala Ala Pro Val
1          5          10          15
Phe Leu Asp Ala Lys Ala Thr Val Asp Lys Ala Ile Gly Leu Met Ala
20          25          30
Glu Ala Gly Ala Lys Gly Ala Lys Leu Leu Ala Phe Pro Glu Val Phe
35          40          45
Ile Pro Gly Tyr Pro Trp Trp Leu Trp Leu Gly Thr Pro Ala Trp Gly
50          55          60
Met Gln Phe Val Ala Lys Tyr His Ala Asn Ser Leu Arg Ala Asp Gly
65          70          75          80
Pro Glu Leu Ala Ala Leu Ala Ala Ala Ala Lys Ser Asp Ile Asn
85          90          95
Ala Val Ile Gly Phe Ser Glu Ile Asp Gly Gly Ser Leu Tyr Ile Ser
100          105          110
Gln Ala Leu Ile Ser Asp Lys Gly Glu Ile Met Phe Lys Arg Arg Lys
115          120          125
Leu Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly
130          135          140
Ser Asp Phe Gln Val Val Asp Thr Ser Val Gly Arg Leu Gly Ala Leu
145          150          155          160
Cys Cys Ala Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ser
165          170          175
Met His Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Thr Leu Tyr
180          185          190
Arg Gly Thr Ala Tyr Ala Leu Gly His Glu Val Asn Leu Ala Ala Ser
195          200          205
Gln Ile Tyr Ala Leu Glu Gly Gly Cys Phe Val Leu His Ala Ser Ala
210          215          220
Ile Thr Gly Gln Asp Met Phe Asp Val Leu Cys Asp Thr Pro Glu Arg
225          230          235          240
Thr Gln Leu Leu Asn Ser Asp Gly Gly Lys Val Gly Gly Gly Tyr Ser
245          250          255
Met Ile Phe Gly Pro Asp Gly Gln Pro Leu Val Gly His Leu Pro Gln
260          265          270
Asp Thr Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Ala Asn Ile Ser
275          280          285

```

Val Ala Lys Ala Ala Tyr Asp Pro Ser Gly His Tyr Ala Arg Gly Asp
 290 295 300
 Val Val Arg Leu Met Val Asn Arg Asn Pro Arg His Thr Ser Val Ala
 305 310 315 320
 Phe Gly Gly Gly Ala Gly Glu Ala Ala Thr Trp Thr Glu Ala Lys Ala
 325 330 335
 Glu

<210> 271
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 271
 atgtccagcg agaataacaa cgctacattc aaagttgccg cagttcaggc cacacctgtg 60
 tatcttgatc gtgaagcaac catcgacaag gcttgcgagt tgatcgctac tgctggcagc 120
 gaaggagctc gcctgattat ctttccagaa gcgttccatcc caacctatcc tgagtgggta 180
 tgggggtattc cttctggtga gcaaggttta ctcaacgagc tctattcaga gttgctcacc 240
 aattcgggtca cgattcccag cgacgcgact gacagactgt gcgaggccgc gaagcttgct 300
 aatgcctacg tgggtgatggg aatgagtga cggaatgtcg aagcgagtgg tgcaagcctg 360
 tataatacgc tcttgtacat agatgcgcag ggggagattt tagggaaaca tcgaaagttg 420
 gtaccaacgg gcggtgagcg cctggtatgg gcgcaagggt atggcagcac gctgcaggtc 480
 tacgatactc cattgggaaa actcgggtggt ttaatttgct gggaaaatta tatgccactg 540
 gcacgctacg ctatgtatgc ctggggtaca caaatctatg tcgcagcaac gtgggatcgc 600
 ggccaaccct ggctctcaac gttacggcat attgccaaag aaggcagggt atacgtaatt 660
 ggttgctgta ttgcgatgcg taaagatgat attccagatc gttactccat gaagcagaag 720
 tattacgctg aaatggagga atggattaat attggtgaca gcgcgattgt caatcccga 780
 ggacacttta ttgcagggcc tgtgcgcaag caagaagaaa ttctttacgc ggagatcgat 840
 ccacgcatgg tgcaaggccc gaagtggatg ctcgatgtgg ctgggcacta tgcgagacca 900
 gatgtgttcc agttgacggg gcatacggat gtgaggcaga tgattcgggt ggaacatgat 960
 tcataa 966

<210> 272
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 272
 Met Ser Ser Glu Asn Asn Asn Ala Thr Phe Lys Val Ala Ala Val Gln
 1 5 10 15
 Ala Thr Pro Val Tyr Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
 20 25 30
 Glu Leu Ile Ala Thr Ala Gly Ser Glu Gly Ala Arg Leu Ile Ile Phe
 35 40 45
 Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
 50 55 60
 Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ser Glu Leu Leu Thr
 65 70 75 80
 Asn Ser Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
 85 90 95
 Ala Lys Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
 115 120 125

Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ser Met Lys Gln Lys
 225 230 235 240
 Tyr Tyr Ala Glu Met Glu Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Val Glu His Asp
 305 310 315 320
 Ser

<210> 273
 <211> 1023
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 273
 atgaataact caccaccaac catccgcgct gctgccattc agctcagtc agttctgttt 60
 agtcgggatg ggactaccga gaaggtgttg caggcgatcg ctagtgctgc caaggaaggg 120
 gcacaaactgg ttgtttttcc agaaactttc atcccctact acccctattt ctcattcatt 180
 caacccccctg tggtgatggg caaagagcac atgcggtctt atgaggaagc cgtgacgggc 240
 ccgggtccgg tgacagatgc ggtcagtcga gcagcccgtt cttacggcat ggtggtagtg 300
 ctgggggtga atgagcgaga tgggtggctca atttacaata cacagttgat ttctgatgct 360
 gacggcacat tgttgctgaa gcgacgcaaa atcaccoccta cctatcatga gcgcatgggc 420
 tggggggcagg gagacggtgc tggattgaag gtattggata cagcagtcgg taaggtgggt 480
 gcgctggcat gttgggaaca ttacaatccc ctggcacgat ttgcgctgat ggcacagcat 540
 gagcagattc actgcgctca gttccccggt tctctggtgg gacaaatttt cactgatcag 600
 attgaggtaa cgattcggca tcatgcgttg gaatcgggtt gttttgtggt gaatgctact 660
 ggctggctct ctccagaaca ggtggcacia atcaccacgg atgaaaagtt gcaacgggtg 720
 ctgagtggtg ggtgtaatac cgccattatt ggacctgaag gcaatcatct ctgtcctccc 780
 attaccgatg gtgagggcat agcgatcgcc gatctcgact tctcactaat caccaaacgc 840
 aaacgcata tggattgcgt cggctactac tcccgccctg acttggtgaa gctgcaactc 900
 aatgcaacgg catggtcggg gctggctggg gagcaggggg cagggtgccag ggagcagggg 960
 ctaggtgtgc cggatgccat gctgtctacg cctaagccag aatactcaac actggatcag 1020
 tag 1023

<210> 274
 <211> 340
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 274

```

Met Asn Asn Ser Pro Pro Thr Ile Arg Ala Ala Ala Ile Gln Leu Ser
 1          5          10          15
Pro Val Leu Phe Ser Arg Asp Gly Thr Thr Glu Lys Val Leu Gln Ala
      20          25          30
Ile Ala Ser Ala Ala Lys Glu Gly Ala Gln Leu Val Val Phe Pro Glu
      35          40          45
Thr Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Gln Pro Pro Val
      50          55          60
Leu Met Gly Lys Glu His Met Arg Leu Tyr Glu Glu Ala Val Thr Val
      65          70          75          80
Pro Gly Pro Val Thr Asp Ala Val Ser Arg Ala Ala Arg Ser Tyr Gly
      85          90          95
Met Val Val Val Leu Gly Val Asn Glu Arg Asp Gly Gly Ser Ile Tyr
      100          105          110
Asn Thr Gln Leu Ile Phe Asp Ala Asp Gly Thr Leu Leu Leu Lys Arg
      115          120          125
Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly
      130          135          140
Asp Gly Ala Gly Leu Lys Val Leu Asp Thr Ala Val Gly Lys Val Gly
      145          150          155          160
Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Phe Ala Leu
      165          170          175
Met Ala Gln His Glu Gln Ile His Cys Ala Gln Phe Pro Gly Ser Leu
      180          185          190
Val Gly Gln Ile Phe Thr Asp Gln Ile Glu Val Thr Ile Arg His His
      195          200          205
Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser
      210          215          220
Pro Glu Gln Val Ala Gln Ile Thr Thr Asp Glu Lys Leu Gln Arg Val
      225          230          235          240
Leu Ser Gly Gly Cys Asn Thr Ala Ile Ile Gly Pro Glu Gly Asn His
      245          250          255
Leu Cys Pro Pro Ile Thr Asp Gly Glu Gly Ile Ala Ile Ala Asp Leu
      260          265          270
Asp Phe Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Cys Val Gly
      275          280          285
His Tyr Ser Arg Pro Asp Leu Leu Lys Leu Gln Leu Asn Ala Thr Ala
      290          295          300
Trp Ser Val Leu Ala Gly Glu Gln Gly Ala Gly Ala Arg Glu Gln Gly
      305          310          315          320
Leu Gly Val Pro Asp Ala Met Leu Ser Thr Pro Lys Pro Glu Tyr Ser
      325          330          335
Thr Leu Asp Gln
      340

```

<210> 275

<211> 849

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 275

```

atggagacgg ctcacaaagc aaaggtcgat ttccttgtgc tgggtgagac gtggctctca      60
ggctacccgg cttggctgga ccactgcccc gatgttggcc ggtgggatta tgaaccgatg      120
aaaaaagtgt atttgagatt tcgacaaagt gctattttctg ttcctggcaa agaatttgat      180
ttccttactg gcctctgtaa aaaatattca caaacgcttg ccatcggtgt taatgagaaa      240

```

```

gtagatcatg gggtaggtaa tggtagaccatt tataattcat ttctactgat tgattctgat 300
ggaacactgt tgaatcatca tcgcaagtta gttcccactt ttactgagaa attattatac 360
ggccatggag atggccatgg gctgaagtcg atggatactt cggtagggaag aatcggagg 420
agcatttggt gggaacattg gatgccacta tgcagacaag cacttcatga tgcagggtgag 480
caaatccatg ttgccctttg gccgactgtt catgacatcc atcaagtggc aagtagaagc 540
tatgcatttg aagggcgctg ctttgtattg gctgccgggc agatttttgc tgctaaagat 600
tttccaaagg aacttgtctt accagactat ctaaagcaaa atccggatca gctcattttg 660
aatgggggga gctgcgtgat cggccctgat gggaaatatt tgattgagcc cgtgtttgat 720
cggaagaac tgattgtgtg tgaacttgac cttgacgaag cttataaaga aagaatgacg 780
atggacgttt caggtcacta ccaaagacga gacgttttca gttttgacgt gaaccaacat 840
cgacattga 849

```

<210> 276

<211> 310

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 276

```

Met Thr Lys Leu Lys Ile Ala Ile Gly Gln Phe Ser Ser Asn His Leu
 1          5          10          15
Asp Leu Lys Cys Ser Leu Glu Lys Leu Glu Lys Ile Met Glu Thr Ala
 20          25          30
His Lys Ala Lys Val Asp Phe Leu Val Leu Gly Glu Thr Trp Leu Ser
 35          40          45
Gly Tyr Pro Ala Trp Leu Asp His Cys Pro Asp Val Gly Arg Trp Asp
 50          55          60
Tyr Glu Pro Met Lys Lys Val Tyr Leu Arg Phe Arg Gln Ser Ala Ile
 65          70          75          80
Ser Val Pro Gly Lys Glu Phe Asp Phe Leu Thr Gly Leu Cys Lys Lys
 85          90          95
Tyr Ser Gln Thr Leu Ala Ile Gly Val Asn Glu Lys Val Asp His Gly
100          105          110
Val Gly Asn Gly Thr Ile Tyr Asn Ser Phe Leu Leu Ile Asp Ser Asp
115          120          125
Gly Thr Leu Leu Asn His His Arg Lys Leu Val Pro Thr Phe Thr Glu
130          135          140
Lys Leu Leu Tyr Gly His Gly Asp Gly His Gly Leu Lys Ser Met Asp
145          150          155          160
Thr Ser Val Gly Arg Ile Gly Gly Ser Ile Cys Trp Glu His Trp Met
165          170          175
Pro Leu Cys Arg Gln Ala Leu His Asp Ala Gly Glu Gln Ile His Val
180          185          190
Ala Leu Trp Pro Thr Val His Asp Ile His Gln Val Ala Ser Arg Ser
195          200          205
Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Gln Ile Phe
210          215          220
Ala Ala Lys Asp Phe Pro Lys Glu Leu Val Leu Pro Asp Tyr Leu Lys
225          230          235          240
Gln Asn Pro Asp Gln Leu Ile Leu Asn Gly Gly Ser Cys Val Ile Gly
245          250          255
Pro Asp Gly Lys Tyr Leu Ile Glu Pro Val Phe Asp Arg Glu Glu Leu
260          265          270
Ile Val Cys Glu Leu Asp Leu Asp Glu Ala Tyr Lys Glu Arg Met Thr
275          280          285
Met Asp Val Ser Gly His Tyr Gln Arg Arg Asp Val Phe Ser Phe Asp
290          295          300
Val Asn Gln His Arg His
305          310

```

<210> 277
 <211> 1056
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 277
 atgccaaccc ccagcgatca tttcaaaatc gccgctgttc aggcctcgcc cgtgtttctg 60
 gaccgggagg ccaactgtgga aaaggcctgc cgggtgatcg ccgaagccgc aaagcagggc 120
 gcccgccctca tcgtctttcc ggaatctttc atcccgacct acccggaactg ggtatggggc 180
 gttcccccgga gaagggaag aatcctgaac cagctgtatt ctgaattcct ggccaatgcc 240
 gtcgatgttc ccggcgcggc gaccgaacaa cttgccagg ctgcacgaat ggccggcgcc 300
 tatgtgatta tgggcgtcac cgaaagagac acctcggcc aacaccgga gctggttccc 360
 acctgctct acttcagccc cgaaggcatc ctaatgggca aacaccgga gctggttccc 420
 acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac 480
 actccgctgg gaaagatcgg cgggctgac tgctgggaga actacatgcc cctggcccgg 540
 tacacgatgt acgcctgggg caccagatt tacatcgccg aaggaaggaa cgcgggggaa 600
 ccgtggctct ccaccctgcg gcatatcgcc aaggaaggaa gggctctacg catcggtgac 660
 tgcacgcgcc tgcgccagg ggatatcccg gaccggttcg agtacaaggg aaaattttat 720
 tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaaccc ggacggggaa 780
 ttcacgcgcc ggccgggtgc gatgaaggag gagatcctgt atgccgagat agacccccgg 840
 cagatgcggg gccccaagt gatgctcgat gtggccggtc attacgccc gccggatata 900
 ttcgagctca tcgtccaccg gaatccccc ccatgatca aaatcgccga agacaggggc 960
 gcggggatcg cctcaagttt gattcgcccc cgccctaacc ttcccccatc aagggggagg 1020
 aaatcggcaa gaagcaaacg caagcccaaa aaatga 1056

<210> 278
 <211> 351
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 278
 Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
 1 5 10 15
 Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
 20 25 30
 Ile Ala Glu Ala Ala Lys Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
 35 40 45
 Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50 55 60
 Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
 65 70 75 80
 Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
 85 90 95
 Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
 100 105 110
 Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
 115 120 125
 Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130 135 140
 Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145 150 155 160
 Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile

```

<400> 280
Met Gly Ile Thr His Pro Lys Tyr Lys Val Ala Ala Val Gln Ala Ala
 1           5           10           15
Pro Val Trp Leu Asp Leu Asp Ala Thr Val Asp Lys Cys Ile Arg Leu

```

<400> 281						60
atgtccaaga	tcgccgtcgt	ccaagagcct	ccggtgctgc	tcgatcgcg	cgccaccctc	120
gagcgcgccg	tctcgcccat	cgagcggg	gccgacgttg	ggcgcacct	cgtcgtgttc	180
cccagacgt	acgtcccggg	gtaccgccag	tgggtctggg	ggacgcgcc	cgacgacttc	240
aagctcgcg	gcgcgtcgca	cgagcgctc	ctcgcgaa	cggtcgacct	cgaaaaggac	300
cagctcgcgc	cgcctcgcga	ggcgcgcgc	cggcgaggcg	tcaccatcgc	gtgcggcg	360
aacgagcgcg	aggggagcca	cggccgcgcg	accctctaca	acaccgtcgt	cgtcgtcgga	420
cccgcgcgcg	cgatcctcaa	cgcgccaccg	aagctcgtcc	ccacgaaccc	cgagcgcgtg	480
gtctggggcc	cgggtgacgc	gagcgggctg	cgcgtcgtcg	acacgcgcgc	cggcgcgcgtg	540
ggggcgctca	tctgtcgga	gaactacatg	ccgctcgcgc	gcttcgcgc	ctacgcgcag	600
ggcctcgaqg	tctacctcgc	gcgcgcgtgg	gatacgcgcg	acacttggct	cgctccatg	

```

cggcacatcg cgcgcgagggc gcgcgcctgg gtcgtctcgg gggccatctg catgcaggcg      660
aaggacgtcc ccgcgcactt cccgcagcgc gcggcgatct accccgacga ggaggagtgg      720
ctcaaccccc gcgatgccgt cgtcgtcgat cccaccggcg ccgtcgccgc cggcccgtg      780
caccgcgagc gcggcatcct ctacgcgcag tgcgatcccg cgcgggcgtc gtcgcccgc      840
cgcacgctcg acgtctccgg gcactacgga cggcccgcac tctttcacct gcagatcgac      900
cgcacaccgc gcgtgccggc gtcgttccgg gactga                                936

```

<210> 282

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 282

```

Met Ser Lys Ile Ala Val Val Gln Glu Pro Pro Val Leu Leu Asp Arg
 1          5          10          15
Ala Ala Thr Leu Glu Arg Ala Val Ser Ala Ile Glu Arg Ala Ala Asp
          20          25          30
Val Gly Ala His Leu Val Val Phe Pro Glu Thr Tyr Val Pro Gly Tyr
          35          40          45
Pro Asp Trp Val Trp Arg Thr Arg Pro Asp Asp Phe Lys Leu Ala Gly
          50          55          60
Ala Leu His Glu Arg Leu Leu Ala Asn Ala Val Asp Leu Glu Lys Asp
          65          70          75          80
Gln Leu Ala Pro Leu Arg Glu Ala Ala Arg Arg Arg Gly Val Thr Ile
          85          90          95
Ala Cys Gly Val Asn Glu Arg Glu Gly Ser His Gly Arg Ala Thr Leu
          100          105          110
Tyr Asn Thr Val Val Val Val Gly Pro Asp Gly Ala Ile Leu Asn Arg
          115          120          125
His Arg Lys Leu Val Pro Thr Asn Pro Glu Arg Met Val Trp Gly Pro
          130          135          140
Gly Asp Ala Ser Gly Leu Arg Val Val Asp Thr Pro Ala Gly Arg Val
          145          150          155          160
Gly Ala Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Phe Ala
          165          170          175
Leu Tyr Ala Gln Gly Val Glu Val Tyr Leu Ala Pro Thr Trp Asp His
          180          185          190
Gly Asp Thr Trp Leu Ala Ser Met Arg His Ile Ala Arg Glu Ala Arg
          195          200          205
Ala Trp Val Val Ser Gly Ala Ile Cys Met Gln Ala Lys Asp Val Pro
          210          215          220
Ala Asp Phe Pro Gln Arg Ala Ala Ile Tyr Pro Asp Glu Glu Glu Trp
          225          230          235          240
Leu Asn Pro Gly Asp Ala Val Val Val Asp Pro Thr Gly Ala Val Ala
          245          250          255
Ala Gly Pro Leu His Arg Glu Arg Gly Ile Leu Tyr Ala Glu Cys Asp
          260          265          270
Pro Ala Arg Ala Ser Leu Ala Arg Arg Thr Leu Asp Val Ser Gly His
          275          280          285
Tyr Gly Arg Pro Asp Val Phe His Leu Gln Ile Asp Arg Thr Pro Arg
          290          295          300
Val Pro Ala Ser Phe Arg Asp
          305          310

```

<210> 283

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 283

```

atggggcatcg aacatccgaa gtacaaggtc gcggtgggtgc aggcggcacc ggcctggctc      60
gatctcgacg cgtcgatoga caagaccatc gggctgatcg aggaggccgc ccaaaaaggc      120
gccaagctga ttgcattccc cgaggccttc atccccgggt acccctggca catctggatg      180
gactcgccgg cctgggcatg cggccgcggg ttctgtgcagc gctatittga caattcgctc      240
gcctatgaca gcccgcaggc cgagaaaactg cgcgcgcgcg ttcgcaaggc aaagctcacg      300
gccgtgatcg ggctgtccga ggcgcagcggc ggcagtcttt acctcgcgca atggctgac      360
gggcccgcagc gtgagaccat cgccaagcgc cgcaagctgc ggccgacaca tgcggagcgc      420
acggtatacg gcgaggcgga cggcagcgac ctgcggttcc acaaccgtcc ggacattggc      480
cgccttggcg cgtctgtctg ctgggagcat ctccagccgc tgtcgaaata cgcgatgtac      540
gcgcagaacg agcagggtga tgcgcgggcc tggccgagct tttcgctgta cgatcccttc      600
gcggtggcgc tcggcgccga agtgaacaac gcggcctcgc gcgtctatgc ggtcgaaggc      660
tcctgcttcg tgcgtggcgc gtgcgcgacg gtctcgcagg ccatgatcga cgaactctgc      720
gaccggcccg acaagcacgc gctgttgcac gtccggcgcg gttttgccgc gatctacggt      780
cctgacggca gccagatcgg cgacaaaactc gctcccgaac aggaagggtt gctgatcgcg      840
gagatcgatc tcggcgccat cggcgctgcc aagaatgcgg cggatcccgc cgggcattat      900
tcgcggcctg acgtgacgcg actgttgctc aacaagaagc cgtacaagcg cgtcgagcag      960
ttttcgccgc cggccgagcg gctcgagccg acggatatcg cagcagcagc aagctaa      1017

```

<210> 284

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 284

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1              5              10              15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Thr Ile Gly Leu
      20              25              30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
      35              40              45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
      50              55              60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
      65              70              75              80
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
      85              90              95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
      100              105              110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
      115              120              125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
      130              135              140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
      145              150              155              160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
      165              170              175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
      180              185              190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
      195              200              205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
      210              215              220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys

```

```

225          230          235          240
Asp Arg Pro Asp Lys His Ala Leu Leu His Val Gly Gly Gly Phe Ala
245          250          255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
260          265          270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
275          280          285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
290          295          300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
305          310          315          320
Phe Ser Pro Pro Ala Glu Ala Leu Glu Pro Thr Asp Ile Ala Ala Ala
325          330          335
Ala Ser

```

<210> 285
 <211> 918
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 285
atgaatacta atctagtaaa ggtcgcggcg gctcaagttg ctccccattt totcaatttg      60
agcaatacgg tggaaaaaac ctgcaactta atttctgaag caggcaaaaa tggagcaaag      120
ctaatacgat ttccagaagc cttcatctct ggttatcccg attgggtctg gcttattccc      180
aatgcgaatt ctgcaatgct ggatgattta taccaggaat tggttgagaa cgcagtaacg      240
atccctgata caacaacaca taaactatgt caggctgcaa aagatgcagg ggtatatgtt      300
gcggtaggta tacatgagag aaattcagaa gcaagtggct tcacgctttt caatacgctt      360
ctatacatca acgatcaagg cgtaatcatc ggaaaacacc gaaaattaat ccctacaggg      420
ggcgaacggc tgggtctggg gcagggtaat ggggatacac tttctgcatt cgatacagac      480
ttcggcaaat taggaggatt gctttgttgg gaaaattata tgccactcgc gcgtcaagct      540
atgtattccg ttggaactga agtatatgta gcccacacct gggactccag cgagaattgg      600
ttgttaagca tgcgccatat tgcccgagag ggcggtatgt ttgtaattag tgtttgccag      660
gctctccgaa aagacgacat ccctgatcag tatgaattta agaaactcta tcctgataat      720
tcagaatgga tcaatagcgg taacagttag atcatcaacc cgcgcggtga gattattgct      780
ggaccaatct caaaccaaca agaaataact tatgcagatt tagacctgag ttttaattgca      840
aaatctaaac gtatgttcga tgttactggg cattattccc ggccggatgt gtttagctat      900
gaaatcaaca aaagctag                                     918

```

<210> 286
 <211> 305
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 286
Met Asn Thr Asn Leu Val Lys Val Ala Ala Ala Gln Val Ala Pro His
1          5          10          15
Phe Leu Asn Leu Ser Asn Thr Val Glu Lys Thr Cys Asn Leu Ile Ser
20          25          30
Glu Ala Gly Lys Asn Gly Ala Lys Ile Val Phe Pro Glu Ala Phe
35          40          45
Ile Ser Gly Tyr Pro Asp Trp Val Trp Leu Ile Pro Asn Ala Asn Ser
50          55          60
Ala Met Leu Asp Asp Leu Tyr Gln Glu Leu Val Glu Asn Ala Val Thr
65          70          75          80

```

Ile Pro Asp Thr Thr Thr His Lys Leu Cys Gln Ala Ala Lys Asp Ala
 85 90 95
 Gly Val Tyr Val Ala Val Gly Ile His Glu Arg Asn Ser Glu Ala Ser
 100 105 110
 Gly Phe Thr Leu Phe Asn Thr Leu Leu Tyr Ile Asn Asp Gln Gly Val
 115 120 125
 Ile Ile Gly Lys His Arg Lys Leu Ile Pro Thr Gly Gly Glu Arg Leu
 130 135 140
 Val Trp Gly Gln Gly Asn Gly Asp Thr Leu Ser Ala Phe Asp Thr Asp
 145 150 155 160
 Phe Gly Lys Leu Gly Gly Leu Leu Cys Trp Glu Asn Tyr Met Pro Leu
 165 170 175
 Ala Arg Gln Ala Met Tyr Ser Val Gly Thr Glu Val Tyr Val Ala Pro
 180 185 190
 Thr Trp Asp Ser Ser Glu Asn Trp Leu Leu Ser Met Arg His Ile Ala
 195 200 205
 Arg Glu Gly Gly Met Phe Val Ile Ser Val Cys Gln Ala Leu Arg Lys
 210 215 220
 Asp Asp Ile Pro Asp Gln Tyr Glu Phe Lys Lys Leu Tyr Pro Asp Asn
 225 230 235 240
 Ser Glu Trp Ile Asn Ser Gly Asn Ser Cys Ile Ile Asn Pro Arg Gly
 245 250 255
 Glu Ile Ile Ala Gly Pro Ile Ser Asn Gln Gln Glu Ile Leu Tyr Ala
 260 265 270
 Asp Leu Asp Leu Ser Leu Ile Ala Lys Ser Lys Arg Met Phe Asp Val
 275 280 285
 Thr Gly His Tyr Ser Arg Pro Asp Val Phe Ser Tyr Glu Ile Asn Lys
 290 295 300
 Ser
 305

<210> 287

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 287

gtgatcaagg	tagcaatcgc	ccaggtggca	ccggtggttc	tggacaaggc	gcgacaccatt	60
gagaaagcgg	taggaattat	tgcgctgcc	gcgcaagagg	gcattgagct	cctgggttttc	120
ccggagacgt	ttatcccgc	ctatccagcc	tgggtatggc	gcttgcgctcc	gggtactgat	180
tacggcctga	gcgaggaact	gcacgcgctc	ctgctggata	attcggtaga	tatggagagc	240
aaggacctgg	agccattgca	agctgttgct	gcagagacca	gcatgaccgt	ggtaatatgg	300
atgaacgagc	gagacggccg	attcagccgg	ggtacaatct	acaatgccct	ggttgtgatc	360
ggtccagggtg	gcacgatcct	gaacaggcac	cgcaagctta	tgcccaccaa	ccccgagcgt	420
atggttttggg	gtatgggcga	tgccagcggg	ctgaaggtag	tggaaatgtc	ttacggggcgc	480
ctgggtgggc	tgatttgctg	ggagaatttc	atgcctctcg	cgcgctatgg	cttgatatgcc	540
caggggtgtgg	agattttacgt	ggcgcccacc	tatgaccagg	gcgacggctg	ggtcggcagc	600
atgcagcata	tagcccggga	gggtcggttc	tgggtactct	cggccggggac	cctttttgcgt	660
ggcagtgatt	ttctgccgga	ttttccgggc	aagaccgagt	tatatcccga	tgaccaggag	720
tgggtgaatc	cgggtggctc	ggtgatcgtg	gcaccggggg	gagagattgt	ggccggcccc	780
atgtatcgcg	acgaaggtct	gctggtctgc	gagttggatg	cgacgcttag	tgtccgcggc	840
aagcgctcgc	tggtatgtggc	cggccattac	tcccggccgg	atttgtttga	actggaaata	900
gatggcgacc	cgctggaacc	catagagtgg	gattga			936

<210> 288

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 288

```

Val Ile Lys Val Ala Ile Ala Gln Val Ala Pro Val Val Leu Asp Lys
 1           5           10           15
Ala Arg Thr Ile Glu Lys Ala Val Gly Ile Ile Arg Ala Ala Gln
 20           25           30
Glu Gly Ile Glu Leu Leu Val Phe Pro Glu Thr Phe Ile Pro Thr Tyr
 35           40           45
Pro Ala Trp Val Trp Arg Leu Arg Pro Gly Thr Asp Tyr Gly Leu Ser
 50           55           60
Glu Glu Leu His Ala Leu Leu Asp Asn Ser Val Asp Met Glu Ser
 65           70           75           80
Lys Asp Leu Glu Pro Leu Gln Ala Val Ala Ala Glu Thr Ser Met Thr
 85           90           95
Val Val Ile Gly Met Asn Glu Arg Asp Gly Arg Phe Ser Arg Gly Thr
 100          105          110
Ile Tyr Asn Ala Leu Val Val Ile Gly Pro Gly Gly Thr Ile Leu Asn
 115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
 130          135          140
Met Gly Asp Ala Ser Gly Leu Lys Val Val Glu Met Ser Tyr Gly Arg
 145          150          155          160
Leu Gly Gly Leu Ile Cys Trp Glu Asn Phe Met Pro Leu Ala Arg Tyr
 165          170          175
Gly Leu Tyr Ala Gln Gly Val Glu Ile Tyr Val Ala Pro Thr Tyr Asp
 180          185          190
Gln Gly Asp Gly Trp Val Gly Ser Met Gln His Ile Ala Arg Glu Gly
 195          200          205
Arg Cys Trp Val Leu Ser Ala Gly Thr Leu Leu Arg Gly Ser Asp Phe
 210          215          220
Leu Pro Asp Phe Pro Gly Lys Thr Glu Leu Tyr Pro Asp Asp Gln Glu
 225          230          235          240
Trp Val Asn Pro Gly Gly Ser Val Ile Val Ala Pro Gly Gly Glu Ile
 245          250          255
Val Ala Gly Pro Met Tyr Arg Asp Glu Gly Leu Leu Val Cys Glu Leu
 260          265          270
Asp Ala Thr Leu Ser Val Arg Gly Lys Arg Ser Leu Asp Val Ala Gly
 275          280          285
His Tyr Ser Arg Pro Asp Leu Phe Glu Leu Glu Ile Asp Gly Asp Pro
 290          295          300
Leu Glu Pro Ile Glu Trp Asp
 305          310

```

<210> 289

<211> 921

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 289

```

atggtgacgg tggccgccgt acaggcaacg ccggtgttcc tcgaccgcga ggcgacctcg      60
gacaaggtct gcgccttggt caaggaggcg gccggccacg gggcagaact gatcgtcttc      120
cccagagtct tcgtccctgc ctatccggac tgggtgtggc gcacccctgc ctggagtgac      180
accgagttcg tgaagcgctt ctacgcgaac gcggtgaccg tccccggcgc gaccctcgag      240
cgcatcgggc cagcggcggc ggaggcggag gcgtacgtcg tgatcggcgt gaccgagatc      300
gacggcggaa ctctctacaa cacccttctc tacctgggccc cggacggaca gctgttgcaa      360

```

```

cggcatcgca agctcatgcc caccggtggg gagcggaccg tgtggggaat gggagacggc 420
tctgagctcg acgtcgtgag caccgcttc ggcgtcgtcg gtgggttggt gtgctgggag 480
aactacatgc cgctcgcccg ggcggcgatc tacgcccagc actgtgacat ctacctggct 540
ccgacatggg acaacagcga cactgtggta gccacgttgc gtcacatcgc caaggagggg 600
cggcagttcg tcatcggcgt cgcgccgctg ctgcgcggct ccgacgtacc ggaggacctc 660
cgcggcacgc tctacgggct gtccggacgac tggatgtcgc gcggctacac caccatcgtc 720
gcaccaagcg gcgaggtgat cgcgggcccg gtcctggagc gtgaggagat cctcttcgcg 780
gacctcgacc tggccgacgt gcaggagcag agaaggatgt tcgaccctgt cggccactac 840
tcacgacccg acgtcttcac gctccacgtc gacgcacgac cgaagagccc ggctcgtcttc 900
gagagggatg caccgacctg a                                     921

```

<210> 290

<211> 306

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 290

```

Met Val Thr Val Ala Ala Val Gln Ala Thr Pro Val Phe Leu Asp Arg
 1          5          10          15
Glu Ala Thr Ser Asp Lys Val Cys Ala Leu Val Lys Glu Ala Ala Gly
          20          25          30
His Gly Ala Glu Leu Ile Val Phe Pro Glu Ser Phe Val Pro Ala Tyr
          35          40          45
Pro Asp Trp Val Trp Arg Thr Pro Ala Trp Ser Asp Thr Glu Phe Val
          50          55          60
Lys Arg Phe Tyr Ala Asn Ala Val Thr Val Pro Gly Ala Thr Leu Glu
          65          70          75          80
Arg Ile Gly Ala Ala Ala Glu Ala Glu Ala Tyr Val Val Ile Gly
          85          90          95
Val Thr Glu Ile Asp Gly Gly Thr Leu Tyr Asn Thr Leu Leu Tyr Leu
          100          105          110
Gly Pro Asp Gly Gln Leu Leu Gln Arg His Arg Lys Leu Met Pro Thr
          115          120          125
Gly Gly Glu Arg Thr Val Trp Gly Met Gly Asp Gly Ser Glu Leu Asp
          130          135          140
Val Val Ser Thr Pro Phe Gly Val Val Gly Gly Leu Leu Cys Trp Glu
          145          150          155          160
Asn Tyr Met Pro Leu Ala Arg Ala Ala Ile Tyr Ala Gln His Cys Asp
          165          170          175
Ile Tyr Leu Ala Pro Thr Trp Asp Asn Ser Asp Thr Trp Val Ala Thr
          180          185          190
Leu Arg His Ile Ala Lys Glu Gly Arg Gln Phe Val Ile Gly Val Ala
          195          200          205
Pro Leu Leu Arg Gly Ser Asp Val Pro Glu Asp Leu Arg Gly Thr Leu
          210          215          220
Tyr Gly Leu Ser Asp Asp Trp Met Ser Arg Gly Tyr Thr Thr Ile Val
          225          230          235          240
Ala Pro Ser Gly Glu Val Ile Ala Gly Pro Val Leu Glu Arg Glu Glu
          245          250          255
Ile Leu Phe Ala Asp Leu Asp Leu Ala Asp Val Gln Glu Gln Arg Arg
          260          265          270
Met Phe Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Phe Thr Leu
          275          280          285
His Val Asp Ala Arg Pro Lys Ser Pro Val Val Phe Glu Arg Asp Ala
          290          295          300
Pro Thr
305

```

<210> 291
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 291
 atgatgaaaa caactgttac cgttgccctgc gttcaggccg ccccggtatt tatggattta 60
 gaaggcacca tagataaaac gatcacccctc atctctgaag ccgcacagaa aggcgcggag 120
 ctcatcgctt ttccggagac ctggataccc ggttaccctg ggttcttatg gctgaactcg 180
 ccgcgcacaa atatgcccct ggtttatcaa tatcatcaga actctctggt gctggacagt 240
 gcccaggcga agcgaattgc ggatgctgca cagcagaata acatcactgt cgttctggga 300
 ttcagcgagc gcgatcatgg aagcctctat atctcacagt ggctgattgg cagcgacggg 360
 gaaactattg gcatccggcg caagctcaag gccacacacg tggagcgtac gctgttcggc 420
 gaaagcgacg gctcctccct gaccacctgg gagacacctc tgggtaacgt cggggccctc 480
 tgctgctggg agcacctgca gccgctgtct cgctatgcga tgtattccca gcatgaagag 540
 atccatatcg ctgcgtggcc cagcttcagt ctttacacca gcgcaactgc cgcgctcgga 600
 cctgacgtca acacggcggc ttcacgcctc tatgccgcgg aggggcagtg cttcgtgta 660
 gccccatgtg ccgtgggttc tgatgagatc attgatttac tctgtcctga tgatgaccgg 720
 agagcgttac tcagtgccgg agggggacat gcccgatttt acggacctga tgggaagagaa 780
 ctctgcaccc ctctcgggga aaatgaggaa ggactgctta tcgctgagct cgactctgct 840
 gcgatcacct ttgccaaact ggcggcagat cccgtaggcc actattcccg ccctgacgtg 900
 accgccttc tttttaatcc ttcagccaac aagactgtta ttaaacggca ttcgcctcct 960
 gagttaattg ccgaacaggc tccggaagaa gaggaggagt ag 1002

<210> 292
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 292
 Met Met Lys Thr Thr Val Thr Val Ala Cys Val Gln Ala Ala Pro Val
 1 5 10 15
 Phe Met Asp Leu Glu Gly Thr Ile Asp Lys Thr Ile Thr Leu Ile Ser
 20 25 30
 Glu Ala Ala Gln Lys Gly Ala Glu Leu Ile Ala Phe Pro Glu Thr Trp
 35 40 45
 Ile Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asn Ser Pro Ala Thr Asn
 50 55 60
 Met Pro Leu Val Tyr Gln Tyr His Gln Asn Ser Leu Val Leu Asp Ser
 65 70 75 80
 Ala Gln Ala Lys Arg Ile Ala Asp Ala Ala Gln Gln Asn Asn Ile Thr
 85 90 95
 Val Val Leu Gly Phe Ser Glu Arg Asp His Gly Ser Leu Tyr Ile Ser
 100 105 110
 Gln Trp Leu Ile Gly Ser Asp Gly Glu Thr Ile Gly Ile Arg Arg Lys
 115 120 125
 Leu Lys Ala Thr His Val Glu Arg Thr Leu Phe Gly Glu Ser Asp Gly
 130 135 140
 Ser Ser Leu Thr Thr Trp Glu Thr Pro Leu Gly Asn Val Gly Ala Leu
 145 150 155 160
 Cys Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met Tyr Ser
 165 170 175
 Gln His Glu Glu Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu Tyr
 180 185 190
 Thr Ser Ala Thr Ala Ala Leu Gly Pro Asp Val Asn Thr Ala Ala Ser

```

      195              200              205
Arg Leu Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Pro Cys Ala
  210              215              220
Val Val Ser Asp Glu Met Ile Asp Leu Leu Cys Pro Asp Asp Asp Arg
  225              230              235              240
Arg Ala Leu Leu Ser Ala Gly Gly Gly His Ala Arg Ile Tyr Gly Pro
      245              250              255
Asp Gly Arg Glu Leu Val Thr Pro Leu Gly Glu Asn Glu Glu Gly Leu
      260              265              270
Leu Ile Ala Glu Leu Asp Ser Ala Ala Ile Thr Phe Ala Lys Leu Ala
      275              280              285
Ala Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu
      290              295              300
Phe Asn Pro Ser Ala Asn Lys Thr Val Ile Lys Arg His Ser Pro Pro
  305              310              315              320
Glu Leu Ile Ala Glu Gln Ala Pro Glu Glu Glu Glu Glu
      325              330

```

<210> 293

<211> 1008

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 293

```

atgaaaaata tcaaaaactc agaaaaaagc agcacagtaa gagtcgctgc ggtacaaatc      60
agtcgggtgt tgtacaaccg cgaagctacc gttcaaaaag tagtcaacaa aatccttgaa      120
ctaggaaaac aaggggtaca attcgccact tttccggaaa cgatagtgcc ttattatcct      180
tattttctctt ttattcaggc gccttatgcc atgggcaaaag aacacctgcg cttgcttgaa      240
caatcagtta ctgttcogtc agccgcgacc gatgccataa gtgaggcggc aaaggaagcc      300
aatatggtag tgtctatttg tgtcaatgaa cgagacggtg gtaccattta caatacgcaa      360
ctcctttttg atgctgacgg aacattaatt cagcgcagac gtaaacttac accaacgtat      420
catgaaagaa tgatttgggg acaaggtgac gcttcaggtc ttcgtgccac agacagcgct      480
gttggggcgta tcgggcaggt ggcttggttg gaacattaca atccattggt ccgttatgct      540
ttgattgctg atggagaaca aatccattct gccatgtatc ccggatcatt tttagggtgcg      600
ttgcacggtg aacaaaccga aatcaatgta cgccaacacg ctttagaatc ggccagcttc      660
gtcgtagtgg ctaccggttg gttggatgcc gatcaacaag cacaaattgc gaaagacacc      720
ggtggaccaaa tcggaccaat ttcgggaggt tgttttacag ccgttatagg ccctgacgga      780
caactaatcg gggaagccct tacatcaggt gaaggggaag tgattgccga tattgatttg      840
gcacaaattg atgcccgcaa aagattaatg gatgccagtg gtcactacaa ccgtcctgaa      900
ttgttgagct tgcataatcga tcacactccg actgctccta tgcataaaaag agtagtttac      960
actgagccgg gattagcaaaa aagacaaaat gaaaattcat caaattaa      1008

```

<210> 294

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 294

```

Met Lys Asn Ile Lys Asn Ser Glu Lys Ser Ser Thr Val Arg Val Ala
  1              5              10              15
Ala Val Gln Ile Ser Pro Val Leu Tyr Asn Arg Glu Ala Thr Val Gln
      20              25              30
Lys Val Val Asn Lys Ile Leu Glu Leu Gly Lys Gln Gly Val Gln Phe
      35              40              45
Ala Thr Phe Pro Glu Thr Ile Val Pro Tyr Tyr Pro Tyr Phe Ser Phe

```

50	55	60
Ile Gln Ala Pro Tyr	Ala Met Gly Lys Glu His	Leu Arg Leu Leu Glu
65	70	75
Gln Ser Val Thr Val	Pro Ser Ala Ala Thr Asp	Ala Ile Ser Glu Ala
85	90	95
Ala Lys Glu Ala Asn Met	Val Val Ser Ile Gly Val Asn	Glu Arg Asp
100	105	110
Gly Gly Thr Ile Tyr Asn	Thr Gln Leu Leu Phe Asp	Ala Asp Gly Thr
115	120	125
Leu Ile Gln Arg Arg Arg	Lys Leu Thr Pro Thr Tyr His	Glu Arg Met
130	135	140
Ile Trp Gly Gln Gly Asp	Ala Ser Gly Leu Arg Ala Thr	Asp Ser Ala
145	150	155
Val Gly Arg Ile Gly Gln	Leu Ala Cys Trp Glu His Tyr	Asn Pro Leu
165	170	175
Phe Arg Tyr Ala Leu Ile	Ala Asp Gly Glu Gln Ile His	Ser Ala Met
180	185	190
Tyr Pro Gly Ser Phe Leu	Gly Ala Leu His Gly Glu Gln	Thr Glu Ile
195	200	205
Asn Val Arg Gln His Ala	Leu Glu Ser Ala Ser Phe	Val Val Val Ala
210	215	220
Thr Gly Trp Leu Asp Ala	Asp Gln Gln Ala Gln Ile	Ala Lys Asp Thr
225	230	235
Gly Gly Pro Ile Gly Pro	Ile Ser Gly Gly Cys Phe Thr	Ala Val Ile
245	250	255
Gly Pro Asp Gly Gln Leu	Ile Gly Glu Ala Leu Thr Ser	Gly Glu Gly
260	265	270
Glu Val Ile Ala Asp Ile	Asp Leu Ala Gln Ile Asp	Ala Arg Lys Arg
275	280	285
Leu Met Asp Ala Ser Gly	His Tyr Asn Arg Pro Glu	Leu Leu Ser Leu
290	295	300
His Ile Asp His Thr Pro	Thr Ala Pro Met His Glu	Arg Val Val Tyr
305	310	315
Thr Glu Pro Gly Leu Ala	Lys Arg Gln Asn Glu Asn	Ser Ser Asn
325	330	335

<210> 295

<211> 1134

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 295

atggccgcaa	aagtacttgg	aggacgtgac	acagtaaaag	tagcagttgt	tcaaacacca	60
tcagtcttta	tggacaagaa	agcctgtctc	gaacttgcct	gcgataagat	tatcgaagcc	120
ggcaaagagg	gcgcggagct	tgttggtttt	cctgaaacct	ggattccgac	atatccttat	180
tggaccatgg	gatgggatac	catcgcccat	ggcttccatg	atgtgatggc	ggacctgcag	240
gacaattccg	tggtcgtcgg	gagcgaagac	accgacatat	tgggcaaagc	cgcccgggaa	300
gctggcgccct	acgtcgtcat	gggctgtaat	gagctcgatg	accgggtcgg	cagcaggacc	360
ttgttcaact	cgctgggtcta	tatggacaaa	tatggcggcg	tgctcggccg	tcaccgtaaa	420
ttaatcccg	cctttatcga	acgcatctgg	tggggcaatg	gggacagccg	cgatctcaaa	480
gtttacgaca	cggaaattgg	gcgcacgcgc	ggtcaaatct	gctgggaaaa	tcacattgtg	540
aacatcaccg	catggtacat	tgcccaaggc	gtggatatct	atgtctcggg	ttggccggga	600
aatgtgaact	gtggcgcaga	agaaggagaa	tccttcatat	acgccgggtc	cgacatcaac	660
aaatgtgacc	tcacccctgc	tacacgcgga	cgggcattta	cgggtcagtg	ttatgtcctc	720
tcagccaaca	acctactgcg	gatggaagac	attcctgacg	atttcccggt	ccgggatacc	780
atgaactatg	gcgggtccggg	ccaggaggat	tttgtcggat	gggcttgccg	tggcagccat	840
attgttgccg	caacgtctga	atattatggtg	ccgccgacgt	ttgatataga	caccatcatc	900
tatgcagaac	ttcaggcgaa	atacatcaaa	gtgggtgaagt	cggctcttca	ttccctcggc	960

```

cactacgogc ggtgggacct cgtcaacttg accacgccgc caccgccgta tgaacctgaa 1020
accgacgcac cagctctcac ggccgatatc cgtgatcggg tcatcgagag tgtggctaaa 1080
gagttcaagc tcgaaccaga aaaagtggct gaagttgtgc gcaatgccgc ctag 1134

```

<210> 296
 <211> 377
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 296

Met	Ala	Ala	Lys	Val	Leu	Gly	Gly	Arg	Asp	Thr	Val	Lys	Val	Ala	Val	1	5	10	15
Val	Gln	Thr	Pro	Ser	Val	Phe	Met	Asp	Lys	Lys	Ala	Cys	Leu	Glu	Leu	20	25	30	35
Ala	Cys	Asp	Lys	Ile	Ile	Glu	Ala	Gly	Lys	Glu	Gly	Ala	Glu	Leu	Val	40	45	50	55
Val	Phe	Pro	Glu	Thr	Trp	Ile	Pro	Thr	Tyr	Pro	Tyr	Trp	Thr	Met	Gly	60	65	70	75
Trp	Asp	Thr	Ile	Ala	His	Gly	Phe	His	Asp	Val	Met	Ala	Asp	Leu	Gln	80	85	90	95
Asp	Asn	Ser	Val	Val	Val	Gly	Ser	Glu	Asp	Thr	Asp	Ile	Leu	Gly	Lys	100	105	110	115
Ala	Ala	Arg	Glu	Ala	Gly	Ala	Tyr	Val	Val	Met	Gly	Cys	Asn	Glu	Leu	120	125	130	135
Asp	Asp	Arg	Val	Gly	Ser	Arg	Thr	Leu	Phe	Asn	Ser	Leu	Val	Tyr	Met	140	145	150	155
Asp	Lys	Tyr	Gly	Gly	Val	Leu	Gly	Arg	His	Arg	Lys	Leu	Ile	Pro	Ser	160	165	170	175
Phe	Ile	Glu	Arg	Ile	Trp	Trp	Gly	Asn	Gly	Asp	Ser	Arg	Asp	Leu	Lys	180	185	190	195
Val	Tyr	Asp	Thr	Glu	Ile	Gly	Arg	Ile	Gly	Gly	Gln	Ile	Cys	Trp	Glu	200	205	210	215
Asn	His	Ile	Val	Asn	Ile	Thr	Ala	Trp	Tyr	Ile	Ala	Gln	Gly	Val	Asp	220	225	230	235
Ile	His	Val	Ser	Val	Trp	Pro	Gly	Met	Trp	Asn	Cys	Gly	Ala	Glu	Glu	240	245	250	255
Gly	Glu	Ser	Phe	Ile	Tyr	Ala	Gly	His	Asp	Ile	Asn	Lys	Cys	Asp	Leu	260	265	270	275
Ile	Pro	Ala	Thr	Arg	Gly	Arg	Ala	Phe	Thr	Gly	Gln	Cys	Tyr	Val	Leu	280	285	290	295
Ser	Ala	Asn	Asn	Leu	Leu	Arg	Met	Glu	Asp	Ile	Pro	Asp	Asp	Phe	Pro	300	305	310	315
Phe	Arg	Asp	Thr	Met	Asn	Tyr	Gly	Gly	Pro	Gly	Gln	Glu	Asp	Phe	Val	320	325	330	335
Gly	Trp	Ala	Cys	Gly	Gly	Ser	His	Ile	Val	Ala	Pro	Thr	Ser	Glu	Phe	340	345	350	355
Met	Val	Pro	Pro	Thr	Phe	Asp	Ile	Asp	Thr	Ile	Ile	Tyr	Ala	Glu	Leu	360	365	370	375
Gln	Ala	Lys	Tyr	Ile	Lys	Val	Val	Lys	Ser	Val	Phe	Asp	Ser	Leu	Gly	375	380	385	390
His	Tyr	Ala	Arg	Trp	Asp	Leu	Val	Asn	Leu	Thr	Thr	Pro	Pro	Pro	Pro	390	395	400	405
Tyr	Glu	Pro	Glu	Thr	Asp	Ala	Pro	Ala	Leu	Thr	Ala	Asp	Ile	Arg	Asp	405	410	415	420
Arg	Val	Ile	Glu	Ser	Val	Ala	Lys	Glu	Phe	Lys	Leu	Glu	Pro	Glu	Lys	420	425	430	435
Val	Ala	Glu	Val	Val	Arg	Asn	Ala	Ala								435	440	445	450

<210> 297
 <211> 1059
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 297
 atgacacggtt ttcggggacgt cacggtggcg gcggttcagg ccgcacccgt ctatttcgat 60
 cgaggaggcct ccacagataa ggcgtgccaa ttgattcacg aagcggcgaa gaaaggcgca 120
 gccctcgcg cggttcggcga aacgtgggtg ccgggatatac cgttctttgc atggggggttc 180
 gcgcacaacc ggagcctggt ctggaatgcg gccgccgagt acatcgccaa tgctgtggag 240
 attccgagtc caacgacgga ccgcctctgc gccgcagcga agatcgccgg gattgacgtg 300
 gtaatcgggc tcgtagaact ggatggacga acgcgagcgt cggtttacag cacactgctg 360
 ttcatcgggg gagagggggc gatcctgggg cgccaccgca aattgaagcc aaccacatg 420
 gagcgaacgg tgtgggggtga aggggacgct caggggctcc gcgttcacga gcgtccgtac 480
 ggccgcctca gcgggctgaa ttgctgggaa cacaacatga tgctgcccgg ctatgtgctt 540
 gccgcgcagg gcacgcagtt tcacgtcgcg acatggcctg ggaaagagag gctcacagtt 600
 ccgccgaacg aggcggctta tacgcgccag cttctcctct ctgcgccta tgcattccag 660
 gcgggcgcgt acgtgatcag cgtcgcgggg ctgctcggac ccgactcgat gccggagcgt 720
 tatcgcgaaac tgggacagtc ctatgagttg accggcgaca gcgtcatcat cgatccgcgc 780
 ggcgaggtca tcgcggggcc cgcgaaaggg gagaccatcc tgctcgcgca atgcagccag 840
 gaagccctct tcgccgcaaa gtccgccatt gacgtcggcg gtcattactc gcgcccgat 900
 atttttcagc tgcgtgtcaa cgatcagcta cagcatcagg tccggagact cgaggcgact 960
 ctcacgcccc cagtgcgct agttgtcggg cctgagggta gctcacatga gcaggagacg 1020
 gccttcgggc catccagcct cctggccacg acaagctag 1059

<210> 298
 <211> 352
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 298
 Met Thr Arg Phe Arg Asp Val Thr Val Ala Ala Val Gln Ala Ala Pro
 1 5 10 15
 Val Tyr Phe Asp Arg Glu Ala Ser Thr Asp Lys Ala Cys Gln Leu Ile
 20 25 30
 His Glu Ala Ala Lys Lys Gly Ala Ala Leu Ala Ala Phe Gly Glu Thr
 35 40 45
 Trp Leu Pro Gly Tyr Pro Phe Phe Ala Trp Gly Phe Ala His Asn Arg
 50 55 60
 Ser Leu Phe Trp Asn Ala Ala Ala Glu Tyr Ile Ala Asn Ala Val Glu
 65 70 75 80
 Ile Pro Ser Pro Thr Thr Asp Arg Leu Cys Ala Ala Ala Lys Ile Ala
 85 90 95
 Gly Ile Asp Val Val Ile Gly Val Val Glu Leu Asp Gly Arg Thr Arg
 100 105 110
 Ala Ser Val Tyr Ser Thr Leu Leu Phe Ile Gly Arg Glu Gly Ala Ile
 115 120 125
 Leu Gly Arg His Arg Lys Leu Lys Pro Thr His Met Glu Arg Thr Val
 130 135 140
 Trp Gly Glu Gly Asp Ala His Gly Leu Arg Val His Glu Arg Pro Tyr
 145 150 155 160
 Gly Arg Leu Ser Gly Leu Asn Cys Trp Glu His Asn Met Met Leu Pro
 165 170 175
 Gly Tyr Val Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Thr Trp

```

      180      185      190
Pro Gly Lys Glu Arg Leu Thr Val Pro Pro Asn Glu Ala Ala Tyr Thr
      195      200      205
Arg Gln Leu Leu Leu Ser Arg Ala Tyr Ala Ser Gln Ala Gly Ala Tyr
      210      215      220
Val Ile Ser Val Ala Gly Leu Leu Gly Pro Asp Ser Met Pro Glu Arg
225      230      235      240
Tyr Arg Glu Leu Gly Gln Ser Tyr Glu Leu Thr Gly Asp Ser Val Ile
      245      250      255
Ile Asp Pro Arg Gly Glu Val Ile Ala Gly Pro Ala Lys Gly Glu Thr
      260      265      270
Ile Leu Leu Ala Gln Cys Ser Gln Glu Ala Leu Phe Ala Ala Lys Ser
      275      280      285
Ala Ile Asp Val Gly Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu
      290      295      300
Arg Val Asn Asp Gln Leu Gln His Gln Val Arg Arg Leu Glu Ala Thr
305      310      315      320
Leu Thr Pro Pro Val Ala Val Val Val Gly Pro Glu Gly Ser Ser His
      325      330      335
Glu Gln Glu Thr Ala Phe Gly Pro Ser Ser Leu Leu Ala Thr Thr Ser
      340      345      350

```

<210> 299

<211> 987

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 299

```

atgactgttg ttaaggccgc cgcagtgcag atcagcccgg tgctctacag ccgtgcagga      60
accgtcgaga aggtcgtgaa gaagatcgac gagctgggcc agaagggtgt cgagtttgcc      120
gtcttccctg aaaccgttgt cccctactac ccctacttct ccttcgtgca gccccctac      180
aaactggcca cggagcacct gcgcctgctt gaggagtcgg tgaccgtgcc ctctgccgag      240
acggacgcca tcggcgacgc cgcgcgcaag gccaacatgg tcgtctcgat cgggtgtcaac      300
gaacgtgatg gcggcaccat ttacaacacc caactcctgt tcgacgccga cgggaacctg      360
atccagcgcc gccgcaagat caccgcgacc taccacgagc ggatgatctg gggacaggga      420
gacggatcag gcttgcgcgc ggtcgacagc gtcgtcggcc gcacgggcca gctcgccctgc      480
tgggagcact accagccgct ggcccggttac gctctcatcg ccgacggcga gcagatccac      540
gccgcgatgt accccggcgc cttcgggggc gatctgttcg cagagcagat cgaagtcaat      600
gtccgtcagc acgctctgga atcggccagt ttcgctcgta gcgccaccgc ctggctcgac      660
gccgaccagc aggcccagat tgcgaaggac accggcggcc ccgtacaggc gatctccggc      720
ggcttcttca cagccatcat cgaccccgac ggccgcatca tcggcggaacc gatcacctcc      780
ggcgaaggcg aagtcatcgc tgacctcgac ttgcgctca tcgaccgccc caagcgctg      840
atggacgcca gcggccacta cagccgcccc gaactgctca gcctgcagat cgaccggacg      900
ccggcaccgg ccgtccacga tcgcaatcgc caggggtcct caagcgctcc ggcaactgaa      960
aagggccgct cagccgaggc caagtga

```

<210> 300

<211> 328

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 300

```

Met Thr Val Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
  1      5      10      15
Ser Arg Ala Gly Thr Val Glu Lys Val Val Lys Lys Ile Asp Glu Leu

```

<210>	301
<211>	1032
<212>	DNA
<213>	Unknown

[illegible]

<210>	302
<211>	335
<212>	PRT
<213>	Unknown

```
<210> 303
<211> 1011
```

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 303
atgggcatcg ttcaccccaa gtacaaagtc gctgtcgttc aggctgcccc tgtatggcta 60
gacctggagg ccactgttga taaatgcatt cagttgattg aagaagcagc cagcaagggc 120
tgcaagctca tcgccttccc tgagaccttc attcccggat acccttggta tatctggatg 180
ggaacgcctg cctggactat tcagcgcggc tttgtacagc gctattttga taattctctg 240
tcttatgaca gtccgcaagc ggagaagcta aggcaggcag tcaaaaaggc tgagatcacg 300
gcogtactag gtctttctga gcgcagcggc ggtagcttgt acattgcaca atggaccatt 360
ggccctgacg gagaaacat acacaaacgc agaaaagtgc gtccaacgca tggtagcgt 420
acggtatttg gcgacggtga cggtagtgat cttgcggtgc acgatacccc cctggggcgg 480
ctgggcgcgc ttgcgtgctg ggagaacata ctgtcactga acaagtatgc gatgtattca 540
cagaatgagc aggtgcacgt agccgcttgg cctagcttct cgggtctacga gcctttcgcc 600
catgcattgg gttgggaggt caataacgca gtcagcaagg tttacgcggg agaaggcggc 660
tgttttgtat tggcgccctg cgcagtggtc tccgaggaaa tgatcgaagc actgtgcgat 720
acacccgata agcaccaact ggctcatgcy ggtggagggc atgctgtcat ttacggacca 780
gatggcagtc ctcctggcaga taagttaccc gaaggagagg aggggctatt aattgcagaa 840
attgatctcg gtctcatcag cttggcgaaa aatgccatgg acccggtggg gcattactct 900
cgacctgacg tacatcgctt gctattgaat cgcaatccag caaagcgggt tgaggaattt 960
tctctgcccc ttgatttggc agagacaact ccgccaatat taggcacgta g 1011

<210> 304
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 304
Met Gly Ile Val His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Val Trp Leu Asp Leu Glu Ala Thr Val Asp Lys Cys Ile Gln Leu
20 25 30
Ile Glu Glu Ala Ala Ser Lys Gly Cys Lys Leu Ile Ala Phe Pro Glu
35 40 45
Thr Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Met Gly Thr Pro Ala
50 55 60
Trp Thr Ile Gln Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Gln Ala Val Lys Lys
85 90 95
Ala Glu Ile Thr Ala Val Leu Gly Leu Ser Glu Arg Ser Gly Gly Ser
100 105 110
Leu Tyr Ile Ala Gln Trp Thr Ile Gly Pro Asp Gly Glu Thr Ile His
115 120 125
Lys Arg Arg Lys Val Arg Pro Thr His Gly Glu Arg Thr Val Phe Gly
130 135 140
Asp Gly Asp Gly Ser Asp Leu Ala Val His Asp Thr Pro Leu Gly Arg
145 150 155 160
Leu Gly Ala Leu Ala Cys Trp Glu Asn Ile Leu Ser Leu Asn Lys Tyr
165 170 175
Ala Met Tyr Ser Gln Asn Glu Gln Val His Val Ala Ala Trp Pro Ser
180 185 190
Phe Ser Val Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Val Asn
195 200 205
Asn Ala Val Ser Lys Val Tyr Ala Val Glu Gly Gly Cys Phe Val Leu

```

      210      215      220
Ala Pro Cys Ala Val Val Ser Glu Glu Met Ile Glu Ala Leu Cys Asp
225      230      235      240
Thr Pro Asp Lys His Gln Leu Ala His Ala Gly Gly Gly His Ala Val
      245      250      255
Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Asp Lys Leu Pro Glu Gly
      260      265      270
Glu Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Leu Ile Ser Leu
      275      280      285
Ala Lys Asn Ala Met Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val
      290      295      300
His Arg Leu Leu Leu Asn Arg Asn Pro Ala Lys Arg Val Glu Glu Phe
305      310      315      320
Ser Leu Pro Ile Asp Leu Ala Glu Thr Thr Pro Pro Ile Leu Gly Thr
      325      330      335

```

<210> 305
 <211> 1068
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 305
atgacgatgc aacatcccaa gtttcgcgct gctgccgtgc aggcggcacc ggtcttcctt      60
gaccttgatg cgtcgataga taaagccatc gacctgatcg cgcaagccgc caaaggcggc      120
gcgcaattga ttgcctttcc ggaaacctgg ctgcccggct accccttttt catctggctc      180
gattcgccgg cctggggcat gcaattcatc cagcgctacc atgacaattc cctgggtctac      240
ggcacaccgc aggccgagcg catcgcgagc gctgcgaaaa agcatcgcat catgggtcgtc      300
atggggcaca gcgagcggga tcatggaagt ctgtacatcg ctcaagtggat catcggtgccc      360
gatggggaaa cggttgcgac acgtcgtaag ctcaaaccga ctcatgccga gcgcaccttg      420
tttggggaa gcatggcag tgacctgagc gtgttcgata caccgctggg aagggttggc      480
gcactatgct gctgggagca cctccagccc ctgtcgaaat acgcgctata cgcacagaat      540
gagcaggtcc acattgcttc ctggccaagc ttttcctgt atcgcggggg cgcctacgcg      600
ctcggcgccg aagtgaacaa tgcggccagc cagatttatg ctgtcgaagg ccagtgtttt      660
gtgatcgcg cgtgcggggg ctgcacgaaa gaaatgctgg acgtgctgtg caccgacgaa      720
atgaaaaagc agttgttgg tgaaggcggc gggttcgcgc gaatttacgc gcccgatgga      780
cagatgatgc acgcgccgct ggcgaaaaac gaagagggcc tgggtgtatgc cgatctcgac      840
ctgggcatga tctcgctggc caaagtagtc gccgacccgg ccgggcatta tgcgcggccc      900
gacgtaaccc gggtactgct ggacaagact ccgggagacc gcgtcatgct ggcgagccgt      960
cgcggaagg aggtcagccg cgctggtaac gacgagccgc aagtgtgtgt ctcgcgcaac     1020
gacacgtga cctcgccgaa gccagcgtct tcgcgcaaag caagctga      1068

```

<210> 306
 <211> 355
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 306
Met Thr Met Gln His Pro Lys Phe Arg Ala Ala Ala Val Gln Ala Ala
1      5      10      15
Pro Val Phe Leu Asp Leu Asp Ala Ser Ile Asp Lys Ala Ile Asp Leu
20      25      30
Ile Ala Gln Ala Ala Lys Gly Gly Ala Gln Leu Ile Ala Phe Pro Glu
35      40      45
Thr Trp Leu Pro Gly Tyr Pro Phe Phe Ile Trp Leu Asp Ser Pro Ala
50      55      60

```

Trp Gly Met Gln Phe Ile Gln Arg Tyr His Asp Asn Ser Leu Val Tyr
 65 70 75 80
 Gly Thr Pro Gln Ala Glu Arg Ile Ala Gln Ala Ala Lys Lys His Arg
 85 90 95
 Ile Met Val Val Met Gly His Ser Glu Arg Asp His Gly Ser Leu Tyr
 100 105 110
 Ile Ala Gln Trp Ile Ile Gly Ala Asp Gly Glu Thr Val Ala Thr Arg
 115 120 125
 Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Leu Phe Gly Glu Gly
 130 135 140
 Asp Gly Ser Asp Leu Ser Val Phe Asp Thr Pro Leu Gly Arg Val Gly
 145 150 155 160
 Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Leu
 165 170 175
 Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ser Trp Pro Ser Phe Ser
 180 185 190
 Leu Tyr Arg Gly Gly Ala Tyr Ala Leu Gly Ala Glu Val Asn Asn Ala
 195 200 205
 Ala Ser Gln Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Ile Ala Pro
 210 215 220
 Cys Gly Val Val Thr Lys Glu Met Leu Asp Val Leu Cys Thr Asp Glu
 225 230 235 240
 Met Lys Lys Gln Leu Leu Val Glu Gly Gly Gly Phe Ala Arg Ile Tyr
 245 250 255
 Ala Pro Asp Gly Gln Met Met His Ala Pro Leu Ala Glu Asn Glu Glu
 260 265 270
 Gly Leu Val Tyr Ala Asp Leu Asp Leu Gly Met Ile Ser Leu Ala Lys
 275 280 285
 Val Val Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Thr Arg
 290 295 300
 Leu Leu Leu Asp Lys Thr Pro Gly Asp Arg Val Met Leu Ala Ser Arg
 305 310 315 320
 Arg Gly Lys Glu Val Ser Arg Ala Gly Asn Asp Glu Pro Gln Val Leu
 325 330 335
 Val Ser Arg Asn Asp Thr Leu Thr Ser Pro Lys Pro Ala Ser Ser Arg
 340 345 350
 Lys Ala Ser
 355

<210> 307
 <211> 942
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 307
 atggctgaac cggaatcctt tatcgctcgt gctgtacagg ctacaccgat ctttcttgac 60
 cgccaggcaa cccttgagaa agcgtgacgac ctgattgccg aagctggcag caatggcgca 120
 aaactcgttc tttttccga agcctttatc cccacctatc ctgattggat atgggagggtg 180
 acaggctcac aatctgcgct gctcgacgaa ctttatgttg aactactgga aaactccgtg 240
 accatccccg acgcgaccac tgagcaactt tgtgaagcag cacgtaacgc cgggtctctac 300
 gtcgtcatgg gagtgaatga ggcgaacgcc gagggcgagca acgccacact ctataacacc 360
 ctgctctata ttgacgatca gggcaaaatt ctgggcaagc atcgcaaatt ggtcccagacc 420
 gccctggagc gaatcgtctg gggctatggc gatggcagca cgcttgacgc ctttgaaacg 480
 ccgctgggca agattggcgg gctgatctgt tgggaaaatt acatgccact ggcgcgccaa 540
 acactttatg cctgggggggt gcaaattttac ttggccgcaa cgtgggatcg cggcgaaagt 600
 tggcaggcga ccatgcgcca tattgccagg gaaggcgggc tctatgtagt cgctcctgt 660
 attocatttc acatcaaaga cattcctgac cacatgcctg aaatccgcaa tctctatgca 720
 ccgggggacag actggatcaa cgtcggccaa agctgcatca tcaaccccag cggcgactat 780

```

attgcaggcc ctgtcgagtg tcgcgaggag attcttttatg ccgaggtaaa tctgcgccag      840
agtgcggcgg caaaacgtat gttggatgtg gcggggccatt atggacgcc t gatgtcttt      900
cacctcaccg tcaaccgcac gcccaatccg catattcgat aa                          942

```

<210> 308
 <211> 313
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 308

Met	Ala	Glu	Pro	Glu	Ser	Phe	Ile	Val	Ala	Ala	Val	Gln	Ala	Thr	Pro	1	5	10	15
Ile	Phe	Leu	Asp	Arg	Gln	Ala	Thr	Leu	Glu	Lys	Ala	Cys	Asp	Leu	Ile	20	25	30	
Ala	Glu	Ala	Gly	Ser	Asn	Gly	Ala	Lys	Leu	Val	Leu	Phe	Pro	Glu	Ala	35	40	45	
Phe	Ile	Pro	Thr	Tyr	Pro	Asp	Trp	Ile	Trp	Ala	Val	Thr	Gly	Ser	Gln	50	55	60	
Ser	Ala	Leu	Leu	Asp	Glu	Leu	Tyr	Val	Glu	Leu	Leu	Glu	Asn	Ser	Val	65	70	75	80
Thr	Ile	Pro	Asp	Ala	Thr	Thr	Glu	Gln	Leu	Cys	Glu	Ala	Ala	Arg	Asn	85	90	95	
Ala	Gly	Leu	Tyr	Val	Val	Met	Gly	Val	Asn	Glu	Arg	Asn	Ala	Glu	Ala	100	105	110	
Ser	Asn	Ala	Thr	Leu	Tyr	Asn	Thr	Leu	Leu	Tyr	Ile	Asp	Asp	Gln	Gly	115	120	125	
Lys	Ile	Leu	Gly	Lys	His	Arg	Lys	Leu	Val	Pro	Thr	Ala	Leu	Glu	Arg	130	135	140	
Ile	Val	Trp	Gly	Tyr	Gly	Asp	Gly	Ser	Thr	Leu	Asp	Ala	Phe	Glu	Thr	145	150	155	160
Pro	Leu	Gly	Lys	Ile	Gly	Gly	Leu	Ile	Cys	Trp	Glu	Asn	Tyr	Met	Pro	165	170	175	
Leu	Ala	Arg	Gln	Thr	Leu	Tyr	Ala	Trp	Gly	Val	Gln	Ile	Tyr	Leu	Ala	180	185	190	
Ala	Thr	Trp	Asp	Arg	Gly	Glu	Val	Trp	Gln	Ala	Thr	Met	Arg	His	Ile	195	200	205	
Ala	Arg	Glu	Gly	Gly	Val	Tyr	Val	Val	Ala	Ser	Cys	Ile	Pro	Phe	His	210	215	220	
Ile	Lys	Asp	Ile	Pro	Asp	His	Met	Pro	Glu	Ile	Arg	Asn	Leu	Tyr	Ala	225	230	235	240
Pro	Gly	Thr	Asp	Trp	Ile	Asn	Val	Gly	Gln	Ser	Cys	Ile	Ile	Asn	Pro	245	250	255	
Ser	Gly	Asp	Tyr	Ile	Ala	Gly	Pro	Val	Glu	Cys	Arg	Glu	Glu	Ile	Leu	260	265	270	
Tyr	Ala	Glu	Val	Asn	Leu	Arg	Gln	Ser	Ala	Ala	Ala	Lys	Arg	Met	Leu	275	280	285	
Asp	Val	Ala	Gly	His	Tyr	Gly	Arg	Pro	Asp	Val	Phe	His	Leu	Thr	Val	290	295	300	
Asn	Arg	Thr	Pro	Asn	Pro	His	Ile	Arg								305	310		

<210> 309
 <211> 951
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 309
ttgaccgact gtctcaaaat agccgcccgc caaatcactc cggtcttctt cgaccgcggt 60
gcgaccacga agaaggtcgt cgaaaccatc gaaaaagcgg ccgccggcgg tgcgcggctg 120
gtcgcattcg gcgaagcgct gttgcccgcg tatccattgt ggctgacgcg caccgacgcc 180
gcgcgggttca attccgacgt gcaaaaaaac ttgcacgcga tctatctcaa gcaatccgtc 240
tcgatagcag gcggtcacct atctccgatt tgcaaaatcg caagcgaacg caagattgcc 300
gtcatcctcg gcatcgccga gcgcgcgacc gaccggggcg accacaccat ttactgctcg 360
tgcgtgttca tcgatgccga cggccgaatc gcgtcgggtc atcgcaagct gatgccgaca 420
tacgaagaac gcctcagttg gggattcggc gacggtgcgg gactcgtcac gcatccggtc 480
gggccgttca cgggtggcgc gttgaactgc tgggaaaact ggatgccctt cgcgcgcacc 540
gcgctgtatg ccggcggaga agatttgcac gttgcgatct ggcccggcgg atcggtgctc 600
acggaagaca tcacgcgctt catcgcacgc gagtgcgctt cgttcgtcct gtccgtcagc 660
ggcatcattc gcgaaagcga catccccagc ggggtcccct atcgcgatga aatgtgtgcy 720
aaaggcga aa catctacaa cggcgggaagc tgcacgcgcg gacccgacgg tcagtggatc 780
atcgcgcccg taaccgaccg tgaagagttg atcttcgccc agatcgacca cgaacacgtc 840
cgccgcgagc ggcagaattt cgaccgggcc gggcattacg cgcggcccga tgtgttgcaa 900
ataaccgttg atcgtcgacg acaaacagcg gcgaatttta ttgatgacta a 951

```

<210> 310

<211> 316

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 310

```

Leu Thr Asp Cys Leu Lys Ile Ala Ala Ala Gln Ile Thr Pro Val Phe
1      5      10      15
Leu Asp Arg Val Ala Thr Thr Lys Lys Val Val Glu Thr Ile Glu Lys
20      25      30
Ala Ala Ala Gly Gly Ala Arg Leu Val Ala Phe Gly Glu Ala Leu Leu
35      40      45
Pro Ala Tyr Pro Leu Trp Leu Thr Arg Thr Asp Ala Ala Arg Phe Asn
50      55      60
Ser Asp Val Gln Lys Asn Leu His Ala Ile Tyr Leu Lys Gln Ser Val
65      70      75      80
Ser Ile Ala Gly Gly His Leu Ser Pro Ile Cys Lys Ile Ala Ser Glu
85      90      95
Arg Lys Ile Ala Val Ile Leu Gly Ile Ala Glu Arg Ala Thr Asp Arg
100     105     110
Gly Asp His Thr Ile Tyr Cys Ser Cys Val Phe Ile Asp Ala Asp Gly
115     120     125
Arg Ile Ala Ser Val His Arg Lys Leu Met Pro Thr Tyr Glu Glu Arg
130     135     140
Leu Ser Trp Gly Phe Gly Asp Gly Ala Gly Leu Val Thr His Pro Val
145     150     155     160
Gly Pro Phe Thr Val Gly Ala Leu Asn Cys Trp Glu Asn Trp Met Pro
165     170     175
Leu Ala Arg Thr Ala Leu Tyr Ala Gly Gly Glu Asp Leu His Val Ala
180     185     190
Ile Trp Pro Gly Gly Ser Val Leu Thr Glu Asp Ile Thr Arg Phe Ile
195     200     205
Ala Arg Glu Ser Arg Ser Phe Val Leu Ser Val Ser Gly Ile Ile Arg
210     215     220
Glu Ser Asp Ile Pro Ser Gly Val Pro Tyr Arg Asp Glu Met Cys Ala
225     230     235     240
Lys Gly Glu Thr Ile Tyr Asn Gly Gly Ser Cys Ile Ala Gly Pro Asp
245     250     255
Gly Gln Trp Ile Ile Ala Pro Val Thr Asp Arg Glu Glu Leu Ile Phe

```

```

                260                      265                      270
Ala Glu Ile Asp His Glu His Val Arg Arg Glu Arg Gln Asn Phe Asp
                275                      280                      285
Pro Ala Gly His Tyr Ala Arg Pro Asp Val Leu Gln Ile Thr Val Asp
                290                      295                      300
Arg Arg Arg Gln Thr Ala Ala Asn Phe Ile Asp Asp
305                      310                      315

```

<210> 311
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 311
atgtcagaaa agcgaataat cagagcagct gcagttcaga tcacacctga atttgactca      60
gcagatggaa cagttaagaa ggtatgcaag gtaatcgatg aagcaggcgc aaaggggtgta      120
caaattatag tattccccga aaccttcatt ccgtattacc catacttctc attcattacc      180
ccccagttt ctgctggcgc tgagcatttg aagctttatg aaaaaagtgt cgtgatacct      240
ggtcctgtca ctcaagcgat cgccgagaga gctagagtga atcaaattggc cgtcgtactc      300
ggtgtaaacg agagagataa cggtagcctc tataacactc aactgatctt cgataccaat      360
ggtgagttga tgttgaagag aagaaaaatc actcctacat atcatgagcg catgatctgg      420
ggacaagggtg atgcttcagg cttaaaagta gttgaaacga gcattgcccgc ggtaggtgct      480
ctagcttgct gggaacatta caaccgctg gccagatatt ctctcatgac acagcatgaa      540
gaaattcact gcgcacaatt cccaggttct atggttggcc aaatatattgc cgaccaaattg      600
gatgtcacta tcagacatca cgcattggaa tctggctggt tcgtcattaa tgccaccggc      660
tggctcacag acgagcaaat ccagtcatt acagatgacc caaaaatgca gaaagcatta      720
cgtggcggct gcaacacagc aatcatttct cccgaagggt tgcacttaac agagccctta      780
cgtgaagggtg aaggcatttt gattgctgac ctggacatgt cactcatcac aaaacgaaaa      840
agaatgatgg attcagtagg tcattattca agacctgaac tattaagtct ggcgatcaat      900
gacaagccag caacaacaaa attttcaatg actgaggggt gtactcaaac tgagcaattt      960
cgaatcgag aggagttgaa aaatgacgac aagcttagca ccggaaacta a      1011

```

<210> 312
 <211> 336
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 312
Met Ser Glu Lys Arg Ile Ile Arg Ala Ala Ala Val Gln Ile Thr Pro
  1                      5                      10                      15
Glu Phe Asp Ser Ala Asp Gly Thr Val Lys Lys Val Cys Lys Val Ile
                20                      25                      30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
                35                      40                      45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Ser
                50                      55                      60
Ala Gly Ala Glu His Leu Lys Leu Tyr Glu Lys Ser Val Val Ile Pro
                65                      70                      75                      80
Gly Pro Val Thr Gln Ala Ile Ala Glu Arg Ala Arg Val Asn Gln Met
                85                      90                      95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
                100                      105                      110
Thr Gln Leu Ile Phe Asp Thr Asn Gly Glu Leu Met Leu Lys Arg Arg
                115                      120                      125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp

```

<210>	313
<211>	987
<212>	DNA
<213>	Unknown

[illegible]

<220>
<223> Obtained from an environmental sample

<400> 314

```

Met Ala Ala Val Gln Ala Ala Pro Val Pro Phe Asp Ala Glu Ala Ser
1      5      10      15
Val Asp Lys Ala Cys Arg Leu Ile Gln Glu Ala Ala Ala Lys Gly Ala
20     25     30
Asp Ile Val Ala Phe Gly Glu Ala Trp Leu Pro Gly Tyr Pro Tyr Phe
35     40     45
Ala Trp Leu Pro Gln Val Thr Pro Glu Trp Tyr Ser Ala Ala Ala Asp
50     55     60
Tyr Leu Ala Ser Ser Val Asp Ile Pro Gly Pro Ile Thr Asp Lys Leu
65     70     75     80
Cys Gln Ala Ala Arg Arg Ala Ser Val Glu Leu Ile Met Gly Val Val
85     90     95
Glu Arg Ser Lys Ser Gln Gly Thr Thr Tyr Cys Thr Leu Leu Phe Ile
100    105    110
Ser Lys Asp Gly Glu Ile Ile Gly Lys His Arg Lys Leu Lys Pro Thr
115    120    125
Leu Ala Glu Arg Thr Val Trp Gly Glu Gly Asp Ala Ser Gly Leu Arg
130    135    140
Val His Asp Arg Pro Ile Ala Arg Ile Ser Gly Leu Ser Cys Trp Glu
145    150    155    160
Asn Lys Met Met Leu Pro Gly Tyr Ala Leu Met Ala Gln Gly Thr Gln
165    170    175
Val His Val Ser Ala Trp Pro Gly Ile Pro Glu Asp Ser Pro Met Glu
180    185    190
Val Pro Ala His Pro Arg Gln Lys Leu Leu Ser Gln Ala Phe Ala Leu
195    200    205
Gln Gly Gly Cys Tyr Val Ile Ser Pro Ser Ile Val Leu Arg Ala Glu
210    215    220
Asp Val Pro Glu Lys His Ala Ala Leu Leu Met Gly Asp Gln Val Gly
225    230    235    240
Gly Ser Tyr Ile Ile Asp Pro Cys Gly Lys Val Ile Ala Glu Ala Gly
245    250    255
Ala Gly Glu Thr Ile Leu Ile Ala Lys Gly Asn Leu Asp Leu Val Arg
260    265    270
Ala Ala Lys Met Ala Ser Asp Val Gly Gly Ser Tyr Ser Arg Pro Asp
275    280    285
Leu Leu Gln Leu Met Ile Asn Asn Arg Pro Leu Glu Gln Leu Ile Glu
290    295    300
Phe Ser Ala Glu Gly Ala Gly Arg Gly Asn Leu Val Ser Asn Ser Pro
305    310    315    320
Glu Val Ser Glu Gln Glu Gly Glu
325

```

<210> 315

<211> 960

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 315

```

atgacaatgc ttaagaccaa attccggggtt gctgcgggtgc aggcagcgcgc tgtattcctg      60
gatcgagagg ctacgctgga gaaagcctgc ggactgattg aggaggcggg tcgcaacggg      120
gccagcctgg tggctcttcc tgagtcgttc attccggcct atcccgattg ggtctgggct      180
gtgccggcgg gtgaagaagc tttacttaat gaactgtatg ctcaactgct ggccaacgcc      240
gttgaaattc ccagcccggc caccgaacgc ttgagccagg cagcgaaaaa ggctaaagtc      300
catgtgggta tgggcctgac cgaacgcaac agcgaggcca gggcggcgag cctctacaat      360
accttgctct atcttgaccc acagggccaa attctgggca aacatcgcaa gctggtgcc      420
accggcgggc agcggctggt ttgggccagc ggcgacggca gtaccctgca agtctacgag      480

```

```

acccccttgg gtaaaactcag cggtttgatt tgctgggaaa attatatgcc gctggcccgc 540
tacgcgctct atgcctgggg tacgcaaata tatatcgccg ccacctggga tcgaggcgag 600
ccgtggcttt cgacgctgcg gcatatcgcc aaagagggcc ggggtgtttgt catcggtgt 660
ggcatggcct tgcgtaaggc tgatattccc gaccattttg aattcaagca gcgcttttat 720
caaaatgccg gcgagtggat caatggaggc gacagcgcca ttgtcaatcc tgagggtgaa 780
tttattgctg gacccctgag cgagcaggaa ggtattttgt acgccgagat tgatcctggc 840
cagatggccg gacaaaaatg gatgctcgat gtggccgggc actatgctcg cccggatgtc 900
tttgaactga ccgtccagac cgtagctcgg cccatgatta cctctactca gccgcgatag 960

```

<210> 316

<211> 319

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 316

```

Met Thr Met Leu Lys Thr Lys Phe Arg Val Ala Ala Val Gln Ala Ala
1      5      10      15
Pro Val Phe Leu Asp Arg Glu Ala Thr Leu Glu Lys Ala Cys Gly Leu
20     25     30
Ile Glu Glu Ala Gly Arg Asn Gly Ala Ser Leu Val Val Phe Pro Glu
35     40     45
Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala Gly
50     55     60
Glu Glu Ala Leu Leu Asn Glu Leu Tyr Ala Gln Leu Leu Ala Asn Ala
65     70     75     80
Val Glu Ile Pro Ser Pro Ala Thr Glu Arg Leu Ser Gln Ala Ala Lys
85     90     95
Lys Ala Lys Val His Val Val Met Gly Leu Thr Glu Arg Asn Ser Glu
100    105    110
Ala Ser Gly Gly Ser Leu Tyr Asn Thr Leu Leu Tyr Leu Asp Pro Gln
115    120    125
Gly Gln Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130    135    140
Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val Tyr Glu
145    150    155    160
Thr Pro Leu Gly Lys Leu Ser Gly Leu Ile Cys Trp Glu Asn Tyr Met
165    170    175
Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
180    185    190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
195    200    205
Ile Ala Lys Glu Gly Arg Val Phe Val Ile Gly Cys Gly Met Ala Leu
210    215    220
Arg Lys Ala Asp Ile Pro Asp His Phe Glu Phe Lys Gln Arg Phe Tyr
225    230    235    240
Gln Asn Ala Gly Glu Trp Ile Asn Gly Gly Asp Ser Ala Ile Val Asn
245    250    255
Pro Glu Gly Glu Phe Ile Ala Gly Pro Leu Ser Glu Gln Glu Gly Ile
260    265    270
Leu Tyr Ala Glu Ile Asp Pro Gly Gln Met Ala Gly Pro Lys Trp Met
275    280    285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Thr
290    295    300
Val Gln Thr Val Ala Arg Pro Met Ile Thr Ser Thr Gln Pro Arg
305    310    315

```

<210> 317

<211> 993

<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

```
<400> 317
atgaccattg taaaagccgc tgccgtccaa ataagccctg tcctttacag ccgcgaaggc      60
accgtggaca aggttggtcca gaagatcctc gaactcggca agcaaggcgt ccagttcgcc      120
actttcccgga agacgggtggt cccctactac ccctacttct ccttcgtcca gtcggggtac      180
gccctcaagg tgggcaagga acatctgcgc ttgctcgaac agtcgggtcac cgtgccatcg      240
gccaccacgc tcgccatcgg cgaagcctgc aagcaggcgg ggatgggtgg gtccatcggc      300
gtcaacgaac gcgacggcag cagcatctac aacacgcagc tgctcttcga tgccgacggc      360
accttgattc agcgccgcgc aaagatcagc ccgaccttcc atgaacgcat ggtctggggc      420
cagggcgacg gctccgggct gcgcgcggtc gacagcgcgg tcggggcgcat cggccagttg      480
gcgtgctggg agcactacaa cccgctggcc cgctacgcca tgatggccga cggcgagcag      540
atccactcgg cgatgtaccc cggtttcctt gcaggcgacg ccttctccga acagatccag      600
gtcaacatcc gccagcacgc attggaagcc ggctgcttcg tcgtgaacgc caccgcgtgg      660
ctggacgccg atcagcaggc gcagatcatg caggacaccg gttgcgccat cggcccgcac      720
tccagtgggt gcttcaccgc catcgcttcg ccggacggcg tgttgctggg cgagcctctg      780
cggtcgggtg agggcgaggt gattgccgat ctgcacttca cgctgatcga caagcgcaag      840
cagatgatgg attcacgcgg gcactatgcg cgcccgaat tgctcagcct gttgatcgac      900
cgcacggcga ccgcgcgatg gcatgagcgc agcgcgcatc cgaaggcgac tgccgagcag      960
cgcgacggtc catccgccgt gaatgcgcag taa                               993
```

<210> 318
<211> 330
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

```
<400> 318
Met Thr Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
  1          5          10          15
Ser Arg Glu Gly Thr Val Asp Lys Val Val Gln Lys Ile Leu Glu Leu
          20          25          30
Gly Lys Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
          35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Ser Gly Tyr Ala Leu Lys Val
          50          55          60
Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ser Val Thr Val Pro Ser
          65          70          75          80
Ala Thr Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val
          85          90          95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Ser Thr Ile Tyr Asn Thr
          100          105          110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
          115          120          125
Ile Ser Pro Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly
          130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu
          145          150          155          160
Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
          165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Phe Ala Gly
          180          185          190
Asp Ala Phe Ser Glu Gln Ile Gln Val Asn Ile Arg Gln His Ala Leu
          195          200          205
Glu Ala Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
```

	210					215					220					
Gln	Gln	Ala	Gln	Ile	Met	Gln	Asp	Thr	Gly	Cys	Ala	Ile	Gly	Pro	Ile	
225					230					235						240
Ser	Ser	Gly	Cys	Phe	Thr	Ala	Ile	Val	Ser	Pro	Asp	Gly	Val	Leu	Leu	
				245					250					255		
Gly	Glu	Pro	Leu	Arg	Ser	Gly	Glu	Gly	Glu	Val	Ile	Ala	Asp	Leu	Asp	
			260					265					270			
Phe	Thr	Leu	Ile	Asp	Lys	Arg	Lys	Gln	Met	Met	Asp	Ser	Arg	Gly	His	
		275					280					285				
Tyr	Ala	Arg	Pro	Glu	Leu	Leu	Ser	Leu	Leu	Ile	Asp	Arg	Thr	Ala	Thr	
	290					295					300					
Ala	His	Val	His	Glu	Arg	Ser	Ala	His	Pro	Lys	Ala	Thr	Ala	Glu	Gln	
305					310					315					320	
Ala	Asp	Gly	Pro	Ser	Ala	Val	Asn	Ala	Gln							
				325					330							

<210>	319
<211>	1017
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

<210>	320
<211>	338
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400> 320																
Met	Thr	Thr	Pro	Arg	Ile	Val	Arg	Val	Ala	Ala	Val	Gln	Met	Ala	Pro	
1				5					10					15		
Asp	Leu	Glu	Ser	Ala	His	Gly	Thr	Val	Asp	Lys	Val	Cys	Arg	Ala	Ile	
			20					25					30			
Leu	Glu	Ala	Gly	Glu	Lys	Gly	Ala	Arg	Met	Val	Val	Phe	Pro	Glu	Thr	
		35				40						45				
Phe	Val	Pro	Tyr	Tyr	Pro	Tyr	Phe	Ser	Phe	Ile	Gln	Pro	Ala	Val	Thr	
50						55					60					
Met	Gly	Ala	Ala	His	Leu	Glu	Leu	Tyr	Glu	Arg	Ala	Val	Thr	Val	Pro	

65 70 75 80
 Gly Pro Val Thr Leu Ala Val Gly Glu Ala Arg Arg Ala Gly Ala
 85 90 95
 Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
 100 105 110
 Thr Gln Leu Ile Phe Asp Glu Thr Gly Ala Leu Val Leu Lys Arg Arg
 115 120 125
 Lys Leu Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp
 130 135 140
 Gly Ser Gly Leu Lys Val Val Asp Thr Gly Ile Gly Arg Ile Gly Ala
 145 150 155 160
 Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Thr Leu Met
 165 170 175
 Ala Gln His Glu Glu Ile His Ala Ala Gln Phe Pro Gly Ser Met Val
 180 185 190
 Gly Gln Ile Phe Ala Asp Gln Met Ala Val Thr Ile Arg His His Ala
 195 200 205
 Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Asp
 210 215 220
 Ala Gln Ile Thr Ala Ile Thr Pro Asp Pro Ala Met Gln Arg Ala Leu
 225 230 235 240
 Arg Gly Gly Cys His Thr Ala Ile Val Ser Pro Glu Gly Ser Tyr Val
 245 250 255
 Cys Glu Pro Leu Thr Glu Gly Glu Gly Met Leu Val Ala Asp Leu Asp
 260 265 270
 Met Arg Leu Val Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
 275 280 285
 Tyr Ala Arg Pro Glu Leu Leu Ser Leu Asn Ala Asp Leu Ala Pro Lys
 290 295 300
 Pro Ala Leu His Thr Gln Pro Ala Ala Ser Leu Pro Leu Ser Leu Gln
 305 310 315 320
 Ala Gly Ala Asp His Val Asp Asp Asp Arg Thr Ala Ser Ala Thr Ala
 325 330 335
 Asp Leu

<210> 321
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 321
 atgagagttg tcaaagccgc tgctgtccaa ctgagtcctg tcctccatag ccgcgacgga 60
 acggtcgaaa aggtcgtgcg gaagatccat gaactcgccg aagagggagt cgagttcgcc 120
 acctttcctg agaccgtggt gccttactac ccgtactttt ccttcgttca gacgcccttg 180
 cagcaaattc tcggaactga gtatctgagg ctgctcgacc aggcagtcac cgtgccatcc 240
 gctgccaccg acgcgatcgg cgaggctgcc aggtgggctg gacttggtgt ctcgatcggc 300
 gtcaacgagc gagacggggg aactctctac aacactcagc ttctcttcga tgccgacggc 360
 agcttaattc agcggcgtcg caagatcaca cccaccatt acgagcgcat gatctggggc 420
 cagggcgacg gctcaggtct gcgggcccgt gatagcaagg ccggccgcat tggtcagctg 480
 gcatgctggg aacacaacaa cccctggcg cgctacgcgc tgatggccga cggcgagcag 540
 atccattcgg ccatgtatcc gggtccatg ttcggcgact cgttttccca aaagaccgaa 600
 atcaatatcc ggcagcatgc gctggaatct gcgtgcttcg tcgtgaacgc aacggcctgg 660
 ctggacgccg atcagcaggc gcaaatcatg aaggacaccg gctgcggcat cggcccgatc 720
 tccggcggtt gcttcaactgc gatcgttgca cccgatggta gcctgctggg cgaacccatc 780
 cgttccgggtg agggcgctcg cgtcgccaac ctgcacttca cgctgatcga caggcgtaag 840
 caggtgatgg actcgcgagg cactacagc cggccggagt tgctcagcct cttaatagac 900
 cgcactccta ccgcgcacgt tcacgaacgc gctacgcacc ccacgacagg agctgagcaa 960

ggctccgagg atgtgttcga ggctcgcat taa

993

<210> 322
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 322
 Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu His
 1 5 10 15
 Ser Arg Asp Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
 20 25 30
 Ala Glu Glu Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Gln Ile Phe
 50 55 60
 Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Trp Ala Gly Leu Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
 180 185 190
 Asp Ser Phe Ser Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Ser Leu Leu
 245 250 255
 Gly Glu Pro Ile Arg Ser Gly Glu Gly Val Val Val Ala Asn Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
 275 280 285
 Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Val His Glu Arg Ala Thr His Pro Thr Thr Gly Ala Glu Gln
 305 310 315 320
 Gly Ser Glu Asp Val Phe Glu Ala Arg Ile
 325 330

<210> 323
 <211> 951
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 323
 atgagcaacg tgaaagtgcg ggtcgtgcaa cgcgcgccgg tgttcggcaa ccgcgccgcc 60
 accctcgatc gcgcgcgtgc cgcgctggcc gaagcggcgc agcagggggc gaagctgggtc 120
 gtgatgcccg agcacttcat ccccggttac ccgccttgga tctggcgccct gcgtccggggc 180
 accgacctgc gattgtgcga acagctgcac gcgatgctgc gcgccaacgc cgtgaggctg 240
 gatgacgggtg acctggcccc gttgaccgag gcgcgcgagc ggcacgcgct caccgtgggtc 300
 tgcggcgctct gcgagatcga caccgaattc agtcgcggca ccctgtacaa caccgtgggtc 360
 gtgatcgggc ccgacggcac gctgctcaac cggcatcgca agctgatgcc caccaacccc 420
 gagcgcatgg tctggggcat gggcgacgcc acggggctga aggtgggtoga cagccctgc 480
 gggcgcatcg gcacgctgat ttgctgggag aactacatgc cattcgcaag cgccgcgctg 540
 tacgcgcagg gggctcgaggt cctgggttgca ccgacctacg acgaaggccc ggtatggctg 600
 gcgtcgatgc agcacatcgc ccgcgaaggc ggctgctggg tgggtgggcaa cggctgcgca 660
 ttccagggcc gcgacatgcc ggacaccttg ccgggcaagg ccagctggt tcccgaggcc 720
 gacgcctggg tcaacgcggg ggactcgggtc atcgtcgcgc caggcgcccg gacagtggcg 780
 ggtccgttgc acgaggcggt cgggctgttc accgcggaga tcgacctctc ccgggtcgga 840
 atggcccgcc gcagcctgga tgtggccggg cactatggac ggcccacat cttctgcctg 900
 caggtcaacg cccgggcgca gccgcgggtt gaggtgacgc accatggctg a 951

<210> 324
 <211> 316
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 324
 Met Ser Asn Val Lys Val Ala Val Val Gln Arg Ala Pro Val Phe Gly
 1 5 10 15
 Asn Arg Ala Ala Thr Leu Asp Arg Ala Val Ala Ala Leu Ala Glu Ala
 20 25 30
 Ala Gln Gln Gly Ala Lys Leu Val Val Met Pro Glu His Phe Ile Pro
 35 40 45
 Gly Tyr Pro Ala Trp Ile Trp Arg Leu Arg Pro Gly Thr Asp Leu Arg
 50 55 60
 Leu Cys Glu Gln Leu His Ala Met Leu Arg Ala Asn Ala Val Arg Leu
 65 70 75 80
 Asp Asp Gly Asp Leu Ala Pro Leu Thr Glu Ala Ala Gln Arg His Ala
 85 90 95
 Leu Thr Val Val Cys Gly Val Cys Glu Ile Asp Thr Glu Phe Ser Arg
 100 105 110
 Gly Thr Leu Tyr Asn Thr Val Val Ile Gly Pro Asp Gly Thr Leu
 115 120 125
 Leu Asn Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val
 130 135 140
 Trp Gly Met Gly Asp Ala Thr Gly Leu Lys Val Val Asp Thr Pro Cys
 145 150 155 160
 Gly Arg Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Phe Ala
 165 170 175
 Arg Ala Ala Leu Tyr Ala Gln Gly Val Glu Val Leu Val Ala Pro Thr
 180 185 190
 Tyr Asp Glu Gly Pro Val Trp Leu Ala Ser Met Gln His Ile Ala Arg
 195 200 205
 Glu Gly Gly Cys Trp Val Val Gly Asn Gly Cys Ala Phe Gln Gly Arg
 210 215 220
 Asp Met Pro Asp Thr Leu Pro Gly Lys Ala Gln Leu Phe Pro Glu Ala
 225 230 235 240
 Asp Ala Trp Val Asn Ala Gly Asp Ser Val Ile Val Ala Pro Gly Gly
 245 250 255
 Arg Thr Val Ala Gly Pro Leu His Glu Ala Phe Gly Leu Phe Thr Ala

```

                260                265                270
Glu Ile Asp Leu Ser Arg Val Gly Met Ala Arg Arg Ser Leu Asp Val
                275                280                285
Ala Gly His Tyr Gly Arg Pro Asp Ile Phe Cys Leu Gln Val Asn Ala
                290                295                300
Arg Ala Gln Pro Pro Val Glu Val Thr His His Gly
305                310                315

```

<210> 325
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 325
atgactgcaa aaaagattgt ccgcgccgcc gctgtccagc tcaatcccgt gctggacagc      60
gccgacggca cccttgtgaa agtggttgag gcgattgccg acgccgcagc gcagggcggtg      120
caactgatcg tctttcccgga gacggtggtg ccctactatc cttacttttc cttcgtcacg      180
cctgcgggtt cgatggggcg gcgcgatctg aaactgtacg aacaatcgcc cacggtgccca      240
gggtccactga ccgacgccgt cgccgcagcc gcgcgggcac atcagatggt ggttgtgctc      300
ggcgtcaacg agcgcgatca cggcacgctc tacaacacgc aactgatctt cgacgccgac      360
ggcacgctcc cactgaagcg tcgcaagatc acgccgacct atcacgagcg catggtcttg      420
ggcatgggag atgggtccgg cctgcgcacg gtgaagaccg aggtcggaac cgttggcgcg      480
ctggcctgct gggaacacta caaccgctg gcacgctacg cgctgatggc gcagcacgaa      540
gagatccatt gcagccagtt ccccggtctg ctggtcggcc cgatcttttc cgagcagatg      600
gaaatcacca tgcgtcatca cgcgctggaa tccggctgct tcgtcgtcaa cgccactgca      660
tggtctgacg ctgagcaggt gcgatcacag gcgccaacac cggcaatgga aaaagccttc      720
tccggtggtt gctacaccgc gatcatttcg ccggaaggaa aacatctggg cgaacctctt      780
cgcgacggcg aaggcatggt catcgccgat cttgattttg atctcatcac caagcgcaag      840
cgaatgatgg attcggtttg ccactacgca cggccggaat tggtgagcct gcagctcgac      900
aaccgatcaa ctgcaaccgt gacaacgtcg ccggtggccg ccgcagcgcc gtcgcttgca      960
gagatggaag cacagcgctt gtcacgttat ctcgatgccg gtcgggcag cgccgcacaa     1020
ggcatcgaag ccgcctacat caatgccctc agctcttttt caggaaaacc ctcatga      1077

```

<210> 326
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 326
Met Thr Ala Lys Lys Ile Val Arg Ala Ala Ala Val Gln Leu Asn Pro
  1                5                10                15
Val Leu Asp Ser Ala Asp Gly Thr Leu Val Lys Val Leu Gln Ala Ile
                20                25                30
Ala Asp Ala Ala Ala Gln Gly Val Gln Leu Ile Val Phe Pro Glu Thr
  35                40                45
Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Thr Pro Ala Val Ser
  50                55                60
Met Gly Ala Ala His Leu Lys Leu Tyr Glu Gln Ser Pro Thr Val Pro
  65                70                75                80
Gly Pro Leu Thr Asp Ala Val Ala Ala Ala Arg Ala His Gln Met
                85                90                95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
                100                105                110
Thr Gln Leu Ile Phe Asp Ala Asp Gly Thr Leu Pro Leu Lys Arg Arg
                115                120                125

```

Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Met Gly Asp
 130 135 140
 Gly Ser Gly Leu Arg Thr Val Lys Thr Glu Val Gly Thr Val Gly Ala
 145 150 155 160
 Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
 165 170 175
 Ala Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
 180 185 190
 Gly Pro Ile Phe Ser Glu Gln Met Glu Ile Thr Met Arg His His Ala
 195 200 205
 Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Thr Pro
 210 215 220
 Glu Gln Val Arg Ser Gln Ala Pro Thr Pro Ala Met Glu Lys Ala Phe
 225 230 235 240
 Ser Gly Gly Cys Tyr Thr Ala Ile Ile Ser Pro Glu Gly Lys His Leu
 245 250 255
 Gly Glu Pro Leu Arg Asp Gly Glu Gly Met Val Ile Ala Asp Leu Asp
 260 265 270
 Phe Asp Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
 275 280 285
 Tyr Ala Arg Pro Glu Leu Leu Ser Leu Gln Leu Asp Asn Arg Ser Thr
 290 295 300
 Ala Pro Leu Thr Thr Ser Pro Val Ala Ala Ala Pro Ser Leu Ala
 305 310 315 320
 Glu Met Glu Ala Gln Arg Leu Ser Arg Tyr Leu Asp Ala Ser Ser Gly
 325 330 335
 Ser Ala Ala Gln Gly Ile Glu Ala Ala Tyr Ile Asn Ala Leu Ser Ser
 340 345 350
 Phe Ser Gly Lys Pro Ser
 355

<210> 327

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 327

atggttgatc	aaataacttaa	cgatcgttct	gaattattaa	cagtttggtt	ggcgcagatt	60
gtccaatct	ggctgaaccg	cgaaaaaaca	cttgcgaaag	tggttgagaa	agtaaatcaa	120
gctgcaaagc	aagattgtca	tcttggtgct	tttggtgaag	ctttggtccc	cggatatccc	180
ttttggattg	aacttacaga	tggcgcgcga	ttcaactcca	atgttcaaaa	agaaattcac	240
gogcactata	tggatcaggc	agtacagata	gagaatgggc	atttaaaagc	gctttgtgaa	300
acatogggccg	caaacaagat	tgccgtgatc	gttggttgca	ttgaacgcgc	agccgatcgc	360
ggcgggcaca	gcttatatgc	ttcattgggt	tttattaatc	ctcaaggggca	aatcggatcg	420
gtgcatcgca	aacttatgcc	aacttatgaa	gaacgtttta	cctggtcacc	tggcgatgga	480
catggtttgc	gaacgcatca	actaggtgct	ttcactgttg	gcggccttgaa	ttgttgggaa	540
aactggatgc	cattgccacg	cgccgcattg	tacgcacaag	gtgaagactt	tcatgtcgca	600
atctggccgg	gaagcattca	caatacgcaa	gatattacgc	gctatattgc	gaaggaatcc	660
agatogtttg	taatgtctac	ttccgggttc	atgcgtaaa	aagactttcc	atctgatacg	720
cctcacttag	acaaaatact	tgcaaaactct	ccgaatgtac	ttgcaaatgg	tggatcctgt	780
ctgcgcggac	cggacgggtca	gtggatcggt	gaaccatttg	tgaatgagga	aaaattagtt	840
gttgcgactg	tgaaccacaa	gcagggtccgt	gaagaaaagac	aaaattttga	tccggtcgga	900
cactattccc	gtcctgatgt	cacgcagttg	attgtgaaca	gacaaagaca	atcaacaatc	960
aagctcaacg	attaa					975

<210> 328

<211> 324

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 328

```

Met Val Asp Gln Ile Leu Asn Asp Arg Ser Glu Leu Leu Thr Val Gly
 1          5          10          15
Leu Ala Gln Ile Ala Pro Ile Trp Leu Asn Arg Glu Lys Thr Leu Ala
          20          25          30
Lys Val Val Glu Lys Val Asn Gln Ala Ala Lys Gln Asp Cys His Leu
          35          40          45
Val Ala Phe Gly Glu Ala Leu Val Pro Gly Tyr Pro Phe Trp Ile Glu
          50          55          60
Leu Thr Asp Gly Ala Arg Phe Asn Ser Asn Val Gln Lys Glu Ile His
          65          70          75          80
Ala His Tyr Met Asp Gln Ala Val Gln Ile Glu Asn Gly His Leu Lys
          85          90          95
Ala Leu Cys Glu Thr Ser Ala Ala Asn Lys Ile Ala Val Ile Val Gly
          100          105          110
Cys Ile Glu Arg Ala Ala Asp Arg Gly Gly His Ser Leu Tyr Ala Ser
          115          120          125
Leu Val Phe Ile Asn Pro Gln Gly Gln Ile Gly Ser Val His Arg Lys
          130          135          140
Leu Met Pro Thr Tyr Glu Arg Leu Thr Trp Ser Pro Gly Asp Gly
          145          150          155          160
His Gly Leu Arg Thr His Gln Leu Gly Ala Phe Thr Val Gly Gly Leu
          165          170          175
Asn Cys Trp Glu Asn Trp Met Pro Leu Pro Arg Ala Ala Leu Tyr Ala
          180          185          190
Gln Gly Glu Asp Phe His Val Ala Ile Trp Pro Gly Ser Ile His Asn
          195          200          205
Thr Gln Asp Ile Thr Arg Tyr Ile Ala Lys Glu Ser Arg Ser Phe Val
          210          215          220
Met Ser Thr Ser Gly Phe Met Arg Lys Glu Asp Phe Pro Ser Asp Thr
          225          230          235          240
Pro His Leu Asp Lys Ile Leu Ala Asn Ser Pro Asn Val Leu Ala Asn
          245          250          255
Gly Gly Ser Cys Leu Ala Gly Pro Asp Gly Gln Trp Ile Val Glu Pro
          260          265          270
Phe Val Asn Glu Glu Lys Leu Val Val Ala Thr Val Asn His Lys Gln
          275          280          285
Val Arg Glu Glu Arg Gln Asn Phe Asp Pro Val Gly His Tyr Ser Arg
          290          295          300
Pro Asp Val Thr Gln Leu Ile Val Asn Arg Gln Arg Gln Ser Thr Ile
          305          310          315          320
Lys Leu Asn Asp

```

<210> 329

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 329

```

gtgccggcca aagtaacgcgc cgccgccgtg cagctcagcc ccgtgctcatt cagccgtgaa      60
ggcaccgacca gcaaggtctg cgacaagatt gccgaggcgg cggcgagagg cgccgagctg      120
gtggtgtttc ccgaaaccgt agtgccgtat taccggtatt tctcgttcat caaggctccg      180

```

```

gccgtgatcg ggcgcgagca cttactcttg ctcgaacaag ccgtcacggt gcccgggccc 240
agcgctgaag ccacgcgaga agccgctcgc aaggcgggcg cggtgggttc gatcggcgtc 300
aacgaacgcg atcacggcac gctgtacaac acccagctgt tggtcgacgc cgacggtcgg 360
ttggcgcaag cccgcgcaa gatcaccccc acgtatcacg agcggatgat ctgggggacg 420
ggcgatggct cgggcttggg ggcggtggat acgcgagtcg gcaggattgg ctccctggcg 480
tgctgggagc actacaaccc gctggctcgc tatgcgctga tggccgacca cgagcaaatt 540
cacgtggcca tggtccctgg ctgcgctcgt ggcgacatct tccgcgagca aatcgaggtc 600
acgattcggc accacgcgct cgagtcgggc tgcttctgcg tcaacgcgac gggctacctg 660
agcgacgcgc aggtgacgca gatcgcgggc gacaccaagc tcgaccgcgc cctgcgcggc 720
ggttgcttca cgcgccatcg atcgccccgag ggcacgctgc tggcgccacc gctcaccgac 780
ggtgagggca tgggtcattgc cgacctcgat ctgtcgctca togcctaacg caaacgcgat 840
atggacagcg tcggccatta cagccggccc gagctgctca gcgtgctgat cgaccgctcg 900
ccgcagccgc atttgcgcga gaaaactgcc tctttaccgc aacctcggat gtcccatgaa 960
tcgctcgctc ccgatagtaa cggcctccgc gacgctgacg cgaaagcctc gaccctctcc 1020
tga 1023

```

<210> 330

<211> 340

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 330

```

Val Pro Ala Lys Val Arg Ala Ala Val Gln Leu Ser Pro Val Leu
1 5 10 15
Phe Ser Arg Glu Gly Thr Thr Ser Lys Val Cys Asp Lys Ile Ala Glu
20 25 30
Ala Ala Ala Gln Gly Ala Glu Leu Val Val Phe Pro Glu Thr Val Val
35 40 45
Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Lys Ala Pro Ala Val Ile Gly
50 55 60
Ala Glu His Leu Leu Leu Leu Glu Gln Ala Val Thr Val Pro Gly Pro
65 70 75 80
Ser Val Glu Ala Ile Ala Glu Ala Ala Arg Lys Ala Gly Ala Val Val
85 90 95
Ser Ile Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn Thr Gln
100 105 110
Leu Leu Phe Asp Ala Asp Gly Arg Leu Ala Gln Ala Arg Arg Lys Ile
115 120 125
Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ser
130 135 140
Gly Leu Val Ala Val Asp Thr Arg Val Gly Arg Ile Gly Ser Leu Ala
145 150 155 160
Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp
165 170 175
His Glu Gln Ile His Val Ala Met Phe Pro Gly Ser Leu Val Gly Asp
180 185 190
Ile Phe Arg Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu
195 200 205
Ser Gly Cys Phe Val Val Asn Ala Thr Gly Tyr Leu Ser Asp Ala Gln
210 215 220
Val Thr Gln Ile Ala Gly Asp Thr Lys Leu Asp Arg Ala Leu Arg Gly
225 230 235 240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Thr Leu Leu Ala Pro
245 250 255
Pro Leu Thr Asp Gly Glu Gly Met Val Ile Ala Asp Leu Asp Leu Ser
260 265 270
Leu Ile Ala Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
275 280 285

```

Arg Pro Glu Leu Leu Ser Val Leu Ile Asp Arg Ser Pro Gln Pro His
 290 295 300
 Leu Arg Glu Lys Thr Ala Ser Leu Pro Glu Pro Arg Met Ser His Glu
 305 310 315 320
 Ser Leu Ala Pro Asp Ser Asn Gly Leu Arg Asp Ala Asp Ala Lys Ala
 325 330 335
 Ser Thr Leu Ser
 340

<210> 331
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 331
 atgtccggaa caggacctat cggaccggtc gtgaagggtcg ccgtcgtaca agccgcgcca 60
 tgtctgctcg atcttgatgc gggcgctcgag aaggcgatcg ccttgatcga ccaagcgggc 120
 aaggctggcg cgcggtcat caattttccc gaaatttggc tgccgggtta tccttggtgg 180
 atctggctga atccaccgc catcaacatg cagtatgtcg cgccttacat gaacaactcc 240
 attgtcgtag gcagcaagca tgaccacgca cttcggggcg ccgcgcgccc caacaatatt 300
 cacgtcgtga tcggtgtctc cgagcgcgcc ggcggcagtc tgtacatggc tcagtggcac 360
 tatgggccc agggcgaggt gatctcgcgt cgctcgtaagc taaaaccac ccatgtcgaa 420
 cgcagcgtct ttggcgaagg cgacggcagc gacatgatcg ttactcagac cgatttcggg 480
 cgcgtcggcg cgctatgctg ttgggaacac ctgcaaccgc tgcgaaata cgcgctcttt 540
 tcccaggacg agcagattca ttgcgcggcg tggcccgtt tcagcctcta tgcaaaactc 600
 tcgaaggcct tcagccccga agtcagcgtc aacgtgaacc aaatctacgc cgtagaaggg 660
 caatgcttcg tcctgtcgtc gtgctcggtt atcgatcagg cgatctacga cacgttggtg 720
 cagaacgaat tgcaccagaa gttcctcgag gtggcgggg gctacagccg aatcttcggg 780
 ccgaacggtg cggaaattcg tgagaatctc ccaccgcgata gggaaggcct ggtggttgcc 840
 gatatcgatc tcggcctgat ctgcactcc aagagtgcg ctgatccggc tggtcactac 900
 gcgagggccc acgctctggc gctcatgcat aaccgtaatc cccgcggtcc gggtatcggg 960
 ttccggcgagg cgacgcgcaa ggttgccgac gcaactgccta aaggcgcgga acccgcgga 1020
 gcgctcgaag cggccgagtg a 1041

<210> 332
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 332
 Met Ser Gly Thr Gly Pro Ile Gly Pro Val Val Lys Val Ala Val Val
 1 5 10 15
 Gln Ala Ala Pro Cys Leu Leu Asp Leu Asp Ala Gly Val Glu Lys Ala
 20 25 30
 Ile Ala Leu Ile Asp Gln Ala Gly Lys Ala Gly Ala Arg Leu Ile Asn
 35 40 45
 Phe Pro Glu Ile Trp Leu Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asn
 50 55 60
 Pro Pro Ala Ile Asn Met Gln Tyr Val Ala Pro Tyr Met Asn Asn Ser
 65 70 75 80
 Ile Val Ala Gly Ser Lys His Asp His Ala Leu Arg Ala Ala Arg
 85 90 95
 Arg Asn Asn Ile His Val Val Ile Gly Val Ser Glu Arg Ala Gly Gly
 100 105 110
 Ser Leu Tyr Met Ala Gln Trp His Tyr Gly Pro Glu Gly Glu Val Ile

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 334

```

Met Ala Ile Glu His Pro Arg Tyr Arg Val Ala Ala Val Gln Ala Ala
 1           5           10           15
Pro Glu Phe Leu Asn Leu Glu Ala Thr Val Asp Lys Thr Ile Ala Leu
      20           25           30
Ile Glu Glu Ala Ala Arg Gly Gly Ala Ser Leu Ile Ala Phe Pro Glu
      35           40           45
Thr Trp Ile Pro Gly Tyr Pro Trp Phe Ala Trp Leu Gly Ala Pro Ile
      50           55           60
Trp Gly Met Lys Phe Ile Gln Ala Tyr His Asp Asn Ser Met Val Ile
      65           70           75           80
Asp Gly Ala Gln Phe Glu Arg Ile Ala Gln Ala Ala Ser Arg Cys Asn
      85           90           95
Ile Thr Val Val Leu Gly Phe Ser Glu Lys Asp Ala Gly Ser Leu Tyr
      100          105          110
Ile Ala Gln Ala Ile Leu Ser Pro Glu Gly Lys Thr Ile Ala Thr Arg
      115          120          125
Arg Lys Leu Lys Pro Thr His Val Glu Arg Ala Ile Phe Gly Glu Gly
      130          135          140
Asp Gly Ser Asp Leu Ala Val His Asp Thr Lys Leu Gly Arg Val Gly
      145          150          155          160
Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Met
      165          170          175
Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ala Trp Pro Ser Phe Ser
      180          185          190
Leu Tyr Val Asp Ala Ala Tyr Ala Leu Gly Pro Glu Val Asn Asn Ala
      195          200          205
Ala Ser Arg Leu Tyr Ala Val Glu Gly Gln Cys Phe Val Val Ala Pro
      210          215          220
Cys Ala Thr Val Ser Gln Lys Met Ile Asp Met Leu Cys Glu Thr Pro
      225          230          235          240
Glu Gln Gln Ala Leu Lys Pro Gly Gly Gly His Ala Gln Ile Tyr
      245          250          255
Gly Pro Asp Gly Arg Ser Leu Ala Asp Pro Leu Pro Pro Asp Ala Glu
      260          265          270
Gly Leu Leu Tyr Ala Asp Ile Asp Leu Ala Ala Ile Thr Leu Ala Lys
      275          280          285
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Gln
      290          295          300
Leu Leu Leu Asp Arg Asn Pro Lys Pro Arg Val Val His Ala Lys Pro
      305          310          315          320
Gly Gln Ser Ala Asn Asn Ser Ser Pro Gly Met Arg Ala Val Glu His
      325          330          335
Thr Glu Leu Glu Glu Gly Glu Gln Ala
      340          345

```

<210> 335

<211> 1053

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 335

atgactacgc gcgtgattaa agtcgctgcc gcgcagctgt ctccggtgct ggcaactgca

60

```

tcggagcaca gccgcgagga cacgattgcg aaagtgatcg acgccatcgc tgcggcgctcg      120
caacagggcg cgcaactgat tgtgtttccg gaaacagtcg ttccgtatta cccgtatttt      180
tcatttatca cgcccgcggt aacgatgggt gccgaacatt tgaaattgta cgaacaggca      240
gtgacggtac ccagcgcagc gacagatgct gtcgctgcgg cggcaaaaaa ttatggcatg      300
gtagtggtgc tcggaattaa tgaacgcgat cacgctcgcg tgtacaacgc gcaattaatt      360
ttcgacgccg atgggtgagct gctattaaag cgtcgaaaaa ttacgccgac ttatcacgaa      420
cgcatggtgt ggggacaagg cgacggcagc ggtttaaaag ttgtcgatac tgctgccggc      480
cgtgtcgggc cgctcgcggt ctgggaacat tacaaccgcg tcgcgcgtta cagcctgatg      540
gcacaacacg aagaaattca ttgcagtcaa tttccgggat cgttggtcgg ccctattttc      600
gccgaacaaa tggaaatcac catgcgtcat cacgcactcg aatccggctg ttttgtgggtg      660
aatgcaacgg octggcttag cgatacacaa atccaatcaa ttacccccga taaagccatg      720
cagaaagcac tgcgcggcgg ttgctacacc gcaatcatct cgcccgaagg caaacatctg      780
tgcccaccgc tgtatgacgg agaaggaata attgtggcgg aattggactt cgcgttaatc      840
accaaacgta aacgcatgat ggattccgtc ggccattacg cgcgaccaga actactttct      900
ttgtcctcgt atgatcgctg aactgcgcgg ctcaaaaact tacagacgac gatggcctct      960
gccaaatccg ctgaagatgg ttttccttta tttgcagacg ttttatatcc agacagttct    1020
ttcattgaga cgtcgaaatt cgcggagtca tga                                1053

```

<210> 336

<211> 350

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 336

```

Met Thr Thr Arg Val Ile Lys Val Ala Ala Ala Gln Leu Ser Pro Val
 1          5          10          15
Leu Ala Thr Ala Ser Glu His Ser Arg Glu Asp Thr Ile Ala Lys Val
          20          25          30
Ile Asp Ala Ile Ala Ala Ala Ser Gln Gln Gly Ala Gln Leu Ile Val
          35          40          45
Phe Pro Glu Thr Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr
          50          55          60
Pro Ala Val Thr Met Gly Ala Glu His Leu Lys Leu Tyr Glu Gln Ala
65          70          75          80
Val Thr Val Pro Ser Ala Ala Thr Asp Ala Val Ala Ala Ala Lys
          85          90          95
Asn Tyr Gly Met Val Val Val Leu Gly Ile Asn Glu Arg Asp His Gly
          100          105          110
Ser Leu Tyr Asn Ala Gln Leu Ile Phe Asp Ala Asp Gly Glu Leu Leu
          115          120          125
Leu Lys Arg Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp
          130          135          140
Gly Gln Gly Asp Gly Ser Gly Leu Lys Val Val Asp Thr Ala Ala Gly
145          150          155          160
Arg Val Gly Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg
          165          170          175
Tyr Ser Leu Met Ala Gln His Glu Glu Ile His Cys Ser Gln Phe Pro
          180          185          190
Gly Ser Leu Val Gly Pro Ile Phe Ala Glu Gln Met Glu Ile Thr Met
          195          200          205
Arg His His Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala
210          215          220
Trp Leu Ser Asp Thr Gln Ile Gln Ser Ile Thr Pro Asp Lys Ala Met
225          230          235          240
Gln Lys Ala Leu Arg Gly Gly Cys Tyr Thr Ala Ile Ile Ser Pro Glu
          245          250          255
Gly Lys His Leu Cys Pro Pro Leu Tyr Asp Gly Glu Gly Ile Ile Val
          260          265          270

```

Ala Glu Leu Asp Phe Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp
 275 280 285
 Ser Val Gly His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Leu Asp
 290 295 300
 Asp Arg Val Thr Ala Pro Leu Lys Asn Leu Gln Thr Thr Met Ala Ser
 305 310 315 320
 Ala Lys Ser Ala Glu Asp Gly Phe Pro Leu Phe Ala Asp Val Leu Tyr
 325 330 335
 Pro Asp Ser Ser Phe Ile Glu Thr Ser Lys Phe Ala Glu Ser
 340 345 350

<210> 337
 <211> 957
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 337
 atgaagggag tgtgtgccat gtcgacgaaa gttgccatcg tccaggcgcc gccggctcctg 60
 ctgcatcgcg acaggacgat tgcgaaggtg cgttcgtoga tgcaggatgc cgccaatgcg 120
 ggcgcctcgc tgatcgtatt tcccgaagct tatgtaccog gctatccgag ttggatcttg 180
 cgtctcaggc ccggaggcga catgggactg tcgtctgaga ttcacgcaag attgcgggaa 240
 aatgccgttg atctcgcgaa cggaggcctg gcgcatgtcc agggggctgc agcaaaattc 300
 ggcgcgactg tcgttatcgg catcaatgaa ctcgacagcg agttcagcgg aacgacattg 360
 ttcaacacccg tgggtggtcat cggccccgac ggaacgcgcc tcaacaggca tcgaaaatta 420
 atgccgacca acccggagcg catggtgttg ggcacgggcg atgcctcggg tctgcgtgtc 480
 atcgatacgc cggcgggacg gctgggaacc atgatctgct gggagagcta catgccgctg 540
 gcgcgctatg ctctctatgc gcaaggcatc gagatatacg tcgctccac gtgggacgca 600
 ggcgagagct ggattgctac gatgcgccac atcgccaagg aggcgggctg ctgggtgatc 660
 ggcacggcaa ccgtcatcca gggcagcgat gttccggacg attttccga acgcgacaag 720
 ctcttcaagc cggaggagtg gatcaacgac ggcgatgcgg tcgtggtcaa gcccatgggc 780
 gcgattgctg ccggaccgca caatcgacag aaaagcatac tctacgcga catcgaccgg 840
 gaggccgcgc ggcgagcccg ccggtcgcctc gatgtctgtg gccactattc ccgccagac 900
 gttttctott tctcggtcaa ccgaaagcca ttccgcctcg ccgactttgt gggttga 957

<210> 338
 <211> 313
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 338
 Met Lys Gly Val Cys Ala Met Ser Thr Lys Val Ala Ile Val Gln Ala
 1 5 10 15
 Pro Pro Val Leu Leu His Arg Asp Gly Arg Leu Arg Arg Cys Val Arg
 20 25 30
 Arg Ser Arg Met Pro Pro Met Arg Ala Pro Arg Ser Tyr Phe Pro Ala
 35 40 45
 Tyr Val Pro Gly Tyr Pro Ser Trp Ile Trp Arg Leu Arg Pro Gly Gly
 50 55 60
 Asp Met Gly Leu Ser Ser Glu Ile Thr Gln Asp Cys Gly Lys Met Pro
 65 70 75 80
 Leu Ile Ser Arg Thr Glu Ala Trp Arg Met Ser Arg Gly Leu Gln Gln
 85 90 95
 Asn Ser Ala Arg Leu Ser Leu Ser Ala Ser Met Asn Ser Thr Ala Ser
 100 105 110
 Ser Ala Glu Arg His Cys Ser Thr Val Val Val Ile Gly Pro Asp Gly

<220>
<223> Obtained from an environmental sample

<400> 340

```

Met Ser Gly Ser Phe Lys Val Ala Ala Val Gln Ala Ala Pro Ala Phe
 1          5          10          15
Leu Asn Leu Asp Ala Gly Ile Asp Gly Gly Gly Ala Asp Arg Ala Ser
 20          25          30
Arg Arg Ala Gly Arg Ser Ala His Arg Leu Ser Arg Asp Leu Val Ala
 35          40          45
Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ala Pro Ala Val Thr Met Gly
 50          55          60
Tyr Val Val Pro Tyr Asn Leu Asn Ser Arg Gly Gly Gln Pro Ala Gly
 65          70          75          80
Gln Ala Ser Gly Lys Cys Arg Ala Glu Gln His Pro Gly Gly Asp Gly
 85          90          95
Leu Ser Glu Arg His Asp Gly Thr Leu Tyr Ile Ala Gln Trp His Tyr
 100          105          110
Gly Glu Asp Gly Glu Val Ile Ala Thr Ala Gln Ala Gln Ala Asp Pro
 115          120          125
Cys Arg Thr His Gly Val Arg Gly Arg Arg Arg Gln Arg His Val Val
 130          135          140
Lys Asp Thr Ser Leu Gly Arg Val Gly Ala Leu Cys Cys Trp Glu His
 145          150          155          160
Leu Gln Pro Leu Asn Lys Thr Arg Cys Thr Pro Arg Thr Ser Arg Ser
 165          170          175
Thr Ser Val Pro Gly Pro Ala Ser Ala Ser Thr Arg Ala Ala Leu Cys
 180          185          190
Ala Trp Gly Arg Pro Gln His Gly Gly Lys Pro Asp Val Cys Gly Arg
 195          200          205
Gly Pro Val Leu Cys Ser Leu Pro Ala Pro Arg Ser Val Arg Thr Cys
 210          215          220
Ser Thr Cys Ser Ala Thr Arg Lys Ser Ser Ser Thr Gly Gly Gly
 225          230          235          240
Phe Ala Arg Ile Phe Gly Pro Asp Gly Ser Pro Met Gly Asn Val Leu
 245          250          255
Glu Glu His Glu Arg Ala Gly Asp Arg Arg Asn Arg Ser His His Asp
 260          265          270
Cys Asp Arg Gln Gly Gly Gly Pro Val Arg Ala Leu Phe Pro Ala Arg
 275          280          285
Cys Val Pro Thr Asp Val Gln Pro Glu Ala Lys Pro Gly Gly Asp Ala
 290          295          300
Ile Arg Lys Thr Trp Pro Ala Arg Leu Ser Arg Pro Pro Arg Ile Arg
 305          310          315          320
Ser Ala Gln Thr Gly Ser Gln Arg Asn
 325

```

<210> 341

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 341

```

atggcactga ccaacccaaa atataaagtc gccgccgtcc aggccgcgcc agcgttcctc      60
gatctggatg cgtccgtcga aaaagcggtc cggctgatcg acgaggccgg cgccaagggc      120
gcgcgcctca ttgcgttccc ggaaacctgg atccccggct atccctggtg gatctggctc      180
ggcgcgccgg cctgggcgat catgaaaggt tttgtctcgg cctatttcga caattcgctc      240
acctatgaca gtccggccgc ggacaaattg cgccaggccg ccaagcgcaa cgatatcgctc      300
gtggtgctcg gcctgtcggg gcgcgacggc ggcagtctct atatcgcgca atggatcatc      360
ggccccgacg gcgaaactgt cgccagcgc cgcaagctca agccgaccca tgtcgagcgt      420
tcggtgttcg gcgagggcga tggcagcgac cttgccgtgc atgagctcgc gatcggggcg      480

```

```

gtcggcgcgcg tgtgctgctg ggagcatctg caaccgctgt cgaaatacgc catgtatgcg      540
cagaacgagc aggttcacgt ggcggcctgg ccgagctttt cgctgtacga tccgttcgcc      600
catgccctcg gtgcggaggt caacaacgcc gccagcaaga tctacgcggt cgagggatcg      660
tgcttcgctg tggcaccctg cgccacogtt tcaaaggaaa tgatcgacct gttgtgcgac      720
acgccggaca agcacggtct gctgcacgcc ggcggcgggt ttgccgcgat ctacggccct      780
gacggctcgc cgatcggcga ccgcctggcg ccgcgaccagg aaggtctgat ctatgccgat      840
gtcgatctcg gcatgatctc ggtcgcgaag gccgcgcgg atccggccgg acattatgcg      900
cggccggatg tcacaagggt gctgctcaac aaacgcccgg gcaatcgtgt cgaggcgctg      960
gcacttcggg tggatcaggt tgcggcaggt gaggagatcc cctcgatatc gcgatcggcc     1020
agagggggtt ccgaactgcc aaacgcggcc gaatag                                1056

```

<210> 342

<211> 342

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 342

```

Met Ala Leu Thr Asn Pro Lys Tyr Lys Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Ala Phe Leu Asp Leu Asp Ala Pro Ser Lys Lys Arg Ser Gly Ser
      20          25          30
Thr Arg Pro Ala Pro Arg Ala Arg Ala Ser Leu Arg Ser Arg Thr Trp
      35          40          45
Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala Trp Ala
      50          55          60
Ile Met Lys Gly Phe Val Ser Pro Ile Ser Thr Ile Arg Ser Pro Met
      65          70          75          80
Thr Val Arg Pro Arg Thr Asn Cys Ala Arg Pro Pro Ser Ala Thr Tyr
      85          90          95
Arg Arg Gly Ala Arg Pro Val Gly Ala Arg Arg Arg Gln Ser Leu Tyr
      100          105          110
Arg Ala Met Asp His Arg Pro Thr Ala Lys Leu Ser Pro Ser Ala Ala
      115          120          125
Ser Ser Ser Arg Pro Met Ser Ser Val Arg Cys Ser Ala Arg Ala Met
      130          135          140
Ala Ala Thr Leu Pro Cys Met Ser Ser Arg Ser Gly Ala Ser Ala Arg
      145          150          155          160
Cys Ala Ala Gly Ser Ile Cys Thr Ala Val Glu Ile Arg His Val Cys
      165          170          175
Ala Glu Arg Ala Gly Ser Arg Gly Gly Leu Ala Glu Leu Phe Ala Thr
      180          185          190
Ile Arg Ser Pro Met Pro Ser Val Arg Arg Ser Thr Thr Pro Pro Ala
      195          200          205
Arg Ser Thr Arg Ser Arg Asp Arg Ala Ser Ser Trp His Pro Ala Pro
      210          215          220
Pro Phe Gln Arg Lys Ser Thr Cys Cys Ala Thr Arg Arg Thr His Gly
      225          230          235          240
Leu Leu His Ala Gly Gly Gly Phe Ala Ala Ile Tyr Gly Pro Asp Gly
      245          250          255
Ser Pro Ile Gly Asp Arg Trp Arg Pro Thr Arg Lys Val Ser Met Pro
      260          265          270
Met Ser Ile Ser Ala Ser Arg Ser Arg Arg Pro Pro Asp Pro Ala Gly
      275          280          285
His Tyr Ala Arg Pro Asp Val Thr Arg Leu Leu Leu Asn Lys Arg Pro
      290          295          300
Gly Asn Arg Val Arg Arg Trp His Phe Arg Trp Ile Arg Leu Arg Gln
      305          310          315          320
Val Arg Arg Ser Pro Arg Tyr Arg Asp Arg Pro Glu Gly Cys Arg Thr

```

325
Ala Lys Arg Gly Arg Ile
340

330

335

<210> 343
<211> 942
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 343
atgaagtcaa aaattgcggt tattcagcga cctcctgtat tgtttagacct tcaggcttca 60
atcgcccggt ccattacttc tgttgaggaa gcggcaggca agggatctga gctccttgtt 120
tttcccagaga catttctgcc tggttatccg tcttgatctt ggcgtctcaa gccgggcgga 180
gacatggtgc tgacatctga aatccacgca aaatatcgcg cgaactctgt tgatgttgag 240
cgcggggatc tggccctttt atgcgaagcg gcggcgaaac acggcggtcac aattgtcatg 300
gggctcagtg aaattgatgg gcgctacagc gggactacac tctttaatac agtggtgacc 360
attggcgcg aaggagagct ccttaataga caccgcaagc tcatgccgac aaacccagag 420
cgtaggtctt gggggcaagg ggatgcctct ggtctgcggg ttgtcgacac gcccggtggg 480
cgcgctggca cgctgatctg ctgggaaaac tacatgcgcg tatcgcgcta tgcgctttat 540
tctcaaaaca ttgacatcta tgtggcgccg acctgggacg cggggcgagag ctggatcgcc 600
tccatgcagc atatcgccaa agaaggtggc tgctgggtga tcggcacggc cacggcgatg 660
gagggctctg atgtcccagc cgacttcctt cagcgggagg tgcttttccc tgatagcagc 720
gaatggatca atgacgggtga cgctgtagtg gttaaaccga tgggggagat tgtcgcgggg 780
ccgcatcacc gggataagag tattctctat gctgagattg acgtcgaagt ggcacgcaat 840
gcgcggcgct cgctcgatgt ggcggggcat tactcccggc cggatatttt ttcctttggc 900
gtggatcgcc ggcctttgcc gccggttacg tttgaggatt ga 942

<210> 344
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 344
Met Lys Ser Lys Ile Ala Val Ile Gln Arg Pro Pro Val Leu Leu Asp
1 5 10 15
Leu Gln Ala Ser Ile Ala Arg Ala Ile Thr Leu Leu Arg Lys Arg Gln
20 25 30
Ala Arg Asp Leu Ser Ser Leu Phe Phe Pro Arg His Phe Cys Leu Val
35 40 45
Ile Arg Pro Gly Ser Gly Val Ser Ser Arg Ala Glu Thr Trp Cys His
50 55 60
Leu Lys Ser Thr Gln Asn Ile Ala Arg Thr Leu Asp Val Glu Arg Gly
65 70 75 80
Asp Leu Ala Pro Leu Cys Glu Ala Ala Ala Lys His Gly Val Thr Ile
85 90 95
Val Met Gly Gln Asn Trp Ala Leu Gln Arg Asp Tyr Thr Leu Tyr Ser
100 105 110
Gly Asp His Trp Arg Gly Arg Arg Leu Leu Asn Arg His Arg Lys Leu
115 120 125
Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly Gln Gly Asp Ala Ser
130 135 140
Val Cys Gly Leu Ser Thr Arg Pro Trp Ala Ala Ser Ala Arg Ser Ala
145 150 155 160
Gly Lys Thr Thr Cys Arg Tyr Arg Tyr Ala Leu Tyr Ser Gln Asn Ile
165 170 175

```

Asp Ile Tyr Val Ala Pro Thr Trp Asp Ala Gly Glu Ser Trp Ile Ala
      180      185      190
Ser Met Gln His Ile Ala Lys Glu Gly Gly Cys Trp Val Ile Gly Thr
      195      200      205
Ala Thr Ala Met Glu Gly Ser Asp Ser Gln Pro Thr Ser Leu Ser Gly
      210      215      220
Arg Cys Phe Ser Leu Ile Ala Ala Asn Gly Ser Met Thr Val Thr Leu
      225      230      235      240
Trp Leu Asn Pro Trp Gly Arg Leu Ser Arg Val Arg Ile Thr Gly Ile
      245      250      255
Arg Val Phe Ser Met Leu Arg Leu Thr Arg Ser Gly Thr Gln Cys Ala
      260      265      270
Ala Leu Ala Arg Cys Gly Gly Ala Leu Leu Pro Ala Gly Tyr Phe Phe
      275      280      285
Leu Trp Val Asp Arg Arg Pro Leu Pro Pro Val Thr Phe Glu Asp
      290      295      300

```

<210> 345

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 345

```

atgaaagcga tcaaggccgc tgccgtgcag gcagcaccgg tattcctgaa cctcgacgca      60
tcgatcacca aggcggaaac attcgtcgcc gaggccgccg cgaatggtgc caagctggtg      120
gcggtttccgg aaacctgggt gccgggctat ccctggttca tctggctcgg tgcgcccgcc      180
gaaggcatgc agttcatccc gcgctatcac gaaaacagca tggagctcgg ctgcgccgag      240
atgcgcogct tgcaggcgat cgcgcgcaag tatgaagtga cgctcgatcat gggctattcc      300
gagcgcgatg gtggcagccg ctacatgtcc caggtcatta ttggcgatca gggcgacatc      360
cttctcaatc gccgtaaatt gaagccaacc catgtcgagc ggacggtcct cggcgaaggc      420
gacggttcgg acctggtggt ggtcgaaacg gcattcggca ggctcgggtg gctcaattgc      480
tgggaaacata tccagccgct cgtcaagatg tcgatgtatg cccagcatga ggaaatccat      540
gtcgcggggtt ggccgagctt ctgcgtctac cgcatctcgg cctatgccct gggaccggaa      600
gtcaacaatg ccgtcagtca ggtctatgcc gtggagggtg gcgcctatgt tctggcacc      660
tgtgcgatcg taagccagga gatgttcgac attctggccg acaagcctga aaaggccttt      720
ctcctcaatc cccgcacatc caagcccggc ggtggcttca cgcagatcta tgcgccgat      780
ggtcgaccgc tttgcgagcc gcttgccgac gatgtggaag gcacacctta tgccgatctc      840
gatccggcaa cgatcgccgt cgcgaaaggc gccgccgatc ctgcggggca ctattcgcg      900
ccggacgcac tctcgctggt gatcaatcgc gaaaagcgcg cggtgatggc tgaaatcaac      960
gcgccggcga cgccgacctt cacccccac tccctggacg ctgcggagta g      1011

```

<210> 346

<211> 329

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 346

```

Met Lys Ala Ile Lys Ala Ala Ala Val Gln Ala Ala Pro Val Phe Leu
  1           5           10          15
Asn Leu Asp Ala Ser Ile Thr Lys Ala Glu Thr Phe Val Ala Glu Ala
      20      25      30
Ala Ala Asn Gly Ala Lys Leu Val Ala Phe Pro Glu Thr Trp Leu Pro
      35      40      45
Gly Tyr Pro Trp Phe Ile Trp Leu Gly Ala Pro Ala Glu Gly Met Gln
      50      55      60

```

<210> 348
 <211> 297
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 348
 Met Lys Val Ala Ala Ile Gln Ala Ala Pro Val Tyr Leu Asp Arg Gln
 1 5 10 15
 Ala Thr Leu Glu Lys Ala Leu Ser Trp Met Lys Arg Pro Gln Thr Ala
 20 30
 Pro Lys Ser Ala Pro Ser Leu Arg Pro Ser Ser Arg Ala Ile Pro Trp
 35 40 45
 Met Asp Leu Thr Asp Gly Ala Lys Trp Asn Asp Asp Lys Gln Lys Ala
 50 55 60
 Ala Tyr Ala Cys Tyr Val Asp Ala Ala Val Glu Ala Asp Gly Pro Glu
 65 70 75 80
 Leu Gln Ala Ile Ala Lys Lys Ser Lys Ala Leu Gly Leu Phe Thr Ile
 85 90 95
 Trp Ala Trp Ser Asn Ala Arg Arg Arg Pro Gly Gln Tyr Ile Val Pro
 100 105 110
 Ser Leu Pro Ser Ile Pro Thr Arg Val Ser Ser Ala Tyr Thr Glu Asn
 115 120 125
 Ser Cys Pro Pro Thr Pro Ser Ala Ser Cys Gly Ala Lys Ala Thr Asp
 130 135 140
 Thr Asp Ser Arg Cys Met Asn Ser Pro Ala Ser Lys Ser Ala Arg Thr
 145 150 155 160
 Ala Gly Lys Ile Gly Cys Pro Ala Arg Tyr Ala Met Tyr Ala Gln Gly
 165 170 175
 Glu Gln Leu His Val Ala Thr Trp Pro Gly Ser Pro Trp Leu Thr Lys
 180 185 190
 Asp Ile Thr Arg Phe Ile Ala Leu Glu Gly Arg Ile Tyr Val Met Ser
 195 200 205
 Val Gly Gly Val Leu Ser Ala Asn Asp Ile Pro Asp Ser Phe Pro Leu
 210 215 220
 Lys Thr Asp Leu Leu Lys Ile Arg Asp Arg Tyr Leu Ser Gly Gly Thr
 225 230 235 240
 Asp Ser Arg Pro Arg Arg His His Pro Arg Arg Pro Arg Gln Lys Arg
 245 250 255
 Arg Asp His Thr Leu Arg Gly Leu Asp Leu Asn Thr Val Leu Gln Glu
 260 265 270
 Arg Gln Asn Phe Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Ser
 275 280 285
 Asn Trp Lys Ser Thr Lys Ile Asp Asp
 290 295

<210> 349
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 349
 atgacgtccc ctgttcaaac caagtacaaa gtgcgctgtg ttcaggcggc gcccgagttt 60
 ctcgatctcg acaaaggcgt tgccaaagcg gtgcgcctga tcgaagaagc cgccacccaa 120
 aaggcctcgc tgatcgcggt tcccgaagtc tggctccccg gctatccgtg gtggatctgg 180
 ctcgactcgc cggcctgggg cttgcagttc gtccagcgct acttcgaaaa cgctctggtc 240

```

gtcggcagcc cccaatggga gcgcttgtgc aaggccgccg ccgacaacaa tatccatggt 300
gtgctcggat tctccgaacg ggacggcagc acgctgtacc tcgcacaggc catcatcgat 360
aacaccggga aggtgatcgc cagcgggcgc aaactcaagc caacacacgc cgaacgcacg 420
gttttcggcg aaggcgacgg gagccacatc gcggtgcatg aaaccacttt gggccgcatg 480
ggtgcactct gctgcgccga gcacatccag ccactgacca agtacgccat gtactcgag 540
cacgagcaga ttcacattgc cgcattggcc agcttctcgg tctaccgcgg agcagcgttc 600
cagctgagcg ccgaagccaa caacgccgcg agccaggctc atgccctgga gggcagttgc 660
tacgtggtgg ccccttgccg gacggtgtcc aaggagatgt tggacatgct ggctgattcg 720
ccgcaaaaga agcagctcct gctggaaggc ggtggctacg ccatgattta tgggcccgac 780
gccaagcccc tgtgcgagcc cattccagag acagaagaag gcattcttta cgcagatgtg 840
gacctgggct tcatcggtgt caccaaggca gcgtatgacc ccgccggtca ctattcacgc 900
cccgacgtgc tgcgcctttt gttcaatcgg aagcctgccc ctcggttca cgatttcgat 960
cctgaataca cggccaccga gcagaagaca gacgcggcct ga 1002

```

<210> 350
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 350

Met	Thr	Ser	Pro	Val	Gln	Thr	Lys	Tyr	Lys	Val	Ala	Cys	Val	Gln	Ala
1				5					10					15	
Ala	Pro	Glu	Phe	Leu	Asp	Leu	Asp	Lys	Gly	Val	Ala	Lys	Ala	Val	Arg
			20					25					30		
Leu	Ile	Glu	Glu	Ala	Ala	Thr	Gln	Lys	Ala	Ser	Leu	Ile	Ala	Phe	Pro
		35					40					45			
Glu	Val	Trp	Leu	Pro	Gly	Tyr	Pro	Trp	Trp	Ile	Trp	Leu	Asp	Ser	Pro
	50					55					60				
Ala	Trp	Gly	Leu	Gln	Phe	Val	Gln	Arg	Tyr	Phe	Glu	Asn	Ala	Leu	Val
65					70					75					80
Val	Gly	Ser	Pro	Gln	Trp	Glu	Arg	Leu	Cys	Lys	Ala	Ala	Ala	Asp	Asn
				85					90					95	
Asn	Ile	His	Val	Val	Leu	Gly	Phe	Ser	Glu	Arg	Asp	Gly	Ser	Thr	Leu
			100					105					110		
Tyr	Leu	Ala	Gln	Ala	Ile	Ile	Asp	Asn	Thr	Gly	Lys	Val	Ile	Ala	Thr
		115					120						125		
Arg	Arg	Lys	Leu	Lys	Pro	Thr	His	Ala	Glu	Arg	Thr	Val	Phe	Gly	Glu
		130				135					140				
Gly	Asp	Gly	Ser	His	Ile	Ala	Val	His	Glu	Thr	Thr	Leu	Gly	Arg	Met
145					150					155					160
Gly	Ala	Leu	Cys	Cys	Ala	Glu	His	Ile	Gln	Pro	Leu	Thr	Lys	Tyr	Ala
				165					170					175	
Met	Tyr	Ser	Gln	His	Glu	Gln	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe
			180					185					190		
Ser	Val	Tyr	Arg	Gly	Ala	Ala	Phe	Gln	Leu	Ser	Ala	Glu	Ala	Asn	Asn
		195					200					205			
Ala	Ala	Ser	Gln	Val	Tyr	Ala	Leu	Glu	Gly	Ser	Cys	Tyr	Val	Val	Ala
	210					215					220				
Pro	Cys	Ala	Thr	Val	Ser	Lys	Glu	Met	Leu	Asp	Met	Leu	Ala	Asp	Ser
225					230					235					240
Pro	Gln	Lys	Lys	Gln	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Ala	Met	Ile
				245					250					255	
Tyr	Gly	Pro	Asp	Ala	Lys	Pro	Leu	Cys	Glu	Pro	Ile	Pro	Glu	Thr	Glu
			260					265					270		
Glu	Gly	Ile	Leu	Tyr	Ala	Asp	Val	Asp	Leu	Gly	Phe	Ile	Gly	Val	Thr
		275					280					285			
Lys	Ala	Ala	Tyr	Asp	Pro	Ala	Gly	His	Tyr	Ser	Arg	Pro	Asp	Val	Leu
	290					295					300				

Arg Leu Leu Phe Asn Arg Lys Pro Ala Pro Arg Val His Asp Phe Asp
 305 310 315 320
 Pro Glu Tyr Thr Ala Thr Glu Gln Lys Thr Asp Ala Ala
 325 330

<210> 351
 <211> 936
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 351
 atgattacag caggcatcgc agtcgccgct ccggtggtgt tggacaaaac aaaaaccatt 60
 gagaaagccg ttggcattat tcacgaggca gcgggtaagg gtgtgaacct gcttgtgttt 120
 cccgagggcat ttattccctc ctatcccgcc tgggggttggc gcctgcgtcc cgggtggagat 180
 ttccgggttgt gcgaggagtt gcacgccctg ttgcttgata attcggtaaa tttgcaaggt 240
 gatgacctgg accctgtccg gggcgctgca gccgagcatt caatgaccgt ggtgatggga 300
 ttgaatgagc gcgaaggcca gttcggtcgg gctaccctgt ttaacgccat ggtattttatc 360
 ggtccgggacg gcagcatcct gaaccatcat cggaactta tgccaaccaa tcatgagcgt 420
 acgattcatg gcttcggcga tgcgcgggga ttgaaagtgg tggatacccc gtgcggtcgc 480
 gtgggtggtc tgatttgctg ggagaatttc atgcccctgg ctgcgtacgg cctgtatgcc 540
 cagggcgtag aagtgtatgt tgcgccacc tacgaccagg gtgatgggtg gataggatcc 600
 atgcagcata ttgcccggga aggacggtgc tgggtgttat cggccggaac accgctacgc 660
 ggcagtgatt ttcccgcgga catgccgggc aaggctcaac tgtttccga tgacgatgaa 720
 tgggtgaatc ccggtgggtc agtggttatc gcaccgggtg gggaattagt ggctggaccg 780
 cttttccgtg aggagggcat ccttgtctgt gaattggatc cggcgaaaag tgctcatgcc 840
 aagcggtcct ttgacgtggc cggtcattac gccaggccag atattttcga gttggaaata 900
 gaccgtgatc cacaggatcc cgtcgagtgg gactga 936

<210> 352
 <211> 301
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 352
 Met Ile Thr Ala Gly Ile Ala Val Ala Ala Pro Val Val Leu Asp Lys
 1 5 10 15
 Thr Lys Thr Ile Glu Lys Ala Val Ala Leu Phe Thr Arg Gln Arg Val
 20 25 30
 Arg Val Thr Cys Leu Cys Phe Pro Arg His Leu Phe Pro Pro Ile Pro
 35 40 45
 Pro Gly Val Gly Ala Cys Val Pro Val Glu Ile Ser Gly Cys Ala Arg
 50 55 60
 Ser Cys Thr Pro Cys Cys Leu Ile Ile Arg Asn Leu Gln Gly Asp Asp
 65 70 75 80
 Leu Asp Pro Val Arg Gly Ala Ala Ala Glu His Ser Met Thr Val Val
 85 90 95
 Met Gly Glu Ala Arg Arg Pro Val Arg Ser Gly Tyr Pro Val Arg His
 100 105 110
 Gly Ile Tyr Arg Ser Gly Arg Gln His Pro Glu Pro Ser Ser Glu Thr
 115 120 125
 Tyr Ala Asn Gln Ser Ala Tyr Asp Ser Trp Leu Arg Arg Cys Ala Gly
 130 135 140
 Ile Glu Ser Gly Gly Tyr Pro Val Arg Ser Arg Gly Trp Ser Asp Leu
 145 150 155 160
 Leu Gly Glu Phe His Ala Pro Gly Ser Leu Gly Leu Tyr Ala Gln Gly

```
<210> 353
<211> 1035
<212> DNA
<213> Psuedomonas putida ATCC 700801
```

```
<210> 354
<211> 312
<212> PRT
<213> Psuedomonas putida ATCC 700801
```

Page 231

Leu Trp Leu Gln Arg Thr Leu Val Trp His Pro Leu Pro Arg Ser Ser
 100 105 110
 Asn Tyr Arg Gln Arg Glu Ser Asn Trp Tyr Ala Pro Ala Gln Ala His
 115 120 125
 Pro Cys Ala Tyr Cys Leu Arg Gly Arg Gln Pro Gln Gly Phe Gln Phe
 130 135 140
 Ala Thr Trp Lys Gly Arg Cys Thr Leu Leu Arg Arg Ala Arg Thr Thr
 145 150 155 160
 Thr Leu Glu Val Cys Asp Val Gln Pro Ala Ala Val Ala His Cys Leu
 165 170 175
 Leu Ala Glu Leu Leu Gly Ile Ser Arg Trp Arg Ile Ser Thr Glu Arg
 180 185 190
 Gly Leu Arg Gly His Pro Ser Leu Cys Ser Arg Pro Val Leu Arg Asn
 195 200 205
 Phe Ser Met Arg Asn Val Ser Lys Asp Met Leu Asn Val Leu Ile Asp
 210 215 220
 Thr Pro Asp Lys Gly Asn Leu Leu Gln Asp Gly Gly Gly Phe Ala Met
 225 230 235 240
 Ile Tyr Gly Pro Asp Gly Ala Pro Leu Cys Glu Pro Leu Gly Glu His
 245 250 255
 Glu Glu Gly Ile Leu Tyr Arg Arg Arg Phe Gly Arg His Phe Arg Ser
 260 265 270
 Ser Gly Thr Arg Pro Gly Trp Pro Leu Leu Ala Ala Arg Cys Leu Arg
 275 280 285
 Leu Leu Phe Asn Asp Gln Pro Thr Pro Cys Val Glu Ala Phe Asn Pro
 290 295 300
 Ala Pro Val Gly Thr Asp Ala Pro
 305 310

<210> 355

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 355

atggccgtct	ctaaagacgg	tactgtttca	ggaaagtgcg	ctatccgatt	gcatgtcgcc	60
gcgatacaga	tggtcccaaa	gctgggtgac	gcgcaggcga	acgtgaatca	ggcagaagcc	120
cttattcggg	aggctcttgg	gctgggtgog	cggttgatcg	tgttaccaga	gatgtttacc	180
tccggtgcgg	cgtttcatcc	cgacatgctc	aaagccattc	agccattcga	tggcgccccca	240
ctccagttgc	tgaaagacct	ttctcgcaag	ggcaatgctg	tcacggcgcg	ctcgtttctc	300
gccaagcgtg	ggcaacaagt	attcaatacc	ttcgttttgg	tttctccgga	cgggtcagtc	360
gtaacgcatg	acaaggattc	accgacctat	tgggaaaatt	gctattaccg	ggcggtacc	420
gatgatggcg	tggtgtctac	gcccattggc	ccggtcggct	ccgtcctctg	ttgggaatth	480
atccgctcaa	gaaccgcgag	acggctggcg	aacaagggtca	agatggtcgt	gggaggtcc	540
tgttggtgga	cgctccccga	tgatgctgat	ccagacagcc	cgcgagagc	cgtgaacctc	600
aagatgctgc	aagaagcgcc	ggttcgcatg	gocgggatgc	tggtgttcc	ggtatacat	660
ggctcccacg	cgggcagctt	cgaaggattc	ttcagtcggg	aacttgcgga	tgttccctat	720
aactcgacgt	acctgggcga	gacaatgatt	gtcgacgcgg	gtggccgggt	acttgcccgt	780
agagcgcaag	atgcaggcga	aggcgtggta	acggcagaag	tggttttgcc	cgacaagtcc	840
gtaccaagcg	aacccatccc	ggagactttc	tggattccca	aggaaatgcc	ggatgattgg	900
aaagaagcct	gggagcggtg	gttcgatacc	ggtgcgggatt	actacgagat	ggtgaccgcg	960
ccctttatca	agacgggtgt	gataaacgag	tacacaccgg	aatatcttag	gtag	1014

<210> 356

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 356

```

Met Ala Val Ser Lys Asp Gly Thr Val Ser Gly Lys Ser Pro Ile Arg
 1          5          10          15
Leu His Val Ala Ala Ile Gln Met Val Gln Ser Trp Val Thr Arg Arg
 20          25          30
Arg Thr Ile Arg Gln Lys Pro Leu Phe Gly Arg Leu Leu Gly Trp Val
 35          40          45
Arg Val Gly Ser Cys Tyr Gln Arg Cys Leu Pro Pro Val Arg Arg Phe
 50          55          60
Ile Pro Thr Cys Ser Lys Pro Phe Ser Phe Asp Gly Ala Pro Leu Gln
 65          70          75          80
Leu Leu Lys Asp Leu Ser Arg Lys Gly Asn Ala Val Ile Gly Gly Ser
 85          90          95
Phe Leu Gln Ala Trp Ala Thr Ser Ile Gln Tyr Leu Arg Phe Gly Phe
100          105          110
Ser Gly Arg Val Ser Arg Asn Ala Gln Gly Ser Pro Thr Tyr Trp Glu
115          120          125
Asn Cys Tyr Tyr Arg Gly Gly Thr Asp Asp Gly Val Leu Ser Thr Pro
130          135          140
Ile Gly Pro Ser Ala Pro Ser Ser Val Gly Asn Leu Ser Ala Gln Glu
145          150          155          160
Pro Arg Asp Gly Trp Arg Thr Arg Ser Arg Trp Val Gly Gly Ser Cys
165          170          175
Trp Trp Thr Leu Pro Asp Asp Ala Asp Pro Asp Ser Pro Arg Arg Ala
180          185          190
Val Asn Leu Arg Cys Cys Lys Lys Arg Arg Phe Ala Trp Arg Gly Cys
195          200          205
Trp Val Phe Arg Tyr Met Ala Pro Thr Arg Gln Leu Arg Arg Ile Leu
210          215          220
Gln Ser Gly Thr Cys Gly Cys Ser Leu Leu Asp Val Pro Gly Arg Asp
225          230          235          240
Asn Asp Val Asp Ala Gly Gly Arg Val Leu Ala Arg Arg Ala Gln Asp
245          250          255
Ala Gly Glu Gly Val Val Thr Ala Glu Gly Phe Ala Arg Gln Val Arg
260          265          270
Thr Lys Arg Thr His Pro Gly Asp Phe Leu Asp Ser Gln Gly Asn Ala
275          280          285
Gly Ile Gly Lys Lys Pro Gly Ser Val Gly Ser Ile Pro Val Arg Ile
290          295          300
Thr Thr Arg Trp Pro Arg Pro Leu Ser Arg Arg Val Thr Ser Thr His
305          310          315          320
Arg Asn Ile Leu Gly
325

```

<210> 357

<211> 951

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 357

```

atgacaaaac tagccatcgt acaaaaaccg ccagtctttc tggataagca aaaaaccatt      60
gagctggccg tcgccaacat tgaagaggcc gccgccaagg gtgccgatct cgtggtgttt      120
tctgaagctt tcattcccgg ctatcctgcc tggatctggc gtctacgccc cggcggtgac      180
tgggggcttt cagaagagtt gcaccagcgt ttgctgcgca atgccgtcaa tgtggactcc      240
gatgatctgg ctccgttggt tgaggtcgcc cgcaagcacg aactcaccat cgtttgcggt      300

```

```

atcgaggagc gtgacaacaa actaagtcaa acaaccttat ataacaccgt catcacgatt 360
ggtccccgatg gatcggttact gaacaaacat cgcaagctta tgcccaccaa cccggagcga 420
atgggtgtggg gggtttgggtga cgcattccggg ttaaaagtcg ttgataccaa tgctgggtcga 480
attggctcat taatgtgctg ggaaaattac atgccgctgg ctcgctatgc cctatatgca 540
caaggtgtcg agatctatat cgcaccgacc tacgacagcg gtgatggctg gataggcagc 600
atgcagcaca tcgcacgtga agggggctgt tgggtgggtg gatgtgggtg tctcatgaaa 660
ggcagtgata ttccagatga tttcccgagg aaatccacgt tgtatccaga tgcagatgaa 720
tgggtgaacc cgggtgattc tgtagtgata gcacccggcg gtgaaattat ggccggccca 780
atgaacagag agtccggtat tttgtatcac gagctagaca gagaaaaagt cagcaacgct 840
aaacgagcat tcgatgttgc cgggcattat tcacgtcccg atatctttca gctgcatgta 900
aatacacagg agcagtcacc ctgcgtattc gaaaataatt ccataactta a 951

```

<210> 358

<211> 300

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 358

```

Met Thr Lys Leu Ala Ile Val Gln Lys Pro Pro Val Phe Leu Asp Lys
 1          5          10          15
Gln Lys Thr Ile Glu Leu Ala Val Pro Thr Leu Lys Arg Pro Pro Pro
          20          25          30
Arg Val Pro Ile Ser Trp Cys Phe Leu Lys Leu Ser Phe Pro Ala Ile
          35          40          45
Leu Trp Ile Trp Arg Leu Arg Pro Gly Gly Asp Trp Gly Leu Ser Glu
          50          55          60
Glu Leu His Gln Arg Leu Leu Arg Asn Ala Val Asn Val Asp Ser Asp
          65          70          75          80
Asp Leu Ala Pro Leu Phe Glu Val Ala Arg Lys His Glu Leu Thr Ile
          85          90          95
Val Cys Gly Arg Gly Ala Gln Gln Thr Lys Ser Asn Asn Leu Ile His
          100          105          110
Arg His His Asp Trp Ser Arg Trp Ile Tyr Thr Asn Ile Ala Ser Leu
          115          120          125
Cys Pro Pro Thr Arg Ser Glu Trp Cys Gly Gly Leu Val Thr His Pro
          130          135          140
Leu Lys Val Val Asp Thr Asn Ala Gly Arg Ile Gly Ser Leu Met Cys
          145          150          155          160
Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Gln Gly
          165          170          175          180
Val Glu Ile Tyr Ile Ala Pro Thr Tyr Asp Ser Gly Asp Gly Trp Ile
          180          185          190          195
Gly Ser Ala Ala His Arg Thr Arg Gly Leu Leu Gly Gly Gly Met Trp
          195          200          205
Val Ser His Glu Arg Gln Tyr Ser Met Ile Ser Arg Arg Asn Pro Arg
          210          215          220
Cys Ile Gln Met Gln Met Asn Gly Thr Arg Val Ile Leu Thr Arg Arg
          225          230          235          240
Asn Tyr Gly Arg Pro Asn Glu Gln Arg Val Arg Tyr Phe Val Ser Arg
          245          250          255
Ala Arg Gln Arg Lys Val Ser Asn Ala Lys Arg Ala Phe Asp Val Ala
          260          265          270
Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu His Val Ile His Arg
          275          280          285
Ser Ser His Pro Ala Tyr Ser Lys Ile Ile Pro Leu
          290          295          300

```

<210> 359

<211> 1029

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 359

```

atggcaaacg tcgttcgtgc tgccggccgta cagttgagcc ctgttttggg tagtcgcgag      60
ggtacggtag agaaggtagt tgctgcgata cgtgacgccg cctcgcaggg cgcacagctg      120
tgcgttttcc cggagacggg tggtccctat tatccgtatt tctcgttcat tcggccgccc      180
gcccgcattg gcaaagacca catgcagctg tacgagcaag ctgtggtcgt gccttctccc      240
agcacgaacg cgattgccgc ggccggccaaa caacactcga tcgtcgtttc aatcggcgtc      300
aatgaacgcg atcacggtag gatatacaac acgcagttgt tggtcgatgc cgacgggaca      360
ctcgtgcaac ggcgtcgcaa gataaccccc acgttccacg agcgtatggt gtgggggtcaa      420
ggtgatgggt cgggtttgct ctgtgtcgac acacaaatcg ggccgatcgg tagcctgggt      480
tggtgggaac attacaatcc cttggcgctg tacgcattga tggccgatca cgaagagatc      540
cacgtcgcca tgtttcgggg ttcgatgggt ggtcagatct tcgccgatca aattcaggta      600
accattcgcc accacgcgct cgaaagcggc tgtttcgctg tcaacgctac ggggtatctg      660
agcaaggaaac aggtcgccca gttgtcaciaa ggcacgtcgc tcgacgcggc gttgaccggg      720
ggttgttaca ccgcgattgt atcgctgaa ggcgtcgtac tgggcgaacc gctcaccgac      780
ggcgaaggca tggtcgtggc ggatatggat ctcagcctca tcaccaaacy caaacgcgatg      840
atggatagcg tcgggcacta cagtcgcccg gaattgctgt ctctgctgat caatcgaacg      900
ccaaccacaa cggcggtcga cgtcgaattc aactccaatt ccgagtctca tcatgtcagc      960
aatacacgaa caccaaagcg cacaactggc ccacgttcga acctcaagt tgccgctgat     1020
cgcgagtaa                                     1029

```

<210> 360

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 360

```

Met Ala Asn Val Val Arg Ala Ala Val Gln Leu Ser Pro Val Leu
 1          5          10          15
Gly Ser Arg Glu Gly Thr Val Glu Lys Val Val Ala Ala Ile Arg Asp
 20          25          30
Ala Ala Ser Gln Gly Ala Gln Leu Cys Val Phe Pro Glu Thr Val Val
 35          40          45
Pro Tyr Ser Val Phe Leu Val His Ser Ala Ala Arg Gly His Gly Gln
 50          55          60
Arg Pro His Ala Ala Val Arg Ala Ser Cys Gly Arg Ala Phe Ser Gln
 65          70          75          80
His Glu Arg Asp Cys Arg Gly Gly Gln Thr Thr Leu Asp Arg Arg Phe
 85          90          95
Asn Arg Arg Met Asn Ala Ile Thr Val Arg Tyr Thr Thr Arg Ser Cys
100          105          110
Cys Ser Met Pro Thr Gly His Ser Cys Asn Gly Arg Lys Ile Thr Pro
115          120          125
Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly Leu
130          135          140
Arg Cys Val Asp Thr Gln Ile Gly Arg Ile Gly Ser Leu Ala Cys Trp
145          150          155          160
Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp His Glu
165          170          175
Glu Ile His Val Ala Met Phe Pro Gly Ser Met Val Gly Gln Ile Phe
180          185          190
Ala Asp Gln Ile Gln Val Pro Phe Ala Thr Thr Arg Ser Lys Ala Ala

```

```

      195              200              205
Val Ser Ser Ser Thr Leu Arg Gly Ile Ala Arg Asn Arg Ala Gln Leu
      210              215              220
Ser Gln Gly Thr Ser Leu Asp Ala Ala Leu Thr Gly Gly Cys Tyr Thr
225              230              235              240
Ala Ile Val Ser Pro Glu Gly Val Val Leu Gly Glu Pro Leu Thr Asp
      245              250              255
Gly Glu Gly Met Val Val Ala Asp Met Asp Leu Ser Leu Ile Pro Asn
      260              265              270
Ala Asn Ala Trp Ile Ala Ser Gly Thr Thr Val Ala Arg Asn Cys Cys
      275              280              285
Leu Cys Ser Ile Thr Pro Thr His Thr Ala Val Asp Val Glu Phe Asn
      290              295              300
Ser Asn Ser Glu Ser His His Val Ser Asn Thr Arg His Gln Ser Ala
305              310              315              320
Gln Leu Ala His Val Arg Thr Phe Lys Leu Pro Leu Ile Ala Ser
      325              330              335

```

<210> 361
 <211> 951
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 361
atgctaaacg agaacaatgg cgctactttc aaggttgctg ccgtgcaggc ttcaccggta      60
tttcttgatc gcgctgctac aatcgacaag gcttgcgatt taattgctac ggccggacgc      120
gagggggctc gcctgatcgt ctttccagaa gcgttcgtcc cggcctatcc tgattgggta      180
tgggcgattc ccgcggtgga tgagggcatg ctcaatgagc tgtatgcaga attacttgcc      240
aatgctgtca ccattcccag cgatgcgacc gagagggtgt gtcgcgcggc gcggcttgct      300
aatgcttacg tggatgatgg gatgagcgaa cgcaatgccg aagcgagtgg cgccagcctg      360
tataatacgc tgttgtatat tgatgcacag ggacaaatcc tgggaaagca ccggaagctg      420
gttccaacgg gcggcgagcg cctgggtatg gcacagggag atggcagcac cctggagggt      480
tacgatactc ctttgggaaa actcgggtggc ttaatctgct gggagaatta tatgccgtg      540
gcacgctata ctatgtatgc ctggggcacg caaatctaca ttgcagcgac gtgggatcgc      600
gggcagccat ggctatccac tttgcgacac attgctaaag agggcagagt atatgtgatc      660
ggctgttgta ttgctatgcg caaagatgat atccccgacc attacgcgat gaaggagaag      720
tattacgcgg aagaagacga gtggatcaat attggcgata gcgcaatcgt caatccagaa      780
ggggtattta ttgccgggcc agtgcgtaag caagaagaaa tcctctacgc cgagggttgac      840
ccgcgaatga tgcaggggcc aaagtggatg ctcgacgtgg caggacatta cgcgcgcccg      900
gatgtattcc agttgacggt gcacacggag aggcggcaga tgatccacta g      951

```

<210> 362
 <211> 302
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 362
Met Leu Asn Glu Asn Asn Gly Ala Thr Phe Lys Val Ala Ala Val Gln
1              5              10              15
Ala Ser Pro Val Phe Leu Asp Arg Ala Tyr Asn Arg Gln Gly Leu Arg
      20              25              30
Phe Asn Cys Tyr Gly Arg Thr Arg Gly Gly Ser Pro Asp Arg Leu Ser
      35              40              45
Arg Ser Val Arg Pro Gly Leu Ser Leu Gly Met Gly Asp Ser Arg Gly
      50              55              60

```

Gly His Ala Gln Ala Val Cys Glu Leu Leu Ala Asn Ala Val Thr Ile
 65 70 75 80
 Pro Ser Asp Ala Thr Glu Arg Leu Cys Arg Ala Ala Arg Leu Ala Asn
 85 90 95
 Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn Ala Glu Ala Ser Gly
 100 105 110
 Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Cys Thr Gly Thr Asn Pro Gly
 115 120 125
 Lys Ala Pro Glu Ala Gly Ser Asn Gly Arg Arg Ala Pro Gly Met Gly
 130 135 140
 Thr Gly Arg Trp Gln His Pro Gly Gly Leu Arg Tyr Ser Phe Gly Lys
 145 150 155 160
 Thr Arg Trp Leu Asn Leu Leu Arg Ile Ile Cys Arg Trp His Ala Ile
 165 170 175
 Leu Cys Met Pro Gly Ala Arg Lys Ser Thr Leu Gln Arg Arg Gly Ile
 180 185 190
 Ala Gly Ser His Gly Tyr Pro Leu Cys Asp Thr Leu Leu Lys Arg Ala
 195 200 205
 Glu Tyr Met Ser Ala Val Val Leu Tyr Ala Gln Arg Tyr Pro Arg Pro
 210 215 220
 Leu Arg Asp Glu Gly Glu Val Leu Arg Gly Arg Arg Arg Val Asp Gln
 225 230 235 240
 Tyr Trp Arg Arg Asn Arg Gln Ser Arg Arg Gly Ile Tyr Cys Arg Ala
 245 250 255
 Ser Ala Ala Arg Arg Ile Leu Tyr Ala Glu Val Asp Pro Arg Met Met
 260 265 270
 Gln Gly Pro Lys Trp Met Leu Asp Val Ala Gly His Tyr Arg Ala Arg
 275 280 285
 Met Tyr Ser Ser Arg Cys Thr Arg Arg Gly Gly Arg Ser Thr
 290 295 300

<210> 363

<211> 1053

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 363

atgccgaaaa agtcgaccgt ccgggtcgca gccgtccaga ttgcgccgga tctgacatcg 60
 cgggaaaaaga cgggtggcacg cgtgatcgag gogatcgccc aggcattccgc caaaggtgcg 120
 gagcttgttg tttttcccga gacctttgtg ccgtgggtatc cttatttctc gttcgtgttg 180
 cccccggtct tgtcgggcaa ggagcacctg ccggtctacg aagaggcggt tgcggtgcc 240
 agtgccgcca caagaagcgt agcggctgcc gctgcggaac atggcatcgt cgtggcgctt 300
 ggcgtcaacg agcgcgacta tggcacgctc tacaatacgc aactgctttt cgatgccgat 360
 ggcagtctga tcctgaagcg gcgcaagatc accccgactt tccacgagcg gatgatctgg 420
 ggccagggcg atgcctcagg cctgaaggtt gtcgacagcg ccattggccg catcggcgcg 480
 ctggcctgct gggaacacta caatccgcta gcccgctatg cgctgatggc gcagcacgag 540
 gaaatccaca ttgcgcagtt tcccggctcc atgggtcgggc cgatctttgc cgatcagatg 600
 gaggtgacga tccgccatca cgcgctggaa agcggctgct tcgtcgtcaa tgccacggga 660
 tggctgacgg atgatcagat cgtctcgatc acaccggata ccggcctgca aaaagcgctg 720
 cggggtggct gcatgacggc gatcatttcc cccgaaggca agcatctcgt gccgccgctc 780
 accgaaggtg aggggtatcct cgtcgccgat ctgcacatga gcctcattct caagcgcaag 840
 cgcctgatgg attcggtcgg ccaactatgcc cggcccgagt tgctgcacct cgtcatggac 900
 gcccgcccg ctgcgccgat gagggaatcg tccatgcccc ctgccttccc cggcgaaaca 960
 ttgacaaccg acatgaccga tggagaacag gatgcgtctt tcgacggaaa cgctgatcaa 1020
 cgaattgcag tccttcggag cccggctggt tga 1053

<210> 364

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 364

```

Met Pro Lys Lys Ser Thr Val Arg Val Ala Ala Val Gln Ile Ala Pro
 1          5          10          15
Asp Leu Thr Ser Arg Glu Lys Gly Gly Thr Arg Asp Arg Gly Asp Arg
      20          25          30
Pro Gly Ile Arg Gln Arg Cys Gly Ala Cys Gly Phe Ser Arg Asp Leu
      35          40          45
Cys Arg Gly Ile Leu Ile Ser Arg Ser Cys Cys Pro Arg Ser Cys Arg
      50          55          60
Ala Arg Ser Thr Cys Gly Ser Thr Lys Arg Arg Leu Arg Cys Gln Val
65          70          75          80
Pro Pro Gln Glu Ala Arg Leu Pro Leu Ala Asn Met Ala Ser Ser Trp
      85          90          95
Arg Leu Ala Ser Thr Ser Ala Thr Met Ala Arg Ser Thr Ile Arg Asn
      100          105          110
Cys Phe Ser Met Pro Met Ala Val Ser Ser Gly Ala Arg Ser Pro Arg
      115          120          125
Leu Ser Thr Ser Gly Ser Gly Ala Arg Ala Met Pro Gln Ala Glu Gly
      130          135          140
Cys Arg Gln Arg His Trp Pro His Arg Arg Ala Gly Leu Leu Gly Thr
145          150          155          160
Leu Gln Ser Ala Ser Pro Tyr Ala Leu Met Ala Gln His Glu Glu Ile
      165          170          175
His Ile Ala Gln Phe Pro Gly Ser Met Val Gly Pro Ile Phe Ala Asp
      180          185          190
Gln Met Glu Val Thr Ile Arg His His Ala Leu Glu Ser Gly Cys Phe
      195          200          205
Val Val Asn Ala Thr Gly Trp Arg Met Ile Arg Ser Ser Arg Ser His
210          215          220
Arg Ile Pro Ala Cys Lys Lys Arg Cys Gly Val Ala Ala Gly Asp His
225          230          235          240
Phe Pro Arg Arg Gln Ala Ser Arg Ala Ala Ala His Arg Arg Gly Tyr
      245          250          255
Pro Arg Arg Arg Ser Thr Ala Ser Phe Ser Ser Ala Ser Ala Trp Ile
      260          265          270
Arg Ser Ala Thr Met Pro Gly Pro Ser Cys Cys Thr Ser Ser Trp Thr
      275          280          285
Pro Gly Arg Leu Arg Arg Gly Asn Arg Pro Cys Pro Leu Pro Ser Pro
      290          295          300
Ala Lys Ile Asp Asn Arg His Asp Arg Trp Arg Thr Gly Cys Val Phe
305          310          315          320
Arg Arg Lys Arg Ser Thr Asn Cys Ser Leu Arg Ser Pro Ala Gly
      325          330          335

```

<210> 365

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 365

```

atgacaaagc tagccatcgt tcaaaaaccc cccgtctttc tggataaaga aaaaaccata      60
gcgaagacgg ttgattccat aaaagaggcc gcgacacaaa atgccgactt ggtcatcttc      120

```

```

accgaagcct tcattcccggg ctacccacc tggatatggc gacttaggcc aggcgctgat 180
tggggcctct cagaagagct gcacgagcag ttattgcgta acgcggtgag tatgggatcg 240
accgacctgg atccgcttta tgaagccgcc caacagcata acgtcactat tgtttgcggc 300
atcgtagaaa gagaccacca actcagccaa tcaaccctct acaacagcat ggtcgtcatt 360
gacacagacg gaacccttct caacaagcac cgcaaactca tgccaactaa tcccgaacgc 420
atggtgtggg gctttggcga cgcctcagga ctcaaagccg ttgcaacacc tgcaggccgc 480
atcagcacgt tgttgtgttg ggagaactac atgccattgg ccgatatgc tctgtatgca 540
caaggcgtgg aaatctatat cgcgccaact tacgacagtg gtgcgggttg gataggaagc 600
ttgcaacaca tagcacgcga aggtcgatgc tgggtcgtgg gctgtggcaa cctgattcag 660
gccagtgatc tgctgaaga cttcccgac aaggacaacc tctaccgga cgcagaagag 720
tggtgaacc cgggtgactc catagtcatt gcaccagacg gtgagattgt ggccggtcca 780
atgcacaaag agacaggaat tttgtactgc gagatagatc tggagaaagt cagaattgca 840
aaacgagcat tagacgtgac cgggcattat tcgcgaccgg acgttttcaa actgcatgtg 900
aatacccgac ctcaatcacc tgtggaattt gaaggtcagg agaccaacaa tccaacaaca 960
ggagaaagct catga 975

```

<210> 366

<211> 315

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 366

```

Met Thr Lys Leu Ala Ile Val Gln Lys Pro Pro Val Phe Leu Asp Lys
1      5      10      15
Glu Lys Thr Ile Ala Lys Thr Val Ile Pro Lys Arg Pro Arg His Lys
20     25     30
Met Pro Thr Trp Ser Ser Ser Pro Lys Pro Ser Ser Arg Ala Thr Thr
35     40     45
Trp Ile Trp Arg Leu Arg Pro Gly Ala Asp Trp Gly Leu Ser Glu Glu
50     55     60
Leu His Glu Gln Leu Leu Arg Arg Gly Glu Tyr Gly Ile Asp Arg Pro
65     70     75
Gly Ser Ala Leu Ser Arg Pro Thr Ala Arg His Tyr Cys Leu Arg His
85     90     95
Arg Arg Lys Arg Pro Pro Thr Gln Pro Ile Asn Pro Leu Gln Gln His
100    105    110
Gly Arg His His Arg Arg Asn Pro Ser Gln Gln Ala Pro Gln Thr His
115    120    125
Ala Asn Ser Arg Thr His Gly Val Gly Leu Trp Arg Ala Ser Gly Leu
130    135    140
Lys Ala Val Ala Thr Pro Ala Gly Arg Ile Ser Thr Leu Leu Cys Trp
145    150    155
Glu Asn Tyr Met Ile Gly Pro Ile Cys Ser Val Cys Thr Arg Arg Gly
165    170    175
Asn Leu Tyr Arg Ala Asn Leu Arg Gln Trp Cys Gly Leu Asp Arg Lys
180    185    190
Leu Ala Thr His Ser Thr Arg Arg Ser Met Leu Gly Arg Gly Leu Trp
195    200    205
Gln Pro Asp Ser Gly Ser Asp Leu Pro Glu Asp Phe Pro Asp Lys Asp
210    215    220
Asn Leu Tyr Pro Asp Ala Glu Glu Trp Val Asn Pro Gly Asp Ser Ile
225    230    235
Val Ile Ala Pro Asp Gly Glu Ile Val Ala Gly Pro Met His Lys Glu
245    250    255
Thr Gly Ile Leu Tyr Arg Asp Arg Ser Gly Glu Ser Gln Asn Cys Lys
260    265    270
Thr Ser Ile Arg Arg Asp Arg Ala Leu Phe Ala Thr Gly Arg Phe Gln
275    280    285

```

Thr Ala Cys Glu Tyr Pro Thr Ser Ile Thr Cys Gly Ile Arg Ser Gly
 290 295 300
 Asp Gln Gln Ser Asn Asn Arg Arg Lys Leu Met
 305 310 315

<210> 367
 <211> 981
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 367
 atgactgccc actttgccga taccctgacc gttgccgtgg cccagatcgc gccggtgtgg 60
 ctacagcgcg aagctaccct gcaaaagatg ctgggtctggg tggagcgcg cgcgcgcgaa 120
 ggcgcgggcc tggtcgcctt cagtgaaggc ctgctgcctg gctaccctt ctggattgaa 180
 cacacggacg gcgccgcctt cgagtcgccg ttacagaagc gcctgtacgc ccactactgc 240
 gatcagtcgg tccagatcaa tgctgggcac ctgcgaccac tctgcgctgc cgcgccaga 300
 caccagattt ggggtggtctg cggcgtcatc gagcgcgaca gcgcacgcgg actcagcgtg 360
 tttgcatcaa tggtcaccaa cgatgccgaa ggcgcgatcc gcagtgtgca ccgcaagctg 420
 atgccgacct acgaagaacg cctggtgtgg tcgcccggcg acgcgcacgg actgcgctgc 480
 catccgctcg gccagttccg cctcggcagc ctcaattgct gggagaactg gatgccgctg 540
 gcgcgcgcgc ccctgtacgc ccagggcgag tctttgcatg ttgcatcctg gcccggcagt 600
 cgccgcaaca ccgagaccaa tactcccttc atcgcccgcg aaggccgcag ttacgcgctg 660
 tccgccagtt ccgtgctgca ccgggatgat ctgcccgaact ccgttcgcgg gctgtcgggtg 720
 ctgcgcgact gcctgccgga cgtgatggcc gacggcggtc cctgcgtcgc cggccccgac 780
 ggacatttcc tgatcgagcc ggtcgtcggc cgggaagagc tgctgctcgc gcagatcgat 840
 catgccccggg tacgcgagga acgtcagaac ttcgaccctt tcggccacta ctgcggccgc 900
 gaactcctgt cgctggtggt ggatacgcg cgggcgagcg gagtgcagat agtgaatgct 960
 gaccatggct ttaagccctg a 981

<210> 368
 <211> 317
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 368
 Met Thr Ala His Phe Ala Asp Thr Leu Thr Val Ala Val Ala Gln Ile
 1 5 10 15
 Ala Pro Val Trp Leu Gln Arg Glu Tyr Pro Ala Lys Asp Ala Gly Leu
 20 25 30
 Gly Gly Ala Arg Arg Ala Arg Arg Gly Pro Gly Arg Leu Gln Gly
 35 40 45
 Pro Ala Ala Trp Leu Pro Leu Leu Asp Thr His Gly Arg Arg Pro Leu
 50 55 60
 Arg Val Ala Val Thr Glu Ala Cys Thr Pro Thr Thr Ala Ile Ser Arg
 65 70 75 80
 Ser Arg Ser Met Leu Gly Thr Ser His His Ser Ala Leu Pro Ala Arg
 85 90 95
 His Gln Ile Trp Val Val Cys Gly Val Ile Glu Arg Asp Ser Ala Arg
 100 105 110
 Gly Leu Ser Val Phe Ala Gln Trp Ser Pro Ser Met Pro Lys Ala Arg
 115 120 125
 Ser Ala Val Cys Thr Ala Ser Cys Arg Pro Thr Lys Asn Ala Trp Cys
 130 135 140
 Gly Arg Pro Ala Thr Arg Thr Asp Cys Ala Ala Ile Arg Ser Ala Ser
 145 150 155 160

Ser Ala Ser Ala Ala Gln Leu Leu Gly Glu Leu Asp Ala Ala Gly Ala
 165 170 175
 Arg Arg Pro Val Arg Pro Gly Arg Val Phe Ala Cys Cys Ile Leu Ala
 180 185 190
 Arg Gln Ser Pro Gln His Arg Asp His Tyr Ser Leu His Arg Pro Arg
 195 200 205
 Arg Pro Gln Leu Arg Ala Ser Ala Ser Ser Val Leu His Arg Asp Asp
 210 215 220
 Leu Pro Asp Ser Val Pro Ala Leu Ser Val Leu Arg Asp Cys Leu Arg
 225 230 235 240
 Thr Trp Pro Thr Ala Ala Pro Ala Ser Pro Ala Pro Thr Asp Ile Ser
 245 250 255
 Ser Ser Arg Ser Ser Pro Gly Arg Ala Ala Arg Ala Asp Arg Ser
 260 265 270
 Cys Pro Gly Thr Arg Gly Thr Ser Glu Leu Arg Pro Leu Gly His Tyr
 275 280 285
 Ser Arg Pro Glu Leu Leu Ser Leu Val Val Asp Thr Arg Arg Ala Ser
 290 295 300
 Gly Val Gln Ile Val Asn Ala Asp His Gly Phe Lys Pro
 305 310 315

<210> 369

<211> 1074

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 369

atgtccgaag	agaacaccac	caccgaatca	agctcggacg	cgatctggac	cgttgcggcc	60
gtccaggcgg	cgccggtgtt	cttgaatcgg	gatgcgacgg	tgcgtaaggc	cgtctcgctg	120
attgccgagg	ccgcggcgca	cgcgcgcggt	ctcattgttt	ttcccagggc	gttcattcca	180
tcgtaccocg	attgggcgtg	ggcgggtccc	cccgacaggg	gcggaaccaa	ctcgagactg	240
tatgccaaac	tgctcgacaa	ttcggttacg	gtgcccagcc	cagccaccga	tgccctggcc	300
agggcgggctc	gcgacgcggg	cgcctacgtc	gtcatgggca	taaacgagcg	gaacacggcg	360
gcgagcggcg	gaagtctcta	caacagcttg	ctctatatattg	gtccggacgg	tcgcatcctg	420
ggcattcatc	ggaagtgtgt	gccgacctcg	gcggagcggc	tgatctgggc	acaaggcgat	480
ggaagcacgc	ttggcgtgtt	cgatacgccg	ggcgcccgcc	ttggcggcct	gatctgctgg	540
gaaaactata	tgccgctggc	ccgatattcg	atgtacgcgc	gcggcggtgca	aatatatgtt	600
gcggcgacct	gggacagggg	cgagccatgg	ctttcgacgc	tgcgacacat	agccaaggaa	660
ggccagacct	acgtgatagg	ctgttgcatc	gccatgcgga	cggccgacat	cgacgacgcc	720
gagctcgtcg	agaagtatta	cgcggacgcc	ggtgagtgga	tcaatgaagg	cgacagcgcg	780
attgtcgatc	cgagcgggaac	aatcattgcc	ggtccggccc	atcagaccaa	tgaaatcctc	840
tacgccgcga	tcgatcgcca	gaaggtgctg	gaatcaaaaat	ggatgttgga	cgtggccggg	900
cactacgcgc	gtccggacgt	gttttcattt	ggcggttcgaa	ccgatgccaa	cccgataatg	960
accatgaacg	aaccaagcgc	gacggccgag	ccgaggcaca	atagcgcggg	agccgagggt	1020
cgcgacggcc	tacgcggggc	tcgtgaccct	cgctcgagaa	ttcggcagat	gtag	1074

<210> 370

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 370

Met Ser Glu Glu Asn Thr Thr Thr Glu Ser Ser Ser Asp Ala Ile Trp
 1 5 10 15
 Thr Val Ala Ala Val Gln Ala Ala Gly Val Leu Glu Ser Gly Cys Asp

20 25 30
 Gly Ala Gly Arg Leu Ala Asp Cys Arg Gly Arg Gly Ala Arg Ala Arg
 35 40 45
 Leu Ile Val Phe Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Ala
 50 55 60
 Trp Ala Val Pro Pro Gly Gln Ala Glu Pro Thr Arg Asp Cys Met Pro
 65 70 75 80
 Asn Cys Ser Thr Ile Arg Leu Arg Cys Pro Ala Gln Pro Pro Met Pro
 85 90 95
 Gly Gln Gly Gly Ser Arg Arg Gly Arg Leu Arg Arg His Gly His Lys
 100 105 110
 Arg Ala Glu His Gly Gly Ser Gly Gly Ser Leu Tyr Asn Ser Leu Leu
 115 120 125
 Tyr Ile Gly Pro Asp Gly Arg Ile Leu Gly Ile His Arg Lys Leu Cys
 130 135 140
 Arg Pro Arg Arg Ser Gly Ser Gly His Lys Ala Met Glu Ala Arg Leu
 145 150 155 160
 Ala Cys Ser Ile Arg Arg Ala Ala Gly Leu Ala Ala Ser Ala Gly Lys
 165 170 175
 Thr Ile Cys Arg Trp Pro Asp Ile Arg Cys Thr Arg Ala Val Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Lys Ala Arg Pro Thr Ala Val Ala Ser Pro Cys
 210 215 220
 Gly Arg Pro Thr Ser Thr Thr Pro Ser Ser Ser Arg Ser Ile Thr Arg
 225 230 235 240
 Thr Pro Val Ser Gly Ser Met Lys Ala Thr Ala Arg Leu Ser Ile Arg
 245 250 255
 Ala Glu Ile Ile Ala Gly Pro Ala His Gln Thr Asn Glu Ile Leu Tyr
 260 265 270
 Ala Ala Ile Asp Arg Gln Lys Val Leu Glu Lys Met Asp Val Gly Arg
 275 280 285
 Gly Arg Ala Leu Arg Ala Ser Gly Arg Val Phe Ile Trp Arg Ser Asn
 290 295 300
 Arg Cys Gln Pro Asp Asn Asp His Glu Arg Thr Lys Arg Asp Gly Arg
 305 310 315 320
 Ala Glu Ala Gln Arg Gly Ser Arg Val Ala Thr Ala Tyr Ala Gly Val
 325 330 335
 Val Thr Leu Ala Arg Glu Phe Gly Arg Cys
 340 345

<210> 371
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 371
 atgggtatcg aacatccgaa gtacaagggtt gcggtggtac aggcggcgcc ggccctggctc 60
 gatctcgacg catcgatcgc caagaccatc gcgctgatcg aggaggcggc cgccaagggc 120
 gccaaactga tcgcattccc tgaggccttc attcccggct atccttggca tatctggatg 180
 gactcgccgg cctgggcatg cgggcgcgga tttgtgcagc gctatttcga caattcgctt 240
 tcctacgaca gccgcagcgc cgaacggctg cggctcgcgg tgaagaaggc cggcatcacc 300
 gccgtgctcg gcctgtccga gcgggaaggc ggcagccttt atctcgcgca atggctgatc 360
 ggtcccgacg gcgagaccat cgccaagcgg cgcaagctgc ggccgacgca tgccgagcgc 420
 accgtctacg gcgaaggcga cggcagtgac cttgcgggtc atgaccgcgc tgacattggc 480
 cgtctcggcg cgctgtgctg ctgggaacat ctgcagccgc tgtcgaaata cgccatgtat 540
 gcccaaacg agcaggtgca tgtcgcggcc tggccgagtt tttcgctgta cgaccgcttc 600

```

gcgcgcggcgc tgggctggga ggtcaacaac gcggcatccc gcgtctatgc ggtcgaaggc 660
tcctgcttcg tgctggcgcc gtgtgccacc gtctcgcagg cgatgggtgga cgaactctgc 720
gaccgcgacg acaagcatgc gctgctgcat gtccggcgcg gccacgccgc gatctacgga 780
ccggacggca gctcgatggc gaacaagctc gatcccgagc aggagggcct gctgttcgcc 840
gacatcgatc tcggggcgat cgggggtggca aagaacgccg ccgatccggc cgggcactat 900
tcgcggccgg atgtgacccg tctgctcttg aacagaaaac cctcaaagcg cgtcgagcac 960
tttgcgctgc cgctcgacca tctcgcgac gagggcggtt ctccggtgac ctga 1014

```

<210> 372

<211> 327

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 372

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1      5      10      15
Pro Ala Trp Leu Asp Leu Asp Ala Arg Ser Pro Arg Pro Ser Arg Ser
20     25     30
Arg Arg Arg Pro Pro Arg Ala Pro Ser Ser His Ser Leu Ala Phe Ile
35     40     45
Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala Trp Ala Ile
50     55     60
Gly Arg Gly Phe Val Gln Ala Ile Ser Thr Ile Arg Phe Pro Thr Thr
65     70     75     80
Ala Arg Arg Pro Asn Gly Cys Gly Ser Arg Arg Arg Pro His His Arg
85     90     95
Arg Ala Arg Pro Val Arg Ala Gly Arg Arg Gln Pro Leu Ser Arg Ala
100    105    110
Met Ala Asp Arg Ser Thr Ala Arg Pro Ser Pro Ser Gly Ala Ser Cys
115    120    125
Gly Arg Arg Met Pro Ser Ala Pro Ser Thr Ala Lys Ala Thr Ala Val
130    135    140
Thr Leu Arg Ser Met Thr Ala Leu Thr Leu Ala Val Ser Ala Arg Cys
145    150    155    160
Ala Ala Gly Asn Leu Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ala Gln
165    170    175
Asn Glu Gln Val His Val Ala Ala Trp Pro Ser Phe Ala Val Arg Pro
180    185    190
Val Arg Ala Gly Ala Gly Leu Gly Gln Gln Arg Gly Ile Pro Arg
195    200    205
Leu Cys Gly Arg Gly Ser Cys Phe Val Leu Ala Pro Cys Ala Thr Val
210    215    220
Ser Gln Ala Met Val Asp Glu Leu Cys Asp Arg Asp Gln Ala Cys Ala
225    230    235    240
Ala Ala Cys Arg Arg Arg Pro Arg Arg Asp Leu Arg Thr Gly Arg Gln
245    250    255
Leu Asp Gly Thr Ser Ser Ile Pro Ser Arg Arg Ala Cys Cys Ser Pro
260    265    270
Thr Ser Ile Ser Gly Arg Ser Gly Trp Gln Arg Thr Pro Pro Ile Arg
275    280    285
Pro Gly Thr Ile Arg Gly Arg Met Pro Val Cys Ser Thr Glu Asn Pro
290    295    300
Gln Ala Arg Arg Ala Leu Cys Ala Ala Ala Arg Pro Ser Arg Gly Arg
305    310    315    320
Gly Arg Cys Ser Gly Asp Leu
325

```

<210> 373

<211> 1056
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 373
 atgacgaatt ttctggacgt gacggtggca gcggttcagg cggctcccgt ctatttcgat 60
 cgggaggcat cgacggagaa agcgtgccgg ttgatccacg aagcggcagg gctcggcgcg 120
 acgctcgag cgttcggcga aacctggttg ccagggtatc cgttcttcgt ctgggggttc 180
 ggcacaacc ggagcctgtt ctggcaggcc gccgccgagt acatcgccaa tgcggtggag 240
 attccgagtc ccacaacgga ccgtctctgt gcggcggcga aggctgccgg ggtcgacgtc 300
 gtcattggcg tcgttgaact ggatgaacga acacgagctt cggtttacag tacgtgctt 360
 ttcacgggtc gcgacgggac gatcctgggc cgccaccgca agctgaagcc aacacacatg 420
 gagcggacga tctggggcga aggggacgca tatggactcc gcgctctacga acgttcgtac 480
 gggcggtga gcggcctgaa ttgctgggaa cacaatatga tgctgcccgg ctacgtgctt 540
 gccgcacagg gcacgcagtt tcacgtcgcc gcatggcccg gaaaggagag gctcaccgtc 600
 ccgccgaacg aagcggctta tacgcgccag cttctcctct ctgcgcgcta tgcacccag 660
 gccggcgct acgtgatcag cgtcgccggg ctgctgcac cagactccat gcccgagcgt 720
 tatcgcgagt tagggcggtc atatgagttg accggcgaca gcgtcatcgt cgaccgcgc 780
 ggcgaggtca ttgccgggccc tgcaaaaggc gagaccatcc tgctcgcgca gtgcagtcag 840
 gaagctctoc tcgcggccaa gtccgccatc gacctcggcg gccattactc acgcccgat 900
 atctttcagc tgcgtgtcaa cgatcaactg cagcatcggg tccggagagt tgagccacac 960
 ttcacggcgg cgatcggaac tatcgagcc gagcgccgat cccaggagga tggtagtgg 1020
 cccttcgacc tggcggaatc tctcacgaac tcctag 1056

<210> 374
 <211> 351
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 374
 Met Thr Asn Phe Leu Asp Val Thr Val Ala Ala Val Gln Ala Ala Pro
 1 5 10 15
 Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile
 20 25 30
 His Glu Ala Ala Gly Leu Gly Ala Thr Leu Ala Ala Phe Gly Glu Thr
 35 40 45
 Trp Leu Pro Gly Tyr Pro Phe Phe Val Trp Gly Phe Ala His Asn Arg
 50 55 60
 Ser Leu Phe Trp Gln Ala Ala Glu Tyr Ile Ala Asn Ala Val Glu
 65 70 75 80
 Ile Pro Ser Pro Thr Thr Asp Arg Leu Cys Ala Ala Lys Ala Ala
 85 90 95
 Gly Val Asp Val Val Ile Gly Val Val Glu Leu Asp Glu Arg Thr Arg
 100 105 110
 Ala Ser Val Tyr Ser Thr Leu Leu Phe Ile Gly Arg Asp Gly Thr Ile
 115 120 125
 Leu Gly Arg His Arg Lys Leu Lys Pro Thr His Met Glu Arg Thr Ile
 130 135 140
 Trp Gly Glu Gly Asp Ala Tyr Gly Leu Arg Val Tyr Glu Arg Ser Tyr
 145 150 155 160
 Gly Arg Leu Ser Gly Leu Asn Cys Trp Glu His Asn Met Met Leu Pro
 165 170 175
 Gly Tyr Val Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp
 180 185 190
 Pro Gly Lys Glu Arg Leu Thr Val Pro Pro Asn Glu Ala Ala Tyr Thr

```

<400> 376
Met Thr Lys Ile Ala Val Ile Gln Glu Pro Pro Val Tyr Leu Asn Leu
 1          5          10          15
Ser Lys Ser Met Asp Arg Ala Val Asp Leu Ile Ala Asp Ala Ala Ser
 20          25          30
Gln Gly Cys Gln Leu Ile Val Phe Pro Glu Ala Trp Leu Ala Gly Tyr
 35          40          45

```

```

Pro Thr Phe Val Trp Arg Leu Ala Pro Gly Ser Gly Met Gly Lys Thr
 50      55      60
Asp Glu Leu Tyr Ala Arg Leu Leu Ala Asn Ser Val Asp Arg Ser Lys
 65      70      75      80
Glu Gly Leu Arg Pro Leu Gln Glu Ala Ala Lys Glu His Gly Val Val
      85      90      95
Ile Val Leu Gly Tyr Gln Glu Val Asp Gly Ser Gly Ser Ser Ser Thr
      100      105      110
Ile Phe Asn Ser Cys Ala Ile Ile Asp Ala Asp Gly Arg Leu Ala Asn
      115      120      125
Asn His Arg Lys Leu Met Pro Thr Asn Ala Glu Arg Met Val Trp Gly
      130      135      140
Phe Gly Asp Gly Ser Gly Leu Asn Val Val Asp Thr Ala Val Gly Arg
 145      150      155      160
Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
      165      170      175
Ala Leu Tyr Ala Gln Asn Ile Glu Ile Tyr Val Ala Pro Thr Trp Asp
      180      185      190
Ser Gly Ala Met Trp Gln Ala Thr Leu Gln His Ile Ala Arg Glu Gly
      195      200      205
Gly Cys Trp Val Ile Gly Cys Ala Thr Ser Leu Gln Ala Ser Asp Ile
      210      215      220
Pro Asp Asp Leu Pro His Arg Asp Glu Leu Phe Pro Asn Lys Asp Glu
 225      230      235      240
Trp Val Asn Pro Gly Asp Ala Val Val Tyr Lys Pro Phe Gly Gly Leu
      245      250      255
Val Ala Gly Pro Met His Gln Glu Lys Gly Leu Leu Ile Ala Glu Leu
      260      265      270
Asp Val Ala Val Gln Val Ser Arg Arg Lys Phe Asp Ala Thr Gly
      275      280      285
His Tyr Ala Arg Pro Asp Val Phe Gln Leu His Val Asn Arg Ser Ala
      290      295      300
Met Arg Pro Val Glu Phe Thr Asn
305      310

```

<210> 377

<211> 1050

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 377

```

atgtccagca ccacccatcc ccgcctgcgc gtgcgcgcgc tgcaagccgc ccccgctcttc      60
ctcgacctcg acggcaccat cgacaagacc atcgacctga tggcccgggc ggccggccag      120
ggcgtgcagc tgatcgccct tcccgagacc tgggtgcccg gctatccgtg gtggatctgg      180
ctcgattcgc cggcctgggg catgcagttc gtgcagcgct accacgacaa cgccctgggtc      240
gtcggctcgc ccgagttcga ccgcattcgc gaggccgcgc gcaagcaccg catctgggtc      300
tcgctcggct acagcgagaa ggccgcgggc agcctctaca tcgcccaggc gctgatcgac      360
gaccagggca acacgtgca gactcggcgc aagctcaagc cgacgcacgt ggagcgacc      420
gtgttcggcg agggcgacgg atcggacctg agcgtggtcg agacggctat cggcaacatc      480
ggctcgctgt cgtgctggga gcacctgcag ccgctcagca agtacgcgat gtactcgag      540
aacgagcaga tccattgcgg cgcctggccc agcttctcgc tctaccgcgg cggcgctac      600
gcgctcggcg ccgaagtga caacgccgcc agccagggtg acgcggccga gggccagtgc      660
ttcgtgatcg cgccctgcgc caccgtctcg aaggcgatgc acgaactgct gtgcaccgac      720
cctggcaagc agcagatgct gctggctcggc ggccgcttcg cgcgcattcta cggacccgac      780
ggatcgccgc tcggcaagaa cctggcagag gacgaggaag ggctggtggt ggccgacatc      840
gacctcggca tgatctccct ggccaaggcg gcggcgaccc cggccggcca ctattcgcg      900
cccgacgtga cgcagttgct gttcaacagg aagcggcgcg agccggtggt gctgcaaggc      960
ccggccgagc ccgagaaggc ggtcgccgag ccggtgtcca cgccgagcga agcggcggcg      1020

```

gccgccgccc gccagccggt cgtggcctga

1050

<210> 378

<211> 349

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 378

```

Met Ser Ser Thr Thr His Pro Arg Leu Arg Val Ala Ala Val Gln Ala
 1          5          10          15
Ala Pro Val Phe Leu Asp Leu Asp Gly Thr Ile Asp Lys Thr Ile Asp
 20          25          30
Leu Met Ala Arg Ala Ala Gly Gln Gly Val Gln Leu Ile Ala Phe Pro
 35          40          45
Glu Thr Trp Val Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ser Pro
 50          55          60
Ala Trp Gly Met Gln Phe Val Gln Arg Tyr His Asp Asn Ala Leu Val
 65          70          75          80
Val Gly Ser Pro Glu Phe Asp Arg Ile Arg Glu Ala Ala Arg Lys His
 85          90          95
Arg Ile Trp Val Ser Leu Gly Tyr Ser Glu Lys Ala Ala Gly Ser Leu
100          105          110
Tyr Ile Ala Gln Ala Leu Ile Asp Asp Gln Gly Asn Thr Leu Gln Thr
115          120          125
Arg Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu
130          135          140
Gly Asp Gly Ser Asp Leu Ser Val Val Glu Thr Ala Ile Gly Asn Ile
145          150          155          160
Gly Ser Leu Ser Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala
165          170          175          180
Met Tyr Ser Gln Asn Glu Gln Ile His Cys Gly Ala Trp Pro Ser Phe
180          185          190
Ser Leu Tyr Arg Gly Gly Ala Tyr Ala Leu Gly Ala Glu Val Asn Asn
195          200          205
Ala Ala Ser Gln Val Tyr Ala Ala Glu Gly Gln Cys Phe Val Ile Ala
210          215          220
Pro Cys Ala Thr Val Ser Lys Ala Met His Glu Leu Leu Cys Thr Asp
225          230          235          240
Pro Gly Lys Gln Gln Met Leu Leu Val Gly Gly Gly Phe Ala Arg Ile
245          250          255
Tyr Gly Pro Asp Gly Ser Pro Leu Gly Lys Asn Leu Ala Glu Asp Glu
260          265          270
Glu Gly Leu Val Val Ala Asp Ile Asp Leu Gly Met Ile Ser Leu Ala
275          280          285
Lys Ala Ala Gly Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr
290          295          300
Gln Leu Leu Phe Asn Arg Lys Arg Arg Glu Pro Val Val Leu Gln Gly
305          310          315          320
Pro Ala Glu Pro Glu Lys Ala Val Ala Glu Pro Val Ser Thr Pro Ser
325          330          335
Glu Ala Ala Ala Ala Ala Ala Arg Gln Pro Val Val Ala
340          345

```

<210> 379

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 379

```

atggcctaaaa tagcgattgt acaaaaggcg tctgttacct tgaataaaca agaaactgtc      60
gccagtgcctg taagagagggt agagctggca gcggcggaag gtgccgagct ggtagtggtt      120
actgaggcat ttattgctgg gtatccggcc tggatctggc gtttgcgcc aggtgggtgac      180
tgggggctat ctgaagatct tcattcccggt ttgttgacaa gcgccgtaga cctgggtggt      240
gatgacctgg atccacttta tgccgcagct aaagaaaata acgtgacgat agtgtgcggt      300
attaatgaac gtgataaccg gctcagtaag gcaacgctat ataattctat cgttattatt      360
ggttccgatg gttcattggt aaatcgacat cgtaagttga tgccgacgaa tccggagaga      420
atgggtatggg gcttttggtga tgccctctgggt ctgaagggtcg ttgatacccc cgttgggtcgt      480
gttggtacgc ttgtctgttg ggaaaactat atgcccttgg ccagatatgc gttgtattcg      540
cagggggtag aggtttatat tgccgcgacc tacgatagcg gtgatgactg gattttctaca      600
ttacagcata ttgccaggga gggctcgttgt tgggttgttg gctgtggcaa tctattgcgt      660
ggcagcgata taccgatga cttccctgag aagttggcgt tatacccaga tgaggatgag      720
tggtataaatc ctggggattc cgttgtgatt gcacctgggg gtaaaatcat ggccgggcca      780
ttgcgccagg aggcggggat tgtctattgt gatattgcgt ctgaaagtgc cagtcaggca      840
aaacgtgcgc tggatgtggc tggacattat tcccgccctg atatctttga gttgcatgtg      900
aatacgaagg tgcagacccc ggttggtatat gattag                                936

```

<210> 380

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 380

```

Met Ala Lys Ile Ala Ile Val Gln Lys Ala Ser Val Thr Leu Asn Lys
 1          5          10          15
Gln Glu Thr Val Ala Ser Ala Val Arg Glu Val Glu Leu Ala Ala Ala
 20          25          30
Glu Gly Ala Glu Leu Val Val Phe Thr Glu Ala Phe Ile Ala Gly Tyr
 35          40          45
Pro Ala Trp Ile Trp Arg Leu Arg Pro Gly Gly Asp Trp Gly Leu Ser
 50          55          60
Glu Asp Leu His Ser Arg Leu Leu Thr Ser Ala Val Asp Leu Gly Gly
 65          70          75          80
Asp Asp Leu Asp Pro Leu Tyr Ala Ala Ala Lys Glu Asn Asn Val Thr
 85          90          95
Ile Val Cys Gly Ile Asn Glu Arg Asp Asn Arg Leu Ser Lys Ala Thr
100          105          110
Leu Tyr Asn Ser Ile Val Ile Ile Gly Ser Asp Gly Ser Leu Leu Asn
115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
130          135          140
Phe Gly Asp Ala Ser Gly Leu Lys Val Val Asp Thr Pro Val Gly Arg
145          150          155          160
Val Gly Thr Leu Val Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
165          170          175
Ala Leu Tyr Ser Gln Gly Val Glu Val Tyr Ile Ala Pro Thr Tyr Asp
180          185          190
Ser Gly Asp Asp Trp Ile Ser Thr Leu Gln His Ile Ala Arg Glu Gly
195          200          205
Arg Cys Trp Val Val Gly Cys Gly Asn Leu Leu Arg Gly Ser Asp Ile
210          215          220
Pro Asp Asp Phe Pro Glu Lys Leu Ala Leu Tyr Pro Asp Glu Asp Glu
225          230          235          240
Trp Ile Asn Pro Gly Asp Ser Val Val Ile Ala Pro Gly Gly Lys Ile

```

245 250 255
 Met Ala Gly Pro Leu Arg Gln Glu Ala Gly Ile Val Tyr Cys Asp Ile
 260 265 270
 Ala Ser Glu Ser Ala Ser Gln Ala Lys Arg Ala Leu Asp Val Ala Gly
 275 280 285
 His Tyr Ser Arg Pro Asp Ile Phe Glu Leu His Val Asn Thr Lys Val
 290 295 300
 Gln Thr Pro Val Val Tyr Asp
 305 310

<210> 381

<211> 945

<212> DNA

<213> *Clostridium acetobutylicum* ATCC 3625

<400> 381

atggggaat	tcggtgaagt	taccctgggc	gtgggtcagg	ctgctcccg	gtactttgac	60
cgcgaggcct	cgaccgagaa	agcctgtggc	ctgatccgcg	aggcgggcga	aaagggtgta	120
gatcttcttg	cgttcgggtga	aacgtgggta	accggctatc	catactggaa	agatgcgcct	180
tggtctcgcg	aatacaacga	cttgcggtgca	cgttatgttg	cgaacgggtg	gatgattcct	240
ggtcgggaaa	cggacgctct	gtgccaagca	gccgcggaag	caggtgtgga	tgtggcgatc	300
ggagtagtag	aactggagcc	gggctctctt	tcctcggttt	attgcactct	gttatttata	360
agccgcgagg	gcgagatcct	gggtcgtcac	cgaaaactga	aaccgaccga	tagcgaacgt	420
cgttactggg	ctgaaggcga	cgcgactggg	ctgcgcgttt	atgagcgccc	atatggtcgg	480
cttagcgccc	tgaattgctg	ggagcacact	atgatgctgc	cggggtaacg	cctggcggcg	540
cagggcaccc	agttccatgt	ggccgcttgg	ccaaacatgg	catcctcgaa	ttctgaactt	600
ctgtctcggt	cctacgctat	gcaggcgggc	tgctacgttt	tatgcgcggg	tggcctgggc	660
ccggccccag	gtgaactgcc	ggatgggtatc	gcggcggaag	gtttagatca	cttgactgga	720
gagtcattgt	tcattgaccc	gtgggggaaa	gtaattgctg	gtccggtgtc	ttgcgaggaa	780
acccttatca	cggtctcggt	tagcaccgca	tctatttatc	gccgcaaaag	tttgacggac	840
gtgggcgggt	attatagccg	cccgatgttt	ttccgttttg	aagtgcgatc	ctctgagcgt	900
ccccgtgtcg	tggtttcgga	tggtgacgtg	gatgaccgag	gttaa		945

<210> 382

<211> 314

<212> PRT

<213> *Clostridium acetobutylicum* ATCC 3625

<400> 382

Met	Gly	Glu	Phe	Gly	Glu	Val	Thr	Leu	Gly	Val	Ala	Gln	Ala	Ala	Pro
1				5					10					15	
Val	Tyr	Phe	Asp	Arg	Glu	Ala	Ser	Thr	Glu	Lys	Ala	Cys	Gly	Leu	Ile
			20					25					30		
Arg	Glu	Ala	Gly	Glu	Lys	Gly	Val	Asp	Leu	Leu	Ala	Phe	Gly	Glu	Thr
		35					40					45			
Trp	Leu	Thr	Gly	Tyr	Pro	Tyr	Trp	Lys	Asp	Ala	Pro	Trp	Ser	Arg	Glu
	50					55				60					
Tyr	Asn	Asp	Leu	Arg	Ala	Arg	Tyr	Val	Ala	Asn	Gly	Val	Met	Ile	Pro
	65				70					75				80	
Gly	Pro	Glu	Thr	Asp	Ala	Leu	Cys	Gln	Ala	Ala	Ala	Glu	Ala	Gly	Val
				85					90					95	
Asp	Val	Ala	Ile	Gly	Val	Val	Glu	Leu	Glu	Pro	Gly	Ser	Leu	Ser	Ser
		100						105					110		
Val	Tyr	Cys	Thr	Leu	Leu	Phe	Ile	Ser	Arg	Glu	Gly	Glu	Ile	Leu	Gly
		115					120					125			
Arg	His	Arg	Lys	Leu	Lys	Pro	Thr	Asp	Ser	Glu	Arg	Arg	Tyr	Trp	Ser
	130					135					140				
Glu	Gly	Asp	Ala	Thr	Gly	Leu	Arg	Val	Tyr	Glu	Arg	Pro	Tyr	Gly	Arg
	145				150				155					160	
Leu	Ser	Gly	Leu	Asn	Cys	Trp	Glu	His	Thr	Met	Met	Leu	Pro	Gly	Tyr
				165				170						175	

Ala Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp Pro Asn
 180 185 190
 Met Ala Ser Ser Asn Ser Glu Leu Leu Ser Arg Ala Tyr Ala Met Gln
 195 200 205
 Ala Gly Cys Tyr Val Leu Cys Ala Gly Gly Leu Gly Pro Ala Pro Gly
 210 215 220
 Glu Leu Pro Asp Gly Ile Ala Ala Glu Ser Leu Asp His Leu Thr Gly
 225 230 235 240
 Glu Ser Cys Ile Ile Asp Pro Trp Gly Lys Val Ile Ala Gly Pro Val
 245 250 255
 Ser Cys Glu Glu Thr Leu Ile Thr Ala Arg Val Ser Thr Ala Ser Ile
 260 265 270
 Tyr Arg Arg Lys Ser Leu Thr Asp Val Gly Gly His Tyr Ser Arg Pro
 275 280 285
 Asp Val Phe Arg Phe Glu Val Asp Arg Ser Glu Arg Pro Arg Val Val
 290 295 300
 Phe Arg Asp Gly Asp Val Asp Asp Arg Gly
 305 310

<210> 383
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 383
 atgtcggagc ccatgacgaa gtatcgcggc gcggcggtgc aggccgcgcc ggtgttcctc 60
 gatctcgacc gcacagtcga gaaagcgatc ggcctgatcg agcaggcggc caagcaggac 120
 gtgcgcctga tcgcattccc agagacttgg attcccggct atcccttttg gatattggctg 180
 ggcgcgcggc cttggggcat gcgcttcgtc cagcgctatt tcgagaattc gctcgtgcgc 240
 ggcagcaagc agtggcaggc cctggcggat gcggcccgcc gccacggcat gcatgtcgtg 300
 gccggctata gcgagcgcgc gggcggcagc ctctatatgg gccaggcgat cttcggtccc 360
 gatggcgatc tgatgcgcgc gcgccgcaag ctcaagccta cccatgcgga gcgcaccgtg 420
 ttcggcgagg gagacggcag ccatctcgcg gtgcacgata ccgccatcgg gcgcctcggc 480
 gcgctctgtt gctgggagca catccagcca ttgtcgaaat acgccatgta cgccgcccgc 540
 gaacagggtcc acgtgcgcgc gtggccgagc ttcagcctct atcgcgcat ggcctatgcg 600
 ctcggaaccgg aggtcaatac cgccgcaagc cagatctacg cggtcgaggg cggctgctac 660
 gtgctggcgt cgtgcgcgac cgtttcgccg gagatgatca aggtatttgt ggatacgccc 720
 gacaaggaga tgttctctcaa ggccggcggc ggttttgcca tgattttcgg gcccgacggc 780
 cgcgccctgg ccgagccgct cccggagacc gaagagggac tgctggtcgc cgatatcgac 840
 ctcggcgatga tcgcgttggc caaggcggcg gccgatccgg cggggcacta ttcacggccc 900
 gacgtaacgc ggctgctgct ggatcgacgt ccggcccaac gcgtcgtcac gcttgatgcc 960
 gcattcgaac cgcaaacga ggacaaggcg gacgcgcccg cgctgcgcgt ggtggcgga 1020
 agcgccgccg ccgcgcagta g 1041

<210> 384
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 384
 Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu
 20 25 30
 Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu

35	40	45
Thr Trp Ile Pro Gly Tyr	Pro Phe Trp Ile Trp	Leu Gly Ala Pro Ala
50	55	60
Trp Gly Met Arg Phe Val	Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg	
65	70	75
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly		80
	85	90
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr		95
	100	105
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg		110
	115	120
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly		125
	130	135
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly		140
	145	150
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met		155
	160	165
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser		170
	175	180
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala		185
	190	195
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser		200
	205	210
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro		215
	220	225
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe		230
	235	240
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu		245
	250	255
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys		260
	265	270
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg		275
	280	285
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala		290
	295	300
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg		305
	310	315
Val Val Ala Glu Ser Ala Ala Ala Ala Gln		320
	325	330
	335	340
	345	

<210> 385

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 385

atgaaagaag	ctatcaaggt	cgcttgcgtg	caagccgccc	cgatctacat	ggatttgaag	60
gcgacggtgg	acaaaacccat	tgagttgatg	gaagaagcag	cacgtaataa	tgctcgtctg	120
atcgcctttc	cgaaacttg	gattccaggc	tacccatggt	ttctttggct	tgactcacca	180
gcatgggcaa	tgcaatttgt	acgccaatac	catgagaact	cattggagtt	ggatggccct	240
caagctaagc	gcatttcaga	tgagccaag	cggttgggaa	tcatgggtcac	cctgggggatg	300
agtgaacggg	tcggtggcac	cctttacatc	agtcagtggg	tcataggcga	taatgggtgac	360
accattgggg	cccggcgaaa	gttgaaacct	acttttggtg	aacgtacttt	gttcggcgcaa	420
ggggatgggt	catcgctagc	ggttttcgag	acgtctgttg	gaaggctggg	tggccttatgc	480
tggtggggagc	accttcaacc	gctaacaaaa	tacgctttgt	atgcacaaaa	tgaagagatt	540
cattgtgcgg	cttgccgag	ctttagcctt	tatcctaata	cggcgaaagc	cctggggcct	600
gatgtcaatg	tagcggcctc	tcgaatctat	gccgttgaag	ggcaatgctt	cgtactagcg	660
tcgtgtgcgc	tcgtttcaca	atccatgatc	gatatgcttt	gtacagatga	cgaaaagcat	720

```

gcgttgcttc tggctggtgg tggacactca cgtatcatag ggctgatgg tggtgacttg      780
gtcgcgcctc ttgccgaaaa tgaagagggt attctctacg caaaccttga tcctggagta      840
cgcatccttg ctaaaatggc ggcagaccct gctggtcatt attccgtcc cgacattact      900
cgcttgctaa tagatcgag ccctaaatta ccggtagttg aaattgaagg tgatcttcgt      960
ccttacgctt tgggtaaagc gtctgagacg ggtgcgcaac tcgaagaaat ttga      1014

```

<210> 386

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 386

```

Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr
  1           5           10           15
Met Asp Leu Lys Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu
          20           25           30
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
          35           40           45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met
          50           55           60
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro
          65           70           75           80
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val
          85           90           95
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln
          100          105          110
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu
          115          120          125
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
          130          135          140
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys
          145          150          155          160
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln
          165          170          175
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro
          180          185          190
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg
          195          200          205
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
          210          215          220
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His
          225          230          235          240
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp
          245          250          255
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu
          260          265          270
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala
          275          280          285
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile
          290          295          300
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg
          305          310          315          320
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu
          325          330          335
Ile

```